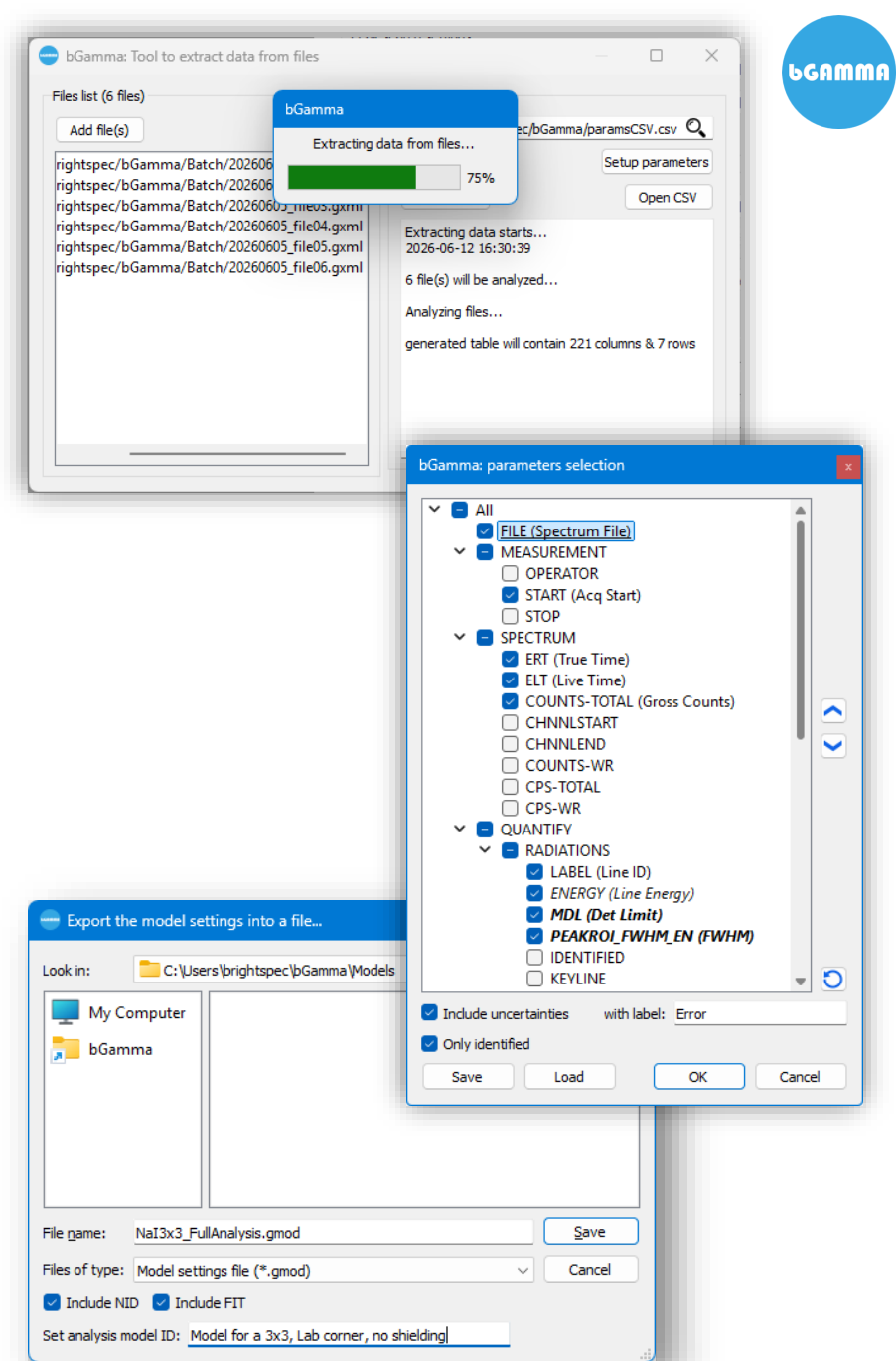


Main highlights

- New file data extraction tool
- New parameters selection tool
- File Batch analysis tool improved
- Analysis model export new options
 - Related updates within batch/procedure analysis
- Further GUI and internal improves
- Revised and updated User's Manual
 - Version 1.7.3, revision 1, July 2026

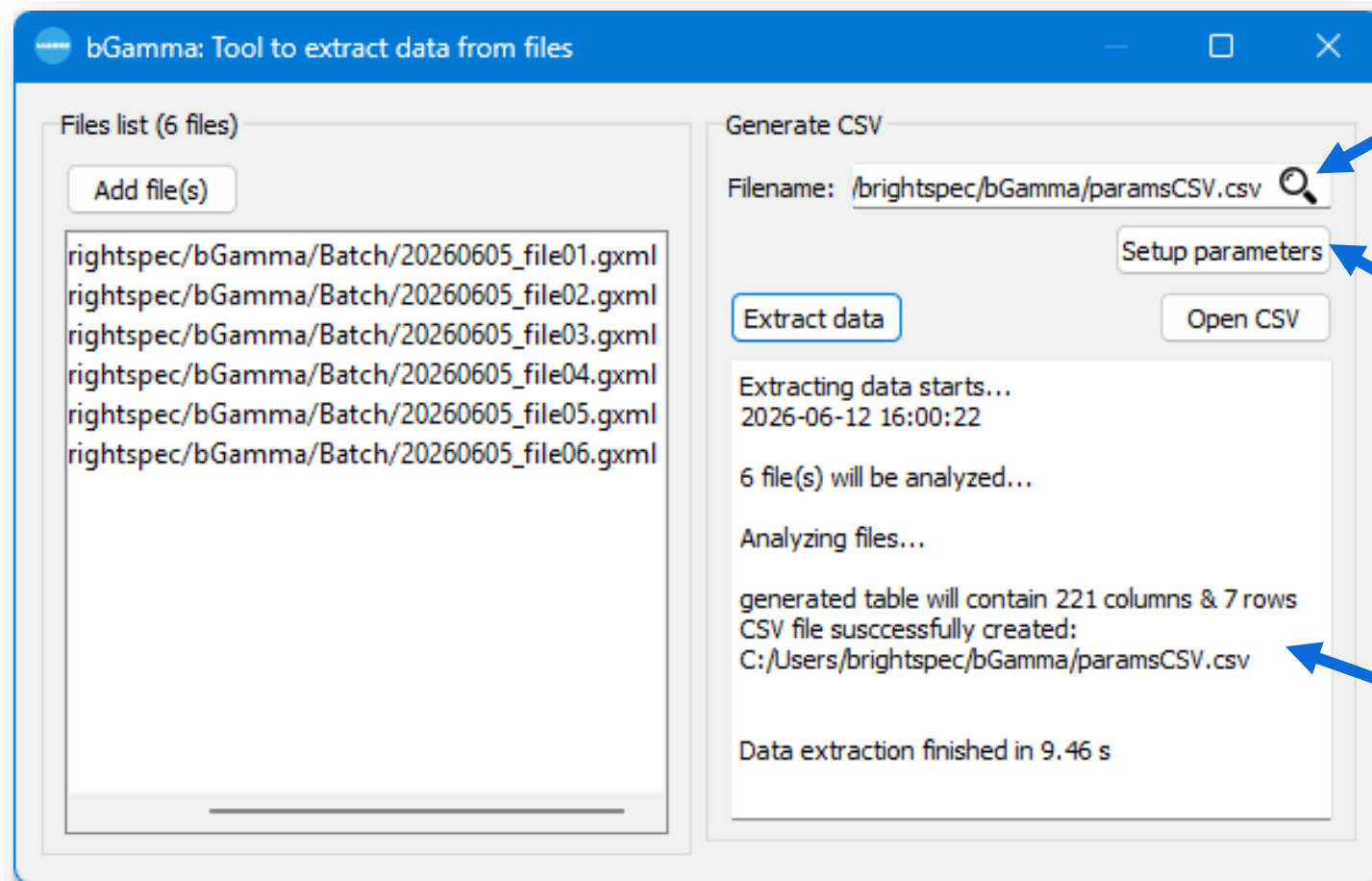


NEW

New tool: Files data extraction

bGamma

This tool allows to extract any existing data from full bGamma file(s) (*.gxml).



Extracted data will be exported into a CSV table formatted file.

Data to extract can be defined using the corresponding tool (check next slide).

Some info will be shown within the log box while executing the data extraction.

Detailed description and use on the bGamma User's Manual, page 198.

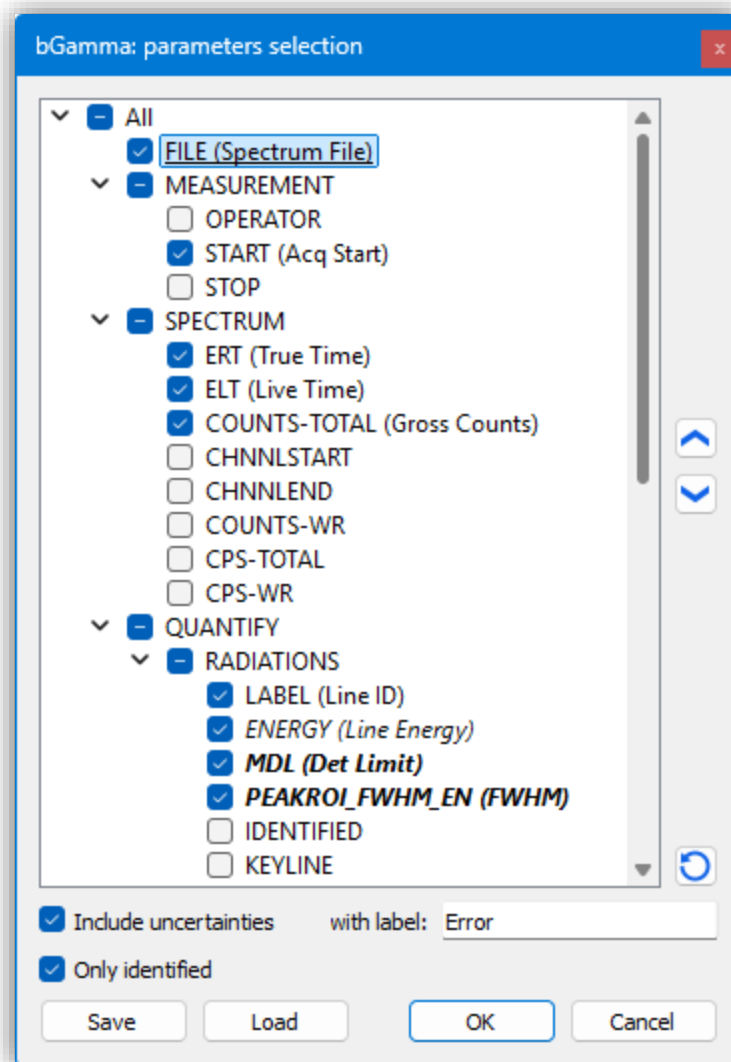
NEW

New tool: Parameters selection

This is a useful tool allows to select parameters and set some extra options for data extraction.

- ✓ Parameters are listed and organized by sections.
- ✓ They can be sorted in the desired order.
- ✓ Their name or label can be customized.
- ✓ Uncertainty values can be included/excluded (if apply), and their labels can be customized too.
- ✓ Option to include only the identified Peaks/ROIs (if they were selected).
- ✓ All selections/customizations can be exported into a dedicated file, which could be imported later for extensive review or analysis.

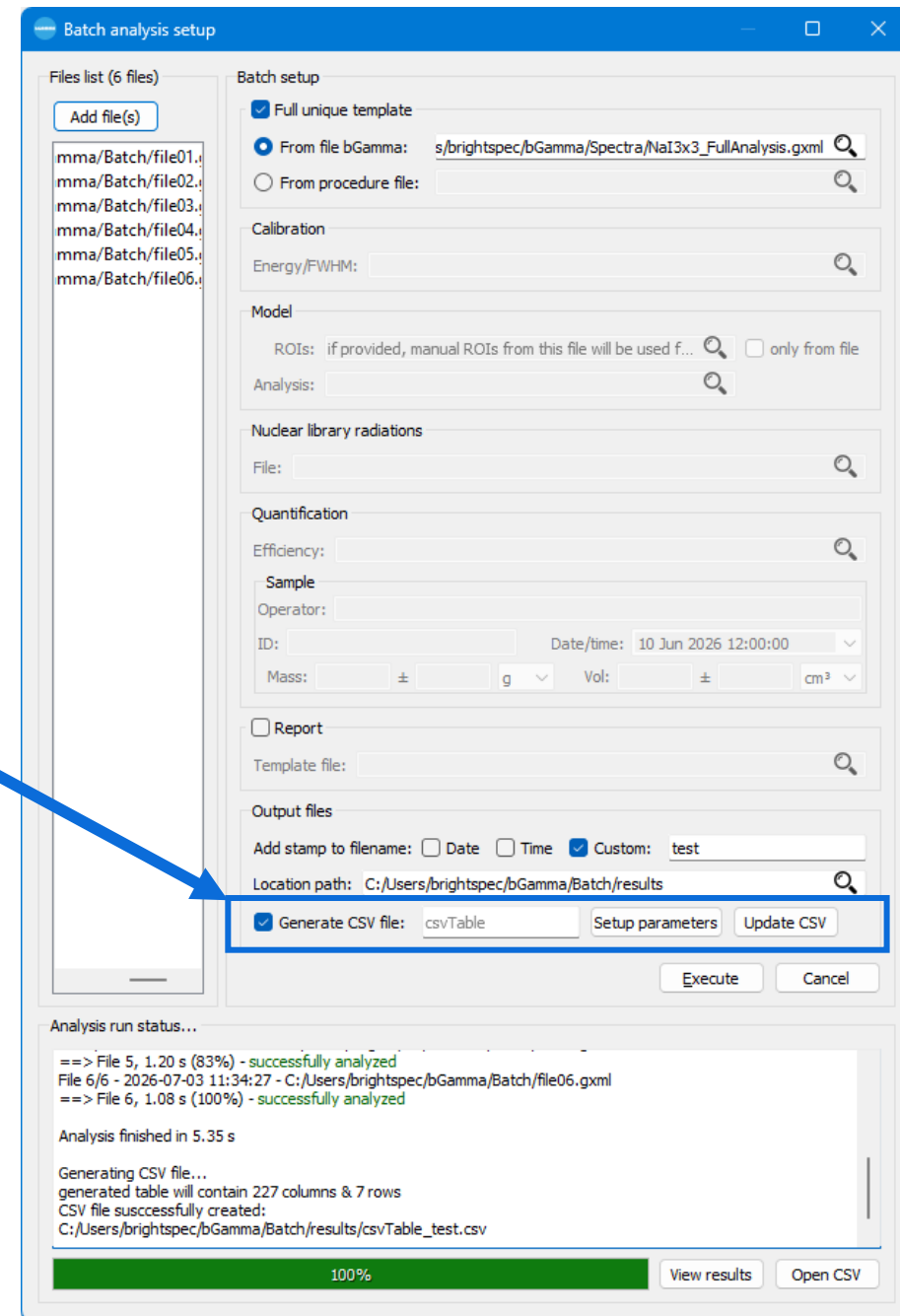
Detailed description and use on the
bGamma User's Manual, page 200.



File Batch analysis update

New option to extract data from analyzed files and export it into a CSV file.

You can setup the exported data using the same parameters selection tool described before.



Batch analysis setup

Files list (6 files)

Add file(s)

mma/Batch/file01.
mma/Batch/file02.
mma/Batch/file03.
mma/Batch/file04.
mma/Batch/file05.
mma/Batch/file06.

Batch setup

☒ Full unique template

☒ From file bGamma: s/brightspec/bGamma/Spectra/NaI3x3_FullAnalysis.gxml

☐ From procedure file:

Calibration

Energy/FWHM:

Model

ROIs: if provided, manual ROIs from this file will be used f... ☐ only from file

Analysis:

Nuclear library radiations

File:

Quantification

Efficiency:

Sample

Operator:

ID: Date/time: 10 Jun 2026 12:00:00

Mass: ± g Vol: ± cm³

☐ Report

Template file:

Output files

Add stamp to filename: ☐ Date ☐ Time ☒ Custom: test

Location path: C:/Users/brightspec/bGamma/Batch/results

☒ Generate CSV file: csvTable Setup parameters Update CSV

Execute Cancel

Analysis run status...

==> File 5, 1.20 s (83%) - successfully analyzed

File 6/6 - 2026-07-03 11:34:27 - C:/Users/brightspec/bGamma/Batch/file06.gxml

==> File 6, 1.08 s (100%) - successfully analyzed

Analysis finished in 5.35 s

Generating CSV file...

generated table will contain 227 columns & 7 rows

CSV file successfully created:

C:/Users/brightspec/bGamma/Batch/results/csvTable_test.csv

100% View results Open CSV

Further details on the bGamma User's Manual, page 214.

Analysis model update

ETH device_SN_12345678

Measurement

Detector: NaI(Tl)

Measurement ID:

Sample ID:

Continuum

Find peaks

NID

Fitting

Quantification

Import Export

Export the model settings into a file...

Look in: C:\Users\brightspec\bGamma\Models

My Computer

bGamma

File name: NaI3x3_FullAnalysis.gmod

Files of type: Model settings file (*.gmod)

☒ Include NID ☒ Include FIT

Set analysis model ID: Model for a 3x3, Lab corner, no shielding

Save Cancel

When exporting the analysis model into a dedicated file (*.gmod), there are now two options to include or not the nuclide identification (NID) and/or the peaks fitting (FIT) steps when running the analysis.

These options will only apply when using the exported file within a Procedure or File Batch analysis execution.

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