SeGaSA

User manual (updated for version 1.0a)

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Preface

SeGaSA (Sequential Gamma Spectra Analysis) is a software complementing the Windows application DPPMCA from Amptek used for radiation spectra acquisition and analysis. SeGaSA analyzes sets of .mca output files and provides the user with results, which display the time dependence of basic spectrometric parameters of a CdTe semiconductor detector. This document contains instructions on how to run the application and instructions on how to interact with the software to achieve the desired outcome.

The software is intended to be used by academic professionals, some experience in gamma spectra analysis is required to successfully interpret the results.

Both the software and this manual are a part of bachelor's thesis *Software design for automation of the spectra processing for a semiconductor detector with polarization effect* written by Filip Frank and supervised by Ing. Katarína Sedlačková, PhD. at the Slovak University of Technology in Bratislava.

The software source code is fully open to modifications, and it is compliant to GNU GPL v3.

Link to the codebase: https://github.com/FilipFr/SeGaSA

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Running the application

Running the application using source code and a pre-installed Python interpreter

We recommend using Python version 3.9. Software requires the following dependencies:

Library name	Version
PyQt5	5.15.4
Matplotlib	3.4.1
SciPy	1.6.3
NumPy	1.20.2

The application should run by running *main.py* included in the root directory of the codebase.

Creating an executable using PyInstaller

This method also requires Python to be installed but does not require additional libraries. This is the preferred method for creating a runnable application from the source code.

1. Check your system for PIP (Pip Installs Packages - Python package installer). If PIP is missing from your system, follow https://pip.pypa.io/en/stable/installing/
2. Execute command `pip install pyinstaller` using cmd.
3. Open new cmd in the root directory of the codebase (contains main.py) and execute command `pyinstaller main.py` using the new cmd.
4. Run *main.exe* created in *main* folder to run the application.

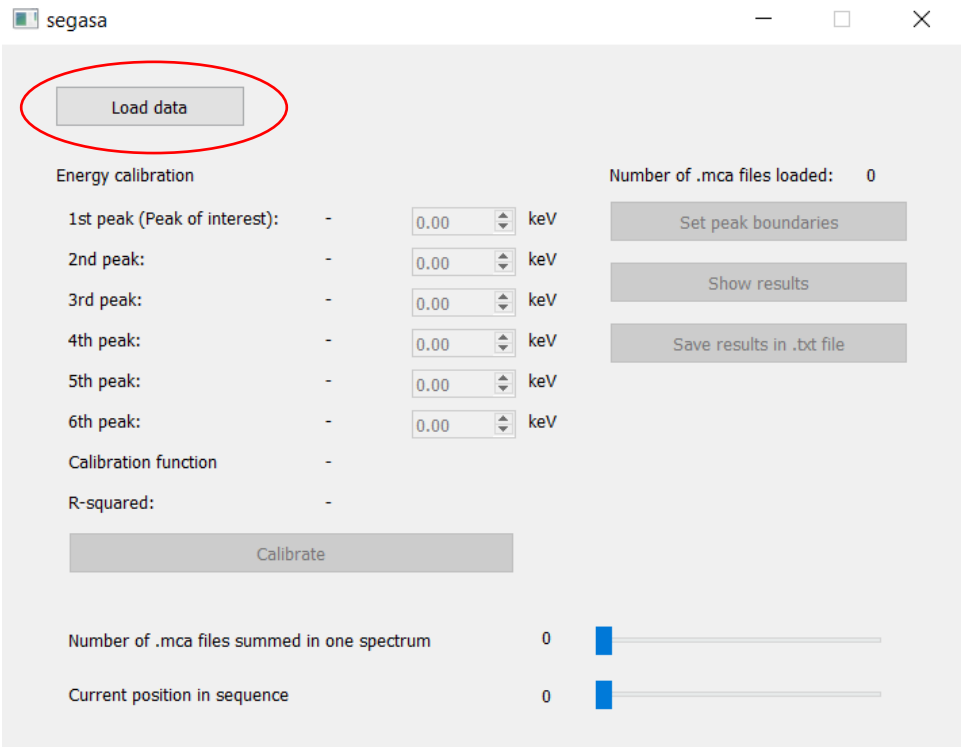
Using Google Drive link to download the application

SeGaSA version 1.0a:
https://drive.google.com/file/d/1XaDNWEAR9vpupCMjxSD7VBni_JutjCBR/view?usp=sharing

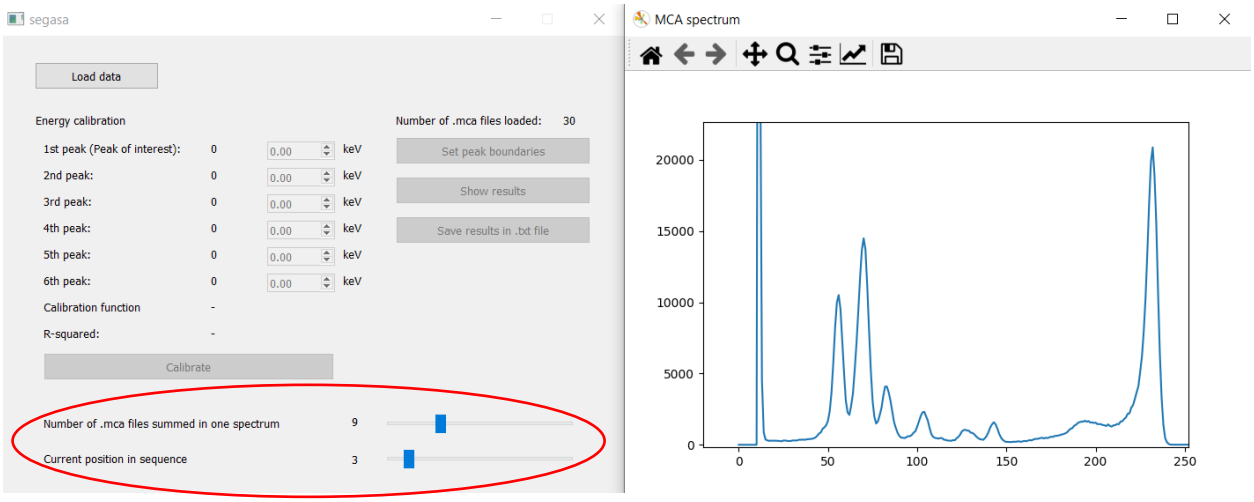
Run *main.exe* in the *main* folder to run the application. Use one of the previous methods if you want to run another version of the application.

How to use the application

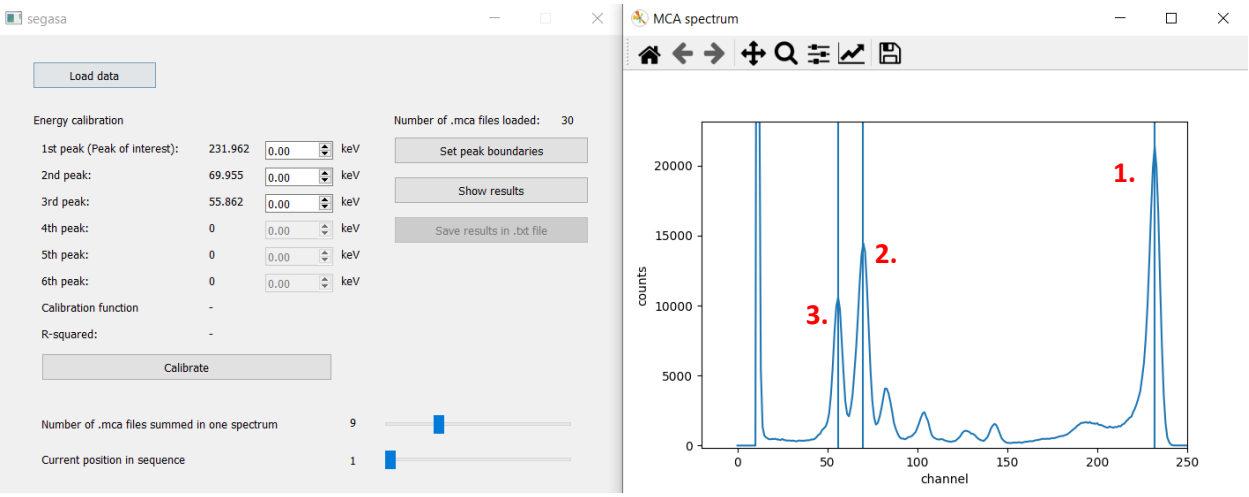
1. Load a folder containing a set of .mca data acquired by the DPPMCA software using the "Load data" button.



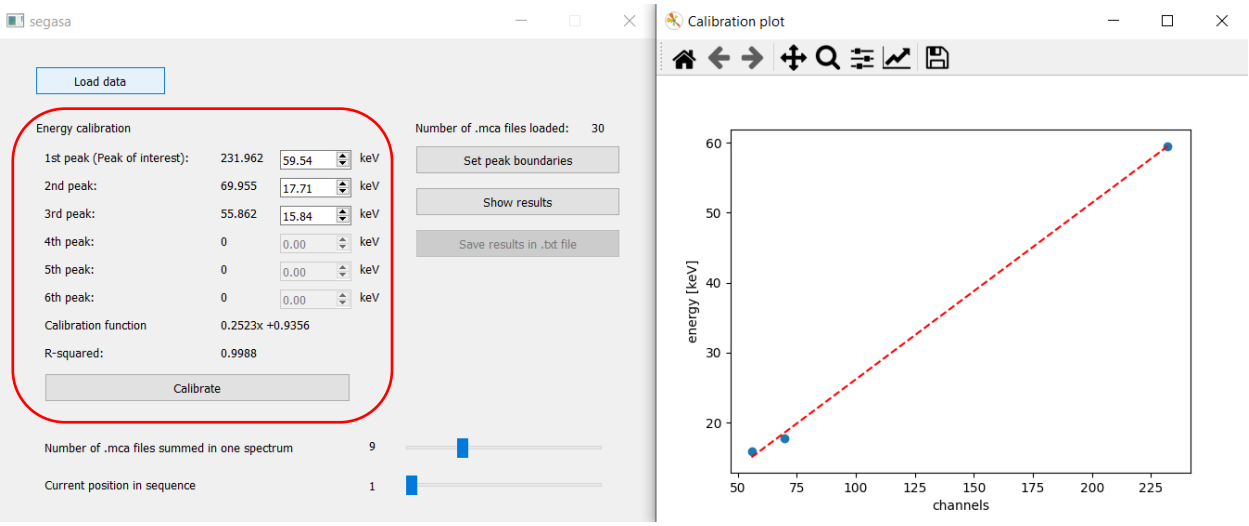
2. Use the sliders to visually analyze any spectrum included in the loaded dataset.
You may create summed spectra (spectra containing summed data of multiple .mca files) by increasing the value of "Number of .mca files summed in one spectrum" slider.



3. Click on a peak in the plot to pick it as a Peak of interest. The selection of five additional peaks may be performed for the purpose of energy calibration. Use sliders to reset your selection. To perform peak selection current position in sequence must be set to 1.

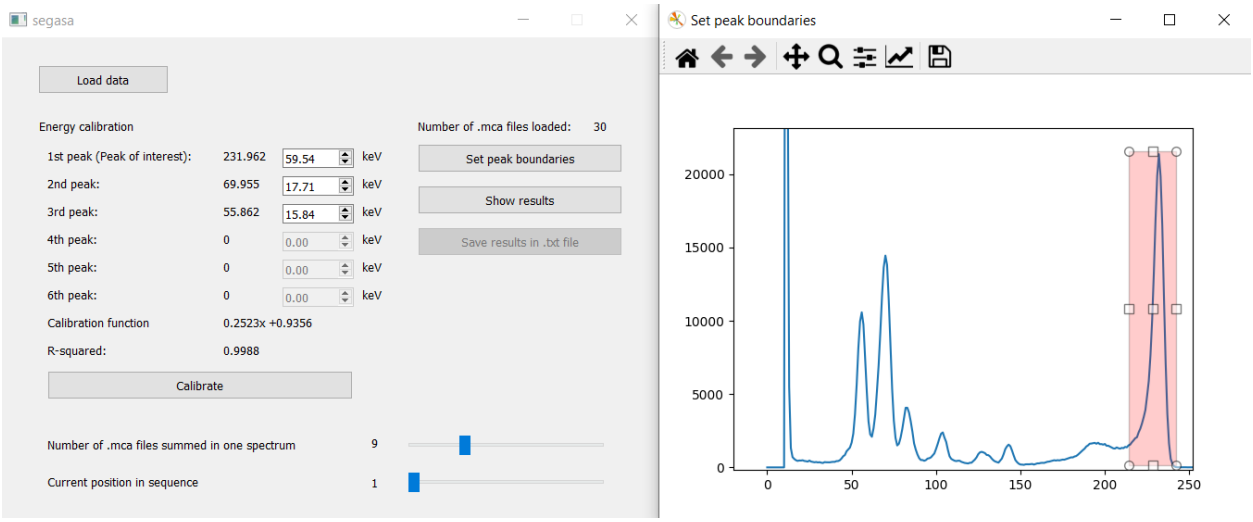


4. **This step is optional and does not have to be performed to obtain the output data.** Energy calibration can be performed by specifying known energies of the selected peaks and clicking "Calibrate". The software allows for calibration quality assessment by displaying the calibration plot, calibration function coefficients and r-squared value. Using the sliders after this step will revert the calibration.

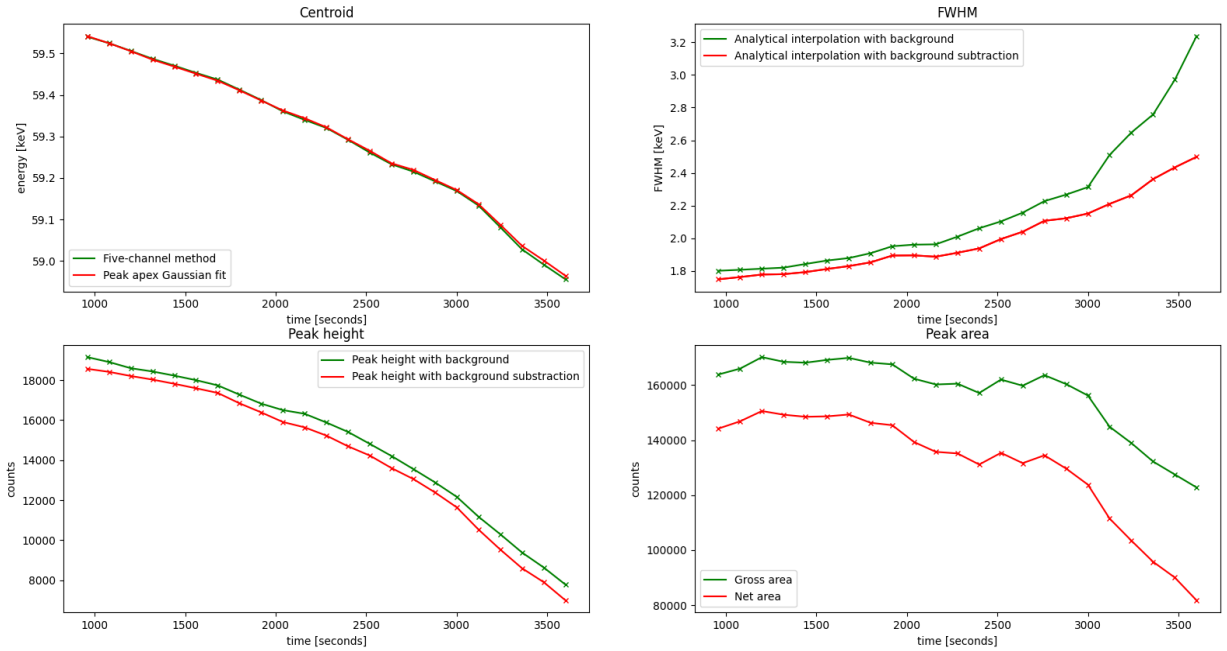


5. **This step is optional and does not have to be performed to obtain the output data. It is, however, required if the user wishes to analyze the peak area. The analysis of peak height and fwhm with background subtraction is also possible only if this step has been executed.**
Peak boundaries (start and end) can be specified after clicking on the "Set peak boundaries" button. Only the boundaries of the selected Peak of interest can be specified.

The application displays a plot for each spectrum of the currently analyzed sequence (displayed spectrum is a product of summation if the value of "Number of .mca files summed in one spectrum" is higher than 1). The boundaries are specified by rectangle selection using a mouse (click, hold and drag to draw a rectangle) on the plot. The boundaries selection for a single displayed spectrum needs to be confirmed by pressing any key on the keyboard (using the key Q is recommended to avoid unwanted interactions). The plot is then closed and the following spectrum of the sequence is displayed. This process repeats for the whole sequence. Once the process is started, it should be fully completed to avoid unwanted behavior. Do not interact with the rest of the application during this process, it will probably cause the application to crash (this is subject to change in later versions of the software).



6. Clicking on the button "Show results" will display the time dependency plots of the analyzed parameters for the currently analyzed sequence. It will also disable interaction with the application except for data export and loading. The following picture contains all time dependency plots the software is currently able to produce.



7. Clicking on "Save results in .txt file" is available only after the results were displayed. It prompts the user to specify a file path for the export file. Created .txt file contains calibration (equation, r-squared) and result data (centroids, fwhms, peak heights, possibly peak areas). It also contains information about the acquisition time of each (possibly summed) spectrum, number of summed .mca files in one spectrum and the number of .mca files loaded.

Parsing the output file

The specific form of the output file is subject to change in the later versions of the software, but it's base structure should remain consistent. The file consists of:

1. a header
2. a specification
3. a matrix of values

These sections are separated by an additional newline character (can be separated using `"\n\n"`)

Header

The header contains one-line statements with descriptive strings followed by values. Statements are separated by a newline character. Currently the statements are[1]:

```
"Number of loaded files: " + str(value) + "\n"
"Calibration plot equation: " + str(tangent) + "x + " + str (offset)+ "z\n"
"Number of files summed in one spectrum: " + str(value)
```

Specification

The specification section is used to describe the result parameters represented by the columns of the matrix. One line contains a column number, a label of the parameter and its unit in brackets, for example:

```
3. Centroid - Five-channel method [keV]
```

According to this statement, the third column of the matrix contains values of centroids determined by the five-channel method. The values are in keV.

Matrix of values

The matrix contains results of the analysis. A row represents a spectrum, a column represents a parameter described in the specification. Values in different columns are separated by the

[1] the z in "z\n" in the "Calibration..." line of the header is a known mistake and it will be fixed in later versions.

character for tabulator. A column full of zeros means that the requirements for the analysis of the corresponding parameter were not met.

Example of an output file

```
Number of loaded files: 60
Calibration plot equation: 0.24446942351158757x + 2.641969188160461z
Number of files summed in one spectrum: 47

Columns should be interpreted as follows:
1. Position in sequence
2. Time of acquisition [seconds]
3. Centroid - Five-channel method [keV]
4. Centroid - Gaussian fit [keV]
5. FWHM - analytic interpolation with background [keV]
6. FWHM - analytic interpolation without background [keV]
7. Peak height with background [counts]
8. Peak height without background [counts]
9. Gross area [counts]
10. Net area [counts]

1       5640    59.261524864826214      59.264994458809966      2.0244489761345394      0       84832   0       0       0
2       5760    59.25357562087775       59.257219797530944      2.028141535222272       0       83446   0       0       0
3       5880    59.24613977017342       59.24893189745905       2.0385711532664685      0       81939   0       0       0
4       6000    59.23830955689919       59.240637076641995      2.0535301653000224      0       80228   0       0       0
5       6120    59.228323830392156      59.231022231893945      2.070461728533383       0       78365   0       0       0
6       6240    59.2207189090683        59.22264730499061       2.0888859819673846      0       76388   0       0       0
7       6360    59.212035304467065      59.21427996383205       2.109780702097974       0       74316   0       0       0
8       6480    59.20203344986077       59.20433384645345       2.1337469029019265      0       72178   0       0       0
9       6600    59.18942934482423       59.191961291918155      2.1514247340722004      0       70206   0       0       0
10      6720    59.17908764894179       59.181541458752584      2.171659099563153       0       68187   0       0       0
11      6840    59.16820747527181       59.170761421567406      2.193665871126834       0       66120   0       0       0
12      6960    59.15795044368187       59.16066337633374       2.2281403339218677      0       63909   0       0       0
13      7080    59.14834458580518       59.15140756190067       2.258331190147253       0       61744   0       0       0
14      7200    59.13715272889736       59.139872696762914      2.289087961619575       0       59631   0       0       0
```