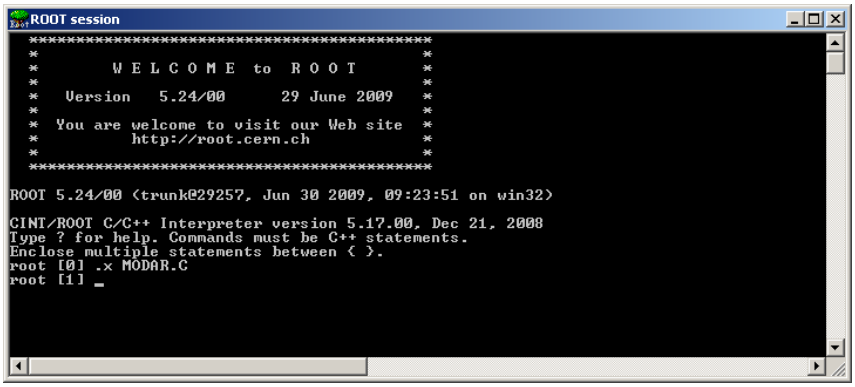
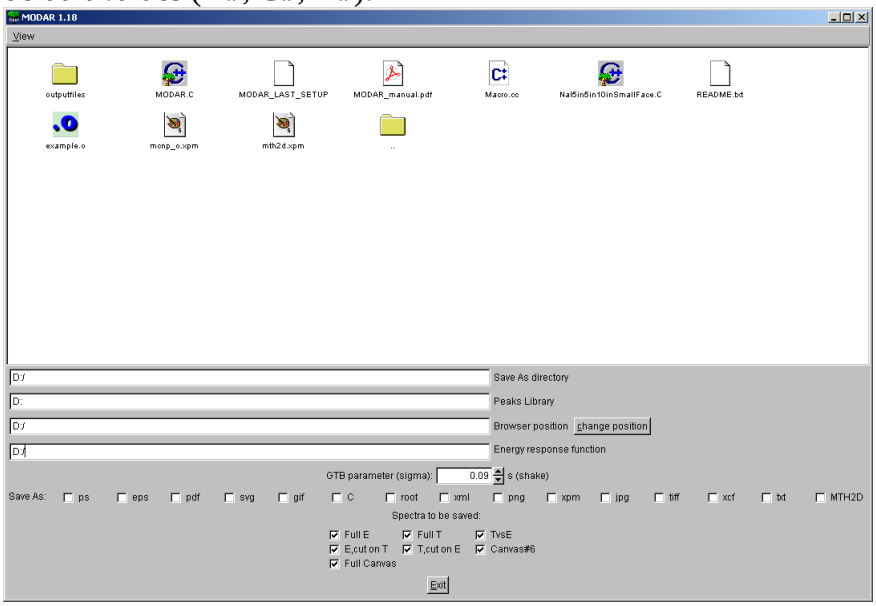
Starting with MODAR

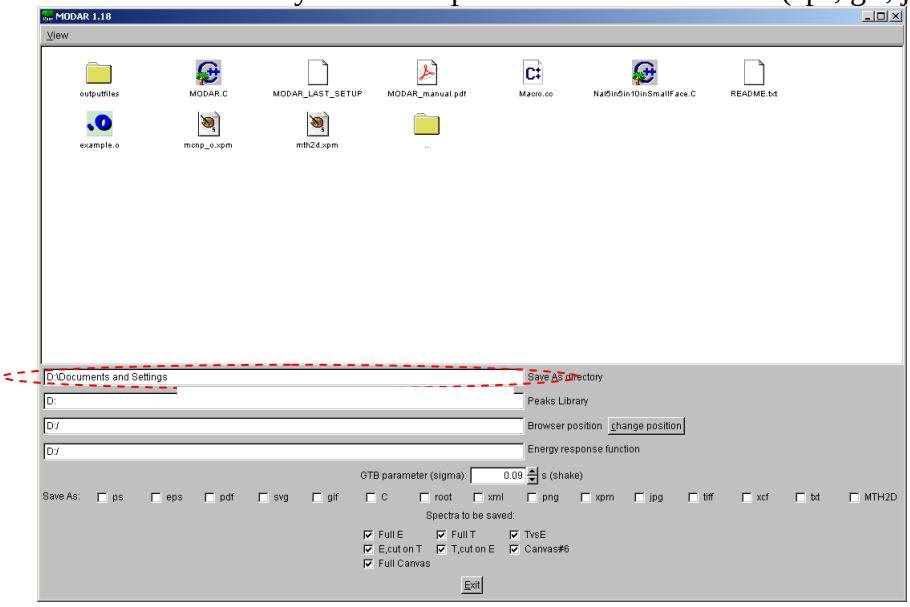
- Call MODAR from ROOT.



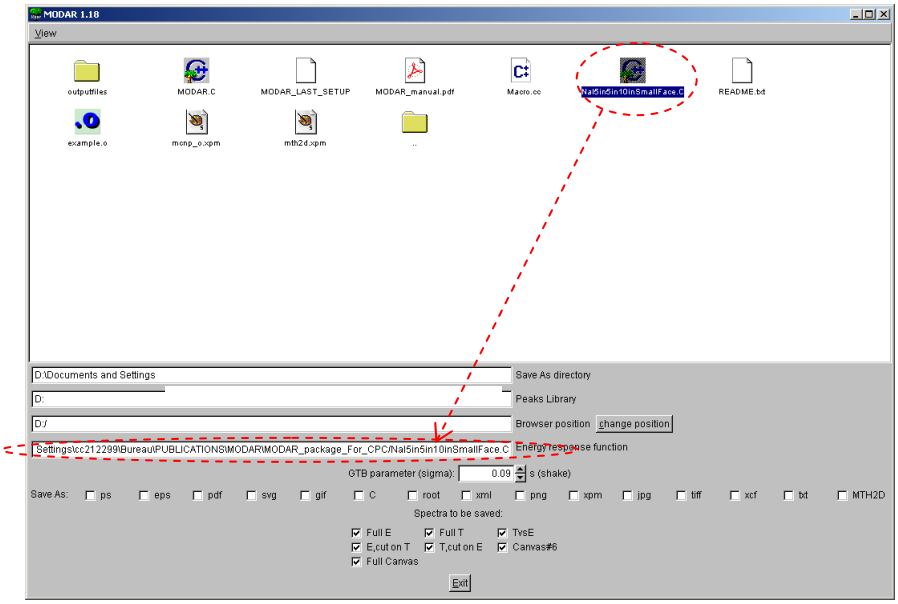
- The main window appears. The first time MODAR is called, the text entries are set to the default values (D:/, C:/, D:/).



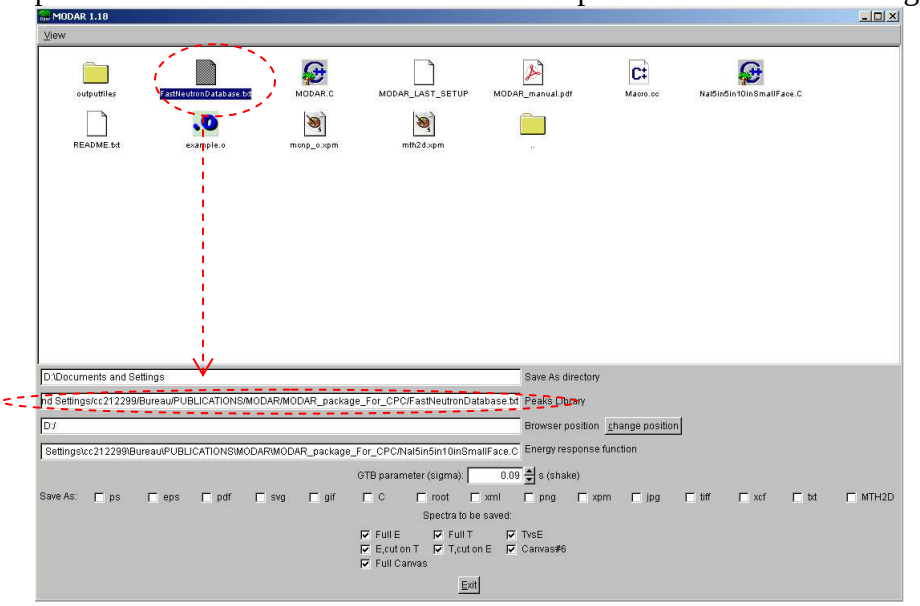
- Enter the directory where the pictures have to be saved (eps, gif, jpeg,…):



● Enter the full path for the detector energy response function. Instead of writing the full path by hand, it is possible to double click on the icon that represents the detector energy response function.



● Enter the full path for the peaks database. Instead of writing the full path by hand, it is possible to double click on the icon that represents the detector energy response function.



Peaks database files are txt files. To be correctly identied by MODAR, the file must starts with the string *//MODAR_PEAKS_DATABASE* (first line of the file).
Then, the file should be built with the following structure:

Name of reaction #1
Energy of Peak #1 Cross section
Energy of Peak #2 Cross section
Energy of Peak #3 Cross section
…
Energy of Peak #N_1 Cross section
Name of reaction #2
Energy of Peak #1 Cross section
…
Energy of Peak #N_2 Cross section
…
Name of reaction #k
Energy of Peak #1 Cross section
…
Energy of Peak #N_k Cross section
…

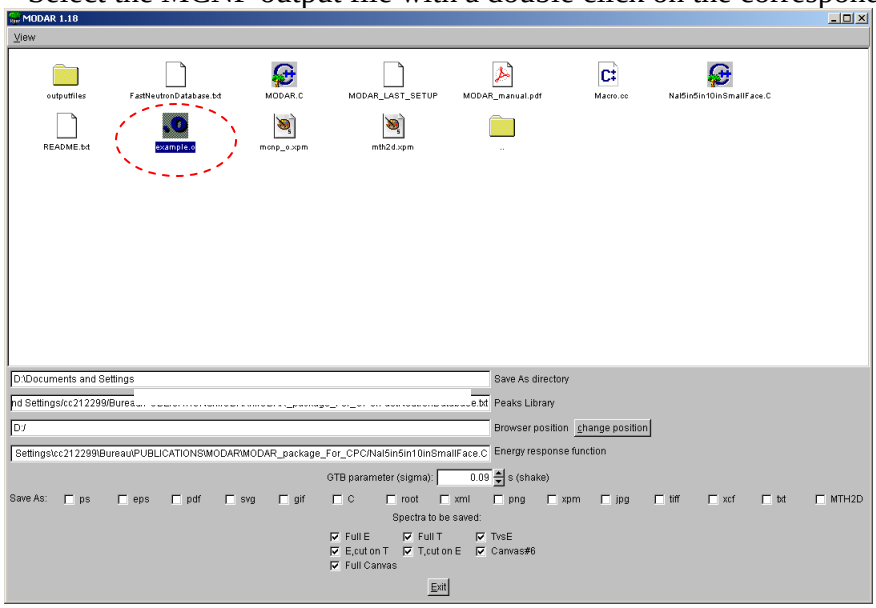
Such a file will serve to identify gamma rays peaks in the energy spectra, corresponding to reactions the user is interested in.

For example, if one is interested by gamma rays produced by 14 MeV neutrons, such a file could look like:

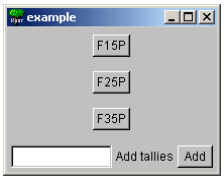
```
//MODAR_PEAKS_DATABASE
C 14MeV n
4.439 187
O 14MeV n
2.742 38
3.089 22
3.684 58
3.854 34
4.439 17
6.130 330
6.917 47
7.117 53
N 14MeV n
0.727 22
1.632 21
2.125 26
2.313 42
3.684 30
4.442 54
5.106 45
6.743 13
7.029 32
Si 14MeV n
0.390 25
0.585 41
0.844 10
0.941 13
0.975 41
0.983 25
1.014 22
1.589 24
1.779 1264
2.839 59
5.100 37
6.879 36
```

MCNP output file analysis

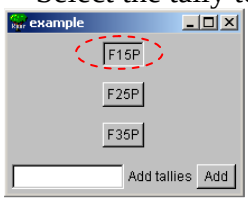
- Select the MCNP output file with a double click on the corresponding icon.



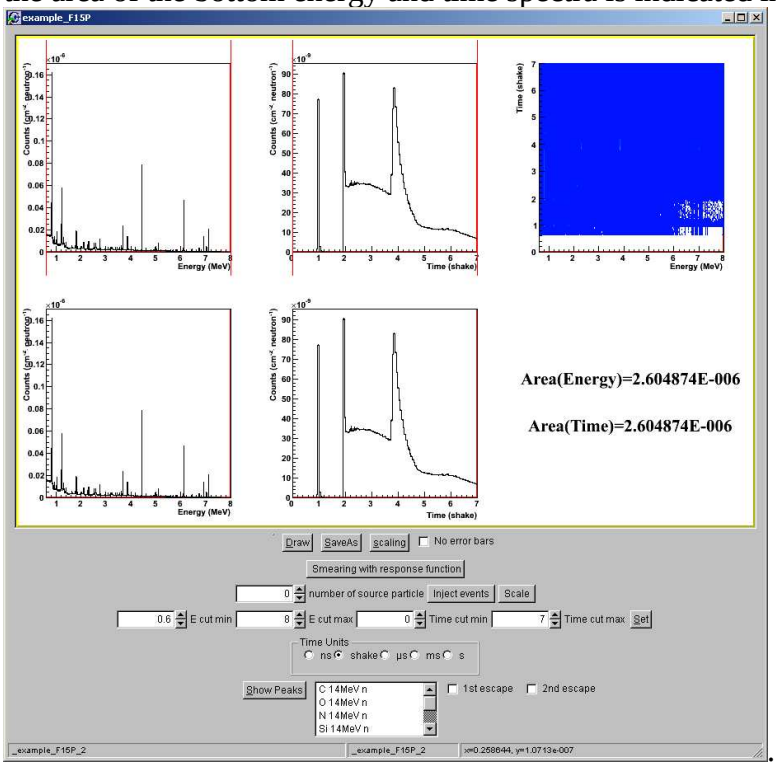
→A small window appears with as many buttons as tallies have identified.



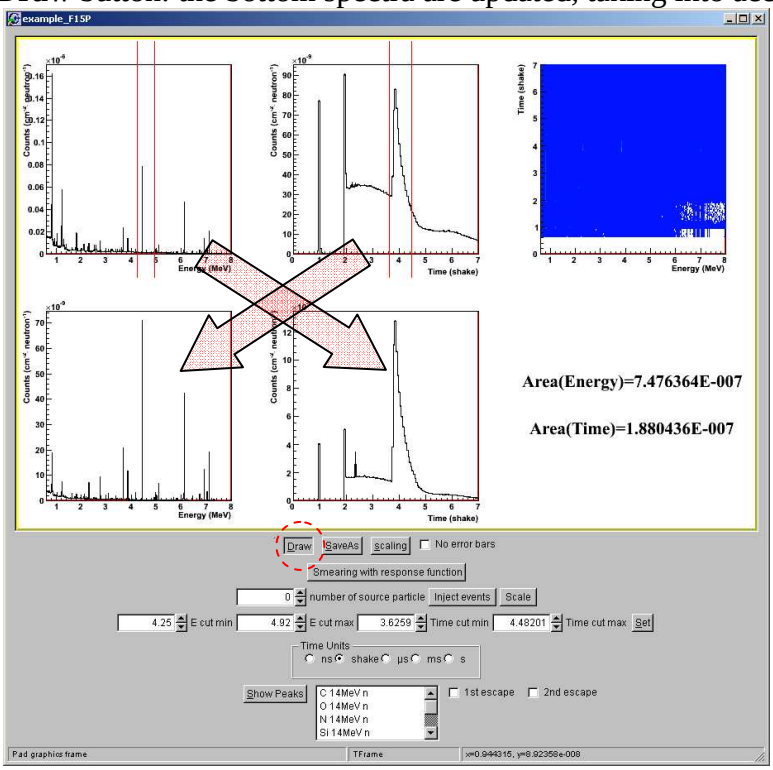
- Select the tally to be visualized.



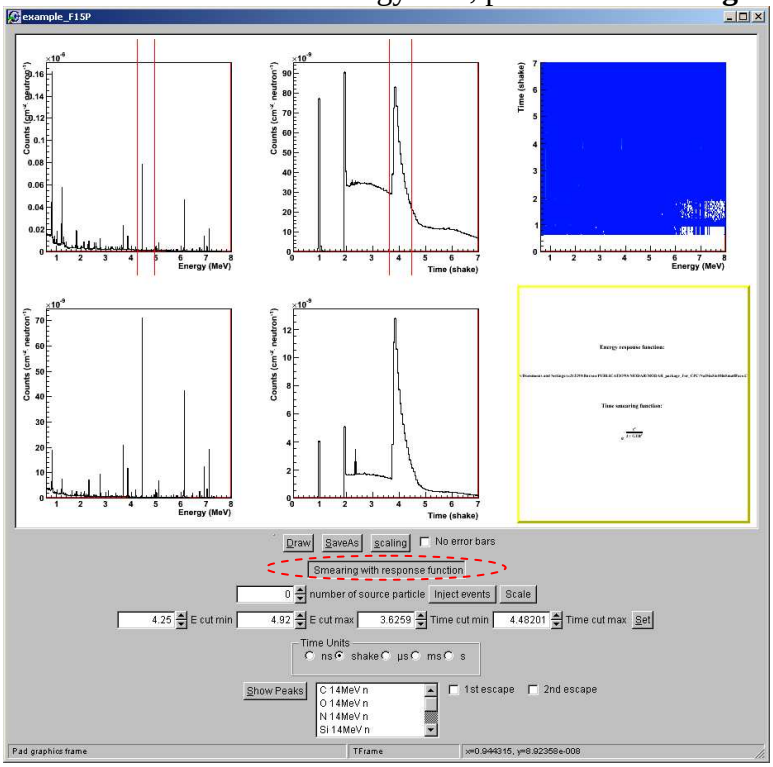
→A canvas appears with the energy and time spectra related to the selected tally. Note that the area of the bottom energy and time spectra is indicated in the bottom right sub-canvas.



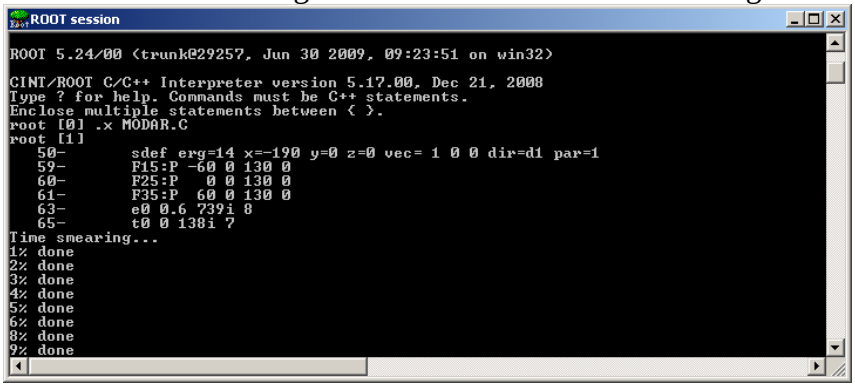
● Move the vertical red lines to select the energy and time windows of interest. Press the **Draw** button: the bottom spectra are updated, taking into account the energy and time cut.



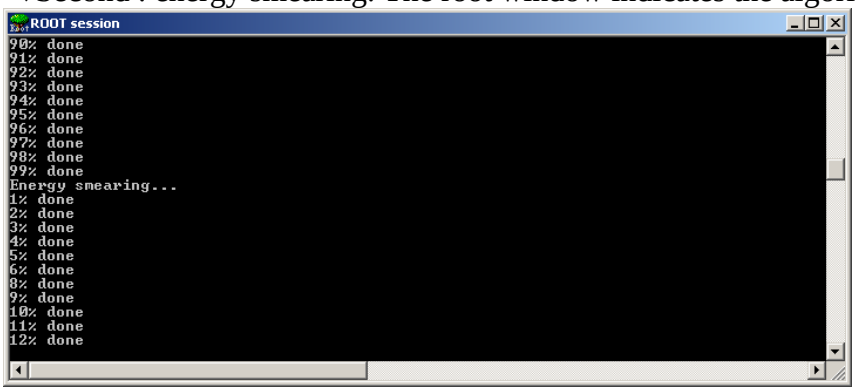
● To smear the time and energy data, press the **Smearing with response function** button.



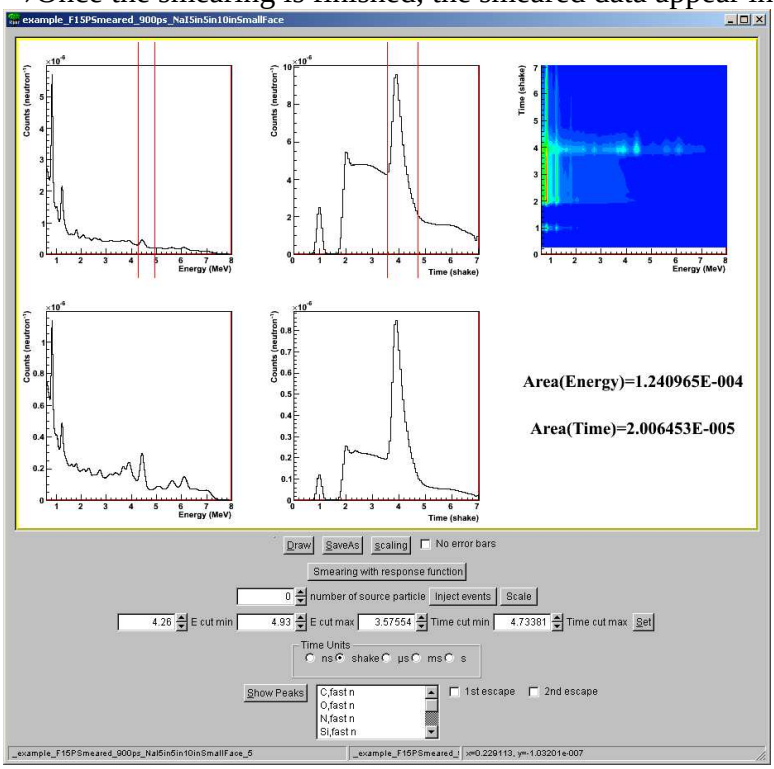
→ First : time smearing. The root window indicates the algorithm progress.



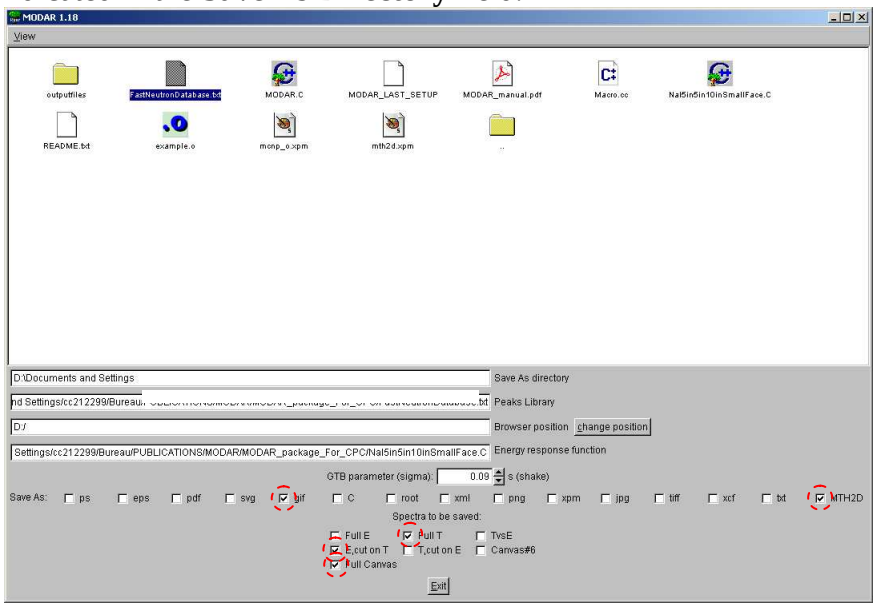
→Second : energy smearing. The root window indicates the algorithm progress.



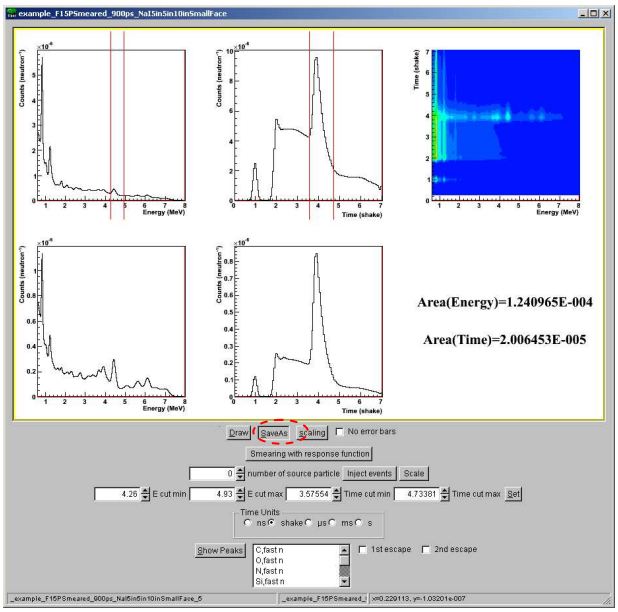
→Once the smearing is finished, the smeared data appear in a new canvas.



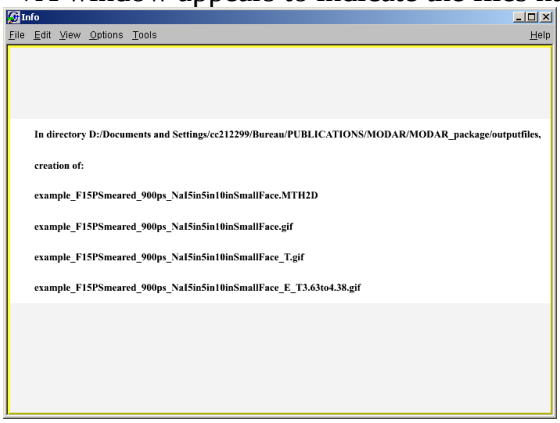
● In the main window, selects the format of the pictures and the spectra to be saved.
In this example, the bottom energy spectrum and top time spectrum, as well as the full tally canvas, are saved as gif pictures and MTH2D file. These files will be saved in the directory indicated in the **Save As Directory** field.



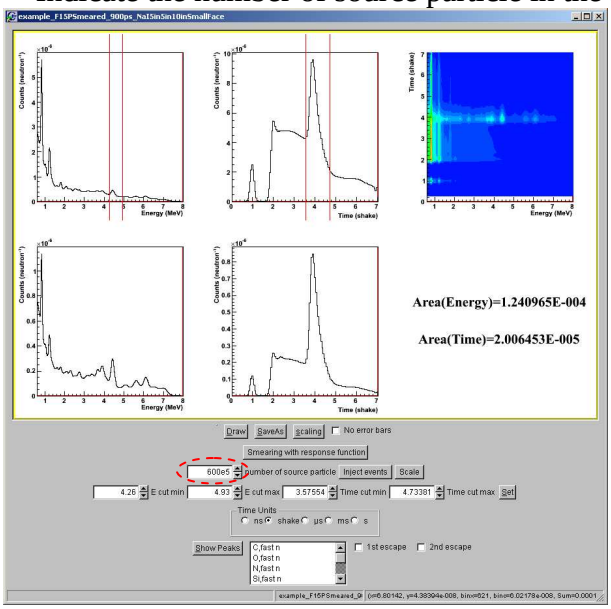
● Press the **Save As** button.



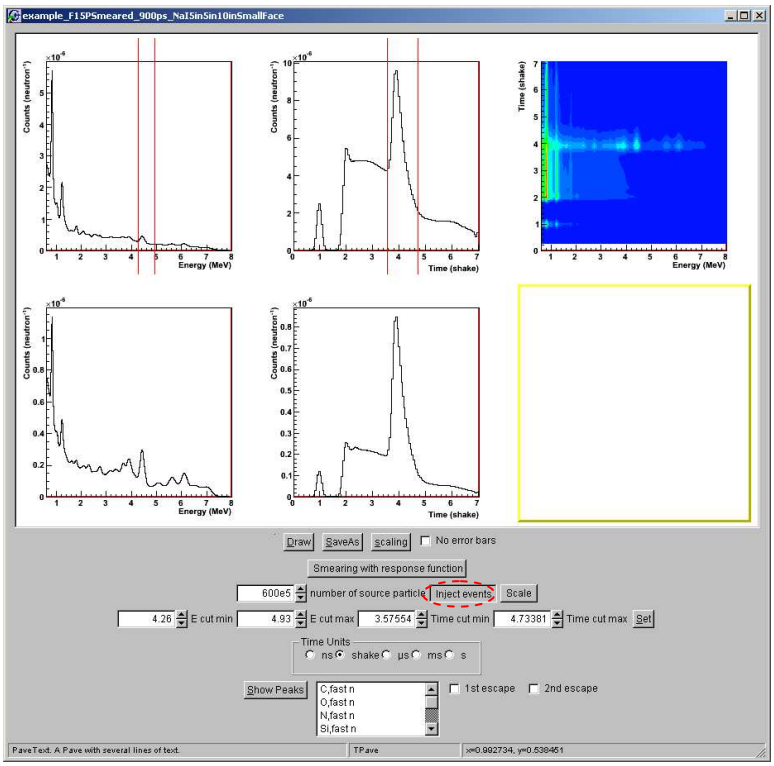
→A window appears to indicate the files have been created.



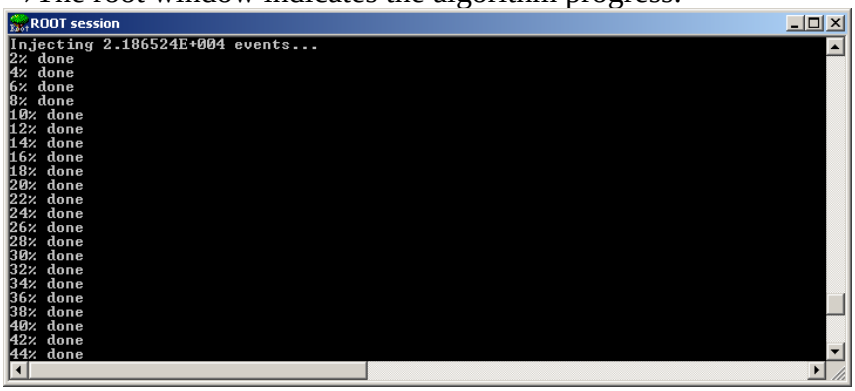
● Indicate the number of source particle in the field number of source particle.



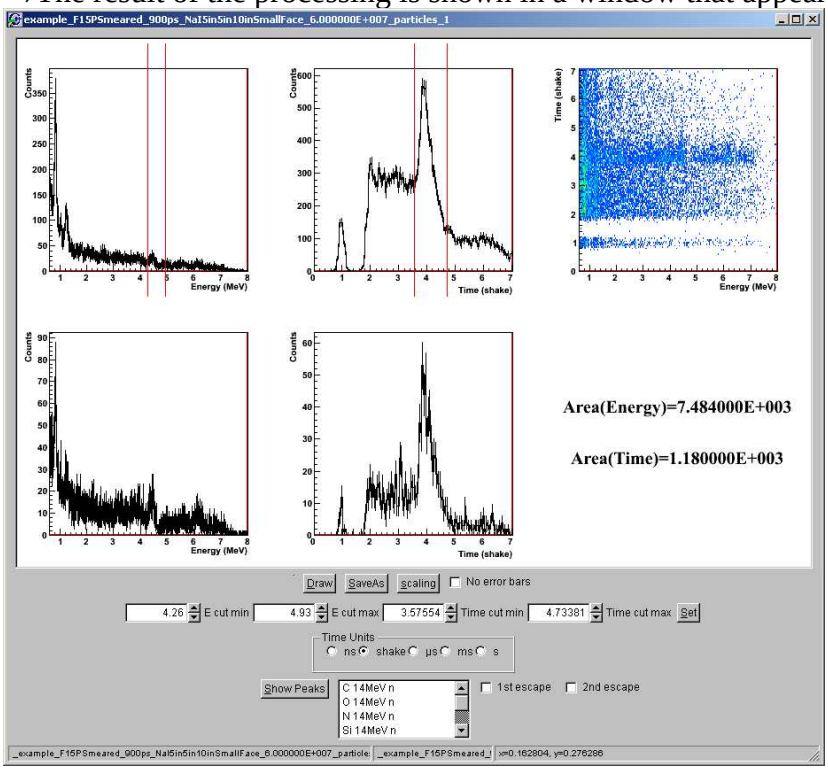
● To sample the 2D histogram by Monte Carlo with indicated number of source particle, press the **Inject events** button.



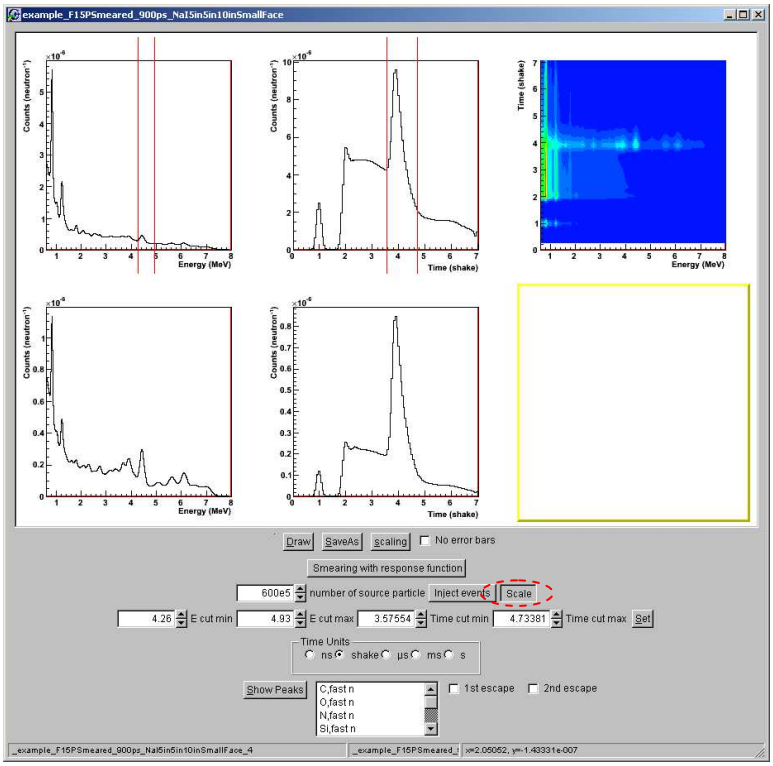
→The root window indicates the algorithm progress.



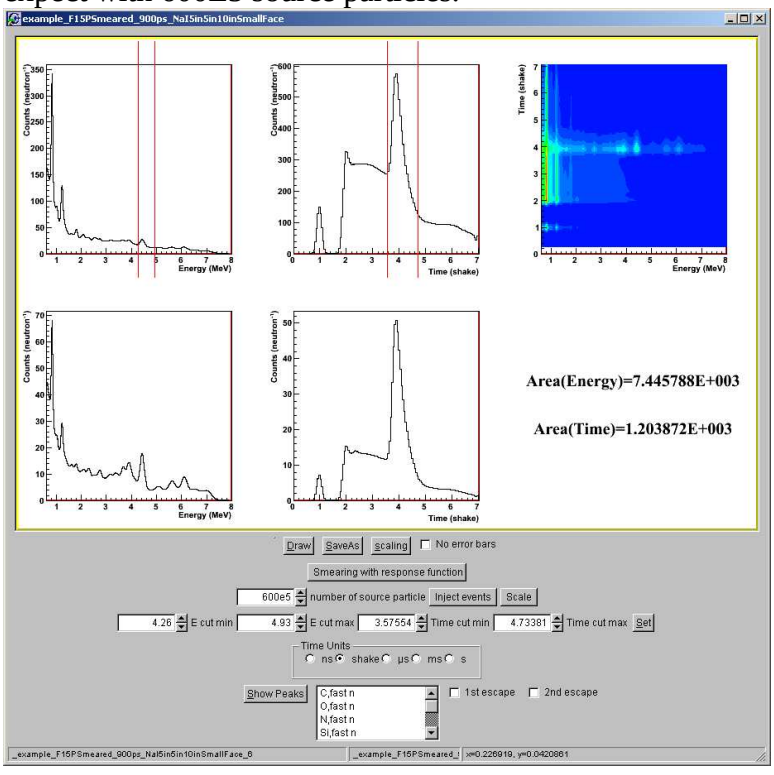
→The result of the processing is shown in a window that appears at the end of the processing.



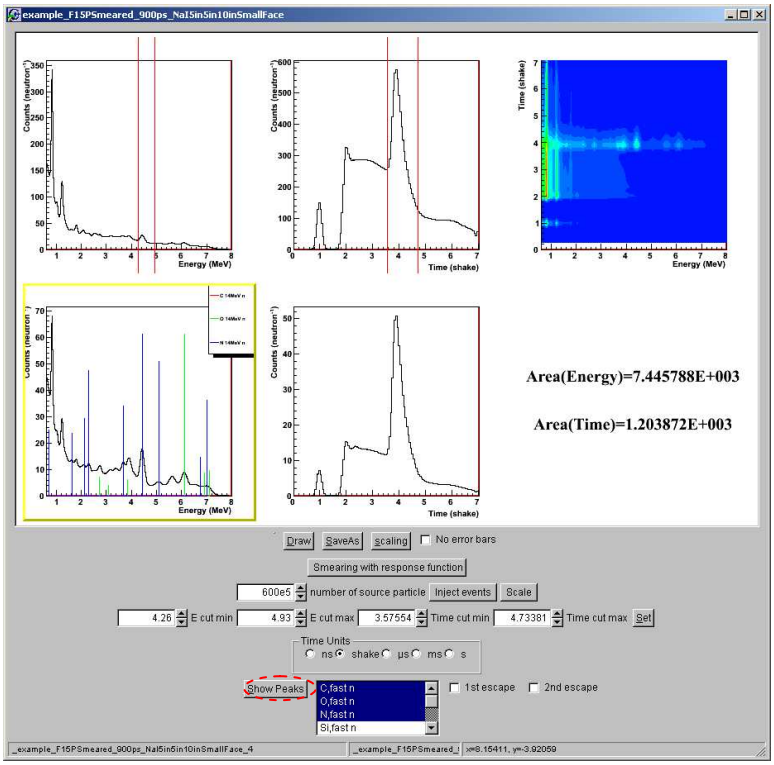
● To scale the 2D histogram with the indicated number of source particle, press the **scale** button.



→The scaled data are shown, corresponding to the average number of events one should expect with 600E5 source particles.



● To show positions of gamma ray of interest in the projected energy spectrum (bottom left), select some reactions and press **Show peaks**. Lines corresponding to the gamma rays energies will be show with the corresponding legend.



Note that one can also display first and second escape peaks: