NECplotter User's guide

The aim of this software is to calculate and plot the optimum NECR for a given dataset acquired with the ClearPEM scanner.

1. Instalation

To run NECplotter the following programs must be pre-installed on the user's computer:

- Amide (http://amide.sourceforge.net/);
- Root (http://root.cern.ch/drupal/).

The following [executable] files are integrating parts of this tool and are provided with it:

- CheckObjectLORs;
- GetNumPandD;
- plotNEC.cxx.

Other tools/files necessary to run NECplotter:

- STIR for planar detectors (including par file and invertsino);
- CorrectScatter_multiCore (including "cross_sectionH2O_2.txt" file);
- MeshCreator.

2. Input/Output

Mandatory Input:

- o a ClearPEM data file with one of the extensions ".elm2", ".bz2" or ".gz";
- o an image obtained from a primary reconstruction (see "Optional Inputs").

Optional Inputs:

In case an image from a primary reconstruction is not provided as input for image segmentation, then a sensitivity image file or a normalization file to calculate the sensitivity image must be provided.

Outputs:

NEC values will be printed to the command line and two plots will pop up showing the counts vs. time window for each type of event and NECR vs. time window.

3. How to run NECplotter

./NECplotter.sh [path_to_input_data_file/data_file.one_of_the_mentioned_extensions]

The following questions will be prompted to the user:

- "Distance between DHs:" - distance between housing boxes and not crystals distance.
- "energy-low (D:400keV):" – Lower limit for energy window in keV. Default is 400keV.
- "energy-high (D:650keV):" – higher limit for energy window in keV. Default is 650keV.
- "Total exam duration (D:1200s):" - default is 300s/angular position.
- "Segmentation mode (1=auto | 2=low-auto | 3=thresholdValue):" – 1 and 2 are automatic options for thresholding based segmentation, 3 is a manual option. If 3 is chosen then "Theshold Value:" will be prompted and the user shall provide a threshold number. This option shall be used after options 1 or 2 fail.
- "Do primary reconstruction (y:n:D=y)?" – This primary reconstruction is needed for segmentation purposes.
    - If "n" : "Input image for segmentation:" – a*.hv file from a primary reconstruction must be provided;
    - If "y" : "Calculate sensitivity image (y:n;D=n)?"
        - If "n" : "Sensitivity Image:" – Provide a *.hv sensitivity image file;
        - If "y" : "Normalization file:" – Provide a normalization file with one of the 3 extensions mentioned for the input data file.
- During execution, the program will pop up an amide window so the user can check the segmentation performed. After closing this window, the question "Accept segmentation result (y:n;D=y)?" will be prompted. In case of "n" the user is prompted to choose again a new segmentation mode. If the user wants to choose option 3, the threshold value shall be obtained from the amide images before closing the amide window.