# PLUGIN DOSIMETRY

Version 2 - 2020

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This plugin allows to obtain information on the counts registered in a SPECT image selecting a manually defined reference ROI or importing one.

The "Dosimetry\_v2" plugin is given as a .class file (Dosimetry\_v2.class).

To install the plugin: open ImageJ and click on "plugin>Install...". Navigate for the .class file and continue to installation. At the end of the operation it will be asked to restart ImageJ.

An analogue procedure is required if using Fiji.

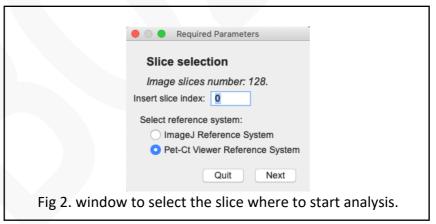
#### How to use...

Launching the plugin, the window in Fig.1 appears. The user is required to open an image. If an image was already opened, this window won't appear.

Clicking on "Browse" it is possible to navigate through the folders to select an image. Clicking on "Quit" the plugin closes.



If more than one image is already open, the user must select the wanted image window before launching the plugin.



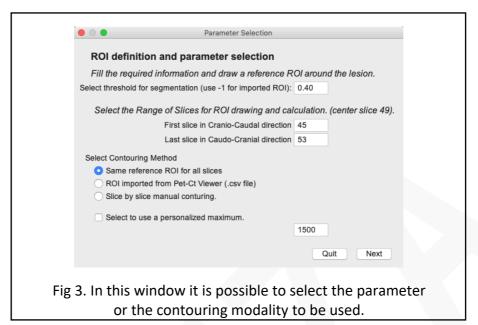
The spatial calibration of the opened image is canceled when the plugin is launched, even if the image was already open. When closing the plugin, the spatial calibration does not reset to the initial state.

A window with the title "Slice selection" opens (Fig.2). The user is asked to insert the number of slice where the lesion is positioned. It is possible to select the reference system used for the given number. If the slice index is the same of ImageJ, please select "ImageJ Reference System". If the slice number is given in the "Pet-Ct Viewer" plugin reference system, select the second option. The difference between the two reference systems is that ImageJ starts counting in Cranio-Caudal direction, while "Pet-CT Viewer" counts in the opposite direction.

The inserted number does not affect the outcome of the analysis. It is used only to move the current

slice view to the one selected by that number.

Clicking on the "Quit" button the plugin closes. Clicking on the "Next" button the window in Fig.3 appears.



All the parameters used during analysis are inserted here.

The software select the lesion/ROI with a thresholding process. The threshold is set equal to the product of the maximum count in the lesion times the threshold index. The threshold index can be inserted in the first field ("Select threshold for segmentation").

Then it is required to insert the first and last slice of the lesion in Cranio-Caudal direction. The slice number has to be given in the imageJ reference system.

There are three different countouring modality available:

### 1. Same reference ROI for all slices:

A reference ROI must be draw on the image (Fig.4 - left). This ROI allows to select the region in which the lesion is present. The plugin looks for the maximum pixel value in the reference ROI for all the slices indicated in the second and third field of the window in Fig.3. Clicking on "Next", the thresholding process starts. It selects in red all the pixel with a value over the selected threshold. The final region in which the analysis is computed is given by the pixel inside the reference ROI with a value over the selected threshold. (Fig.4 - Right).

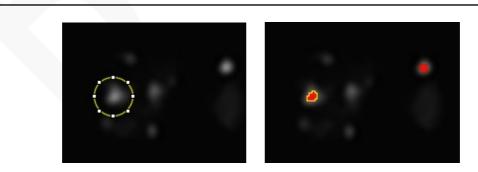


Fig 4. Left: Reference ROI selecting the lesion area. Right: the final selection is given only by the intersection between the region selected via the thresholding process and the reference ROI.

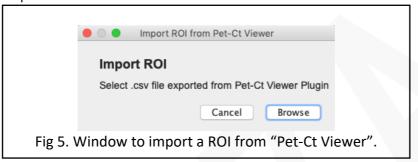
## 2. ROI imported from Pet-Ct Viewer

This contouring modality allows to import a ROI created with the "Pet-Ct viewer" plugin. In

this case the slice values selected in the second and third field of the window inf Fig. 3 are ignored. Only the information in the .csv file exported from "Pet-Ct viewer" plugin are used. Selecting this modality and clicking on "Next", the user is asked to import the .csv file, as shown in Fig. 5

Clicking on "Cancel" the user is redirected to the window in Fig. 2. Clicking on "Browse", it is possible to navigate the folders to select the .csv file exported from Pet-Ct Viewer, that contains the ROI info.

It is important to understand that the ROI is treated as a reference ROI. In order to consider



all the pixel in this region and not only the one above the threshold the user must use a threshold value of "-1" in the first field of the window in Fig. 2

### 3. Slice by slice manual conturing

Analogously to case 1, it is required to draw a reference ROI. The user is aske to draw a reference ROI for each slice of the lesion. At each request, the window in Fig.6 appears.

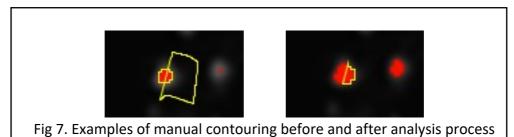


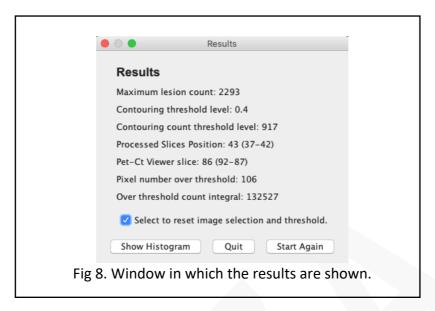
Clicking on "Quit" the plugin closes. Clicking on "Next Slice" the current reference ROI is registered for the current slice and the view moves to the next slice.

Manual contouring ends in two ways: if the last selected slice is reached or clicking on the "End Contouring" button. In the second way the current and following slice are ignored for the analysis.

### Results

Results are shown in a window like the one in Fig.8.





The output parameters are the following:

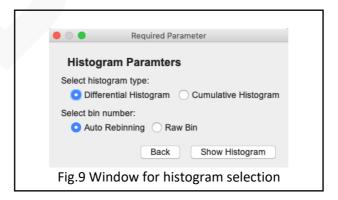
- Maximum pixel value (count) found in the lesion;
- The level of the threshold used;
- o The actual threshold value used:
- The number of the slices processed. The first value is where the maximum was found. The range shows the position of the lesion;
- Same as before, but in the Pet-Ct Viewer reference System;
- Number of pixels in the lesion with value above threshold.
- o Integral of all the pixel above threshold in the lesion.

Clicking on "Quit" the plugin closes. Clicking on "Start Again" the user is redirected to the window in Fig. 2. When closing the plugin, the image is threshold is reset and the selection is canceled.

If the user wants to keep on screen as an overlay the results of the current threshold selection, it is required to deselect the thick "Select to reset image selection and threshold".

Clicking on "Show Histogram" it is possible to select the kind of histogram that the user is interested in (Fig.9).

It is possible to select a cumulative histogram or a differential histogram. The bin dimension is chosen automatically by the system, but it is possible to see the distribution using a bin size of 1 count ("Raw Bin").



Clicking on "Show Histogram" a histogram window opens and a "Save" button appears on the "Histogram Parameter" window. Completing the saving process, a .csv file is saved in the "Downloads" folder. It contains

the points shown in the graph for each bin.

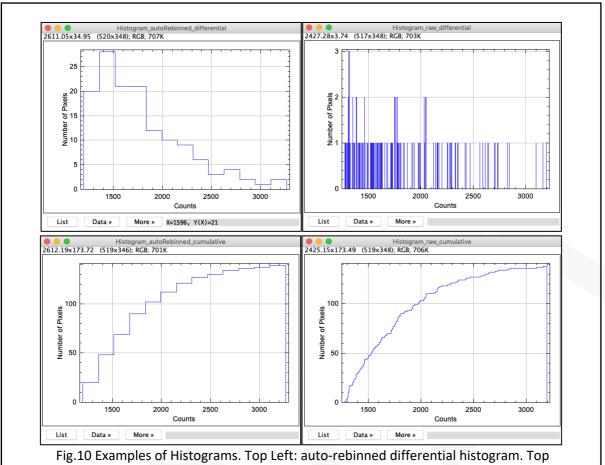


Fig.10 Examples of Histograms. Top Left: auto-rebinned differential histogram. Top Right: raw-bin differential histogram. Bottom Left: auto-rebinned cumulative histogram.

Bottom Right: raw-bin cumulative histogram.