



**EFOMP**

EUROPEAN FEDERATION OF ORGANISATIONS FOR MEDICAL PHYSICS

## **EFOMP GUIDELINE**

### **Quality control in PET/CT and PET/MR**

- software tools user manual

version 30.08.2022

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## General requirements

The easiest way to run the python scripts is through the Anaconda software package (Anaconda Inc.) available at <https://www.anaconda.com/>. The package includes an editor called Spyder as part of the installation that can be used to run the code. After successful installation of Anaconda, the pydicom library will need to be installed. This can be done using the Anaconda Power Shell (run as Administrator) and using the following command:

```
conda install -c conda-forge pydicom
```

The python code downloaded from the EFOMP website should be placed into a single directory. All scripts require the .png files in the same directory and the RC\_analyzer requires the config.cfg file in the same directory. This configuration file contains information about the boundary values of the recovery coefficient (RC) curve. The file is editable, so users can define the shape of the RC curve as required.

It was not tested by the WG members, but the scripts can run without Anaconda installed. In this case, the user will probably have to install additional libraries.

## Possible limitations

All scripts are using DICOM header information. The basic condition for the SUV calculation is that the value of DecayCorrection DICOM tag equals START and that the DecayCorrectionDateTime equals SeriesTime.

Users should carefully observe the results and cross-check them with a vendor delivered processing station. If any discrepancies occur, feel free to modify the code or ask for the modification.

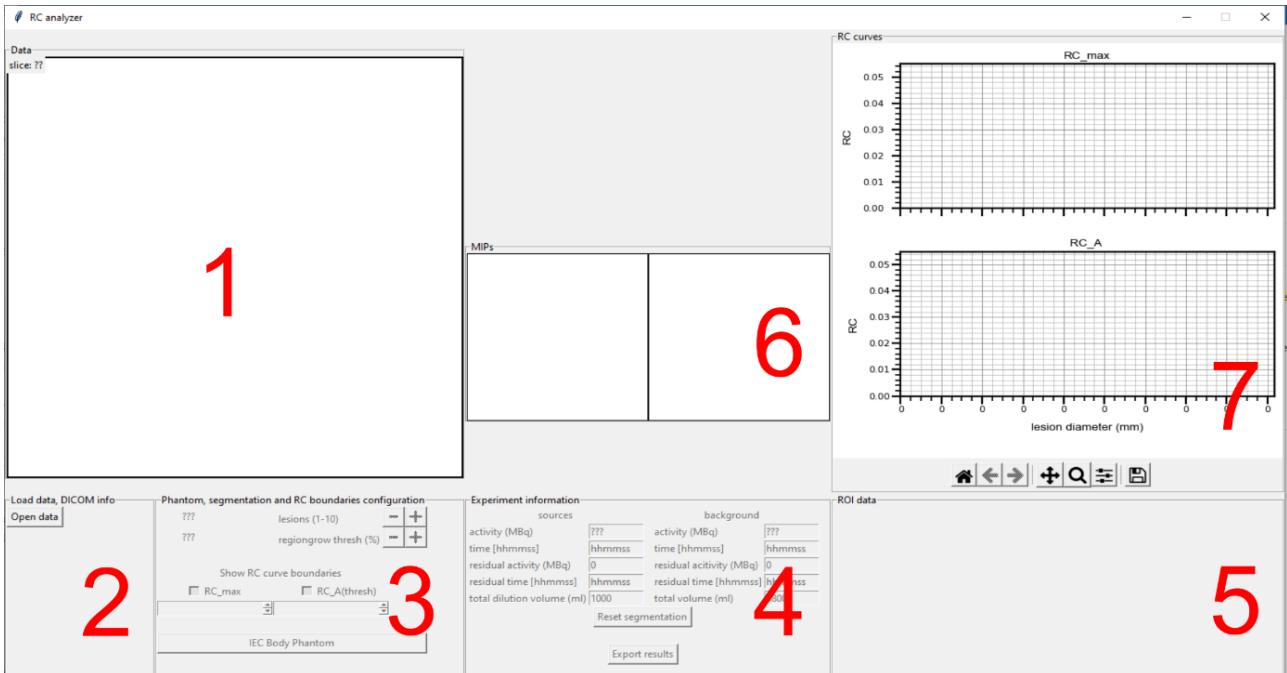
Codes were tested for accuracy with Siemens biograph mCT data. Tests with Philips and GE were done only to a limited extent mainly for compatibility reasons.

## Feedback / issues

Feedback and issues/bugs reporting are highly appreciated. Please use [jaroslav.ptacek@fnol.cz](mailto:jaroslav.ptacek@fnol.cz) for this purpose.

## RC\_analyzer

This code serves to help users in analysing RC curve data from the image quality phantom. It was mainly designed for the IEC Body phantom, but since it uses the region-growing algorithm to delineate 3D volumes of interest (VOI), users are able to use with alternative phantoms. The number of lesions to analyze can be switched from 1 up to 10. The output from the analysis consists of two curves, the  $RC_{max}$  and  $RC_{A??}$ . In the latter case ?? represents the threshold used during the delineation process. For example,  $RC_{A50}$  is the commonly used threshold for EARL accreditation purposes. The threshold is set as (maximum value in the volume of interest plus mean background value) divided by two in the A50 scenario.



The RC\_analyzer window is divided into 7 frames corresponding with the steps needed to obtain the RC curve.

- 1) **Data** frame is used to display the phantom slices. It is also used for seed position selection during the region-growing algorithm. Users can scroll through slices using the mouse scroll button. Using the scroll button together with Shift key pressed, a zoom (positive or negative depending on the scroll button's rotation direction) is applied on the image. The center point for the zoom function is the current mouse cursor location. To reset the zoom the mouse scroll button must be pressed. Data frame is also used for drawing the background region of interest.
- 2) **Load data, DICOM info** frame contains an Open data icon. This is for selection of the directory containing data to be analyzed (only one series of PET attenuation corrected data). After all slices are loaded, brief information regarding the study is shown in this frame.
- 3) **Phantom, segmentation and RC boundaries configuration** frame allows the user to select the number of lesions to be analyzed, a region-growing algorithm threshold in

terms of A?? and RC curve boundaries. The IEC Body phantom button can be used to prefill the region of interest (ROI) data automatically.

- 4) **Experiment information** frame must be filled prior to image segmentation. Information about sources and background, which is vital for a correct RC curve analysis, must be entered manually. The reset segmentation button resets only the result of the segmentation and can be used if there are any issues with the segmentation process. Export results button creates a .csv file containing all data and saves in the user selected location.
- 5) **ROI data** frame displays the measurement results and contains fields to define the lesion sizes.
- 6) **MIPs** frame displays maximum intensity projections of region-growing segmented regions to control the validity of the segmented VOI. Both images are zoomable.
- 7) **RC curves** frame displays the RC curve corresponding to the current PET data, RC curve boundaries (if switched on and selected in frame 2) and tools for graph manipulation and .png export.

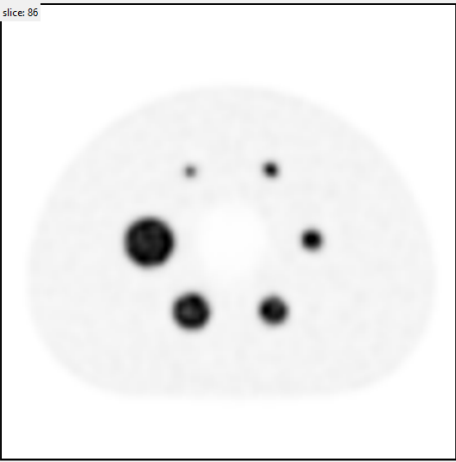
### RC\_curve analysis process

- Open PET corrected data (frame 2).
- Select number of lesions and the threshold used for VOI region-growing segmentation.
- Select whether and which RC boundary curves will be displayed together with the RC curve. This can be done prior the analysis or anytime during the process. Curves can be freely switched anytime.
- Fill in the information regarding phantom preparation. The time of acquisition is taken from the Series Time DICOM tag. This demands a proper synchronization of all clocks used during the experiment with the acquisition workstation.
- State ROI sizes (diameter).
- Scroll through phantom slices to find a suitable one for background ROI delineation. Draw the background ROI using left mouse button directly on the Data frame slice image. The image can be zoomed prior to or after the ROI is drawn. If a better ROI is needed, one just needs to draw a new one. RC\_analyzer holds only the last drawn background ROI, the previous one is deleted automatically. Background ROI data (frame 5) is updated after the release of the left mouse button. The background ROI is automatically created on the selected slice,  $\pm 1$  and  $\pm 2$  slices.
- Adjust the lesion sizes and position by zooming and starting with the RC curve analysis. Use the right mouse button with the pointer above the analyzed lesion and select the appropriate number of the ROI. A suggestion is to start from the largest one having number 1. The ordering must correspond with ROI data frame information. As soon as the right mouse button is released a region-growing algorithm delineates the VOI (this can be verified on the MIP image), ROI data frame gets updated and the RC curve point is added to the graph section.

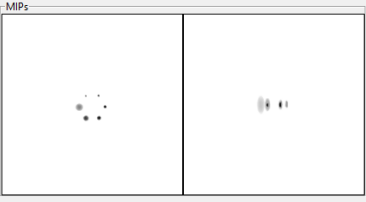
- After the analysis is done, the Export results button can be used to save the results to a .csv file.

RC analyzer

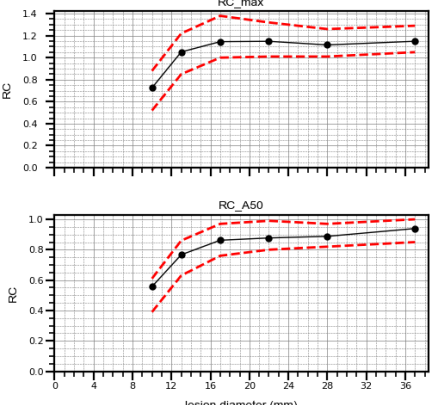
Data  
slice: 86



MIPs



RC curves



Load data, DICOM info

Open data

rows: 256  
columns: 256  
slices: 174  
slices thickness: 2 mm  
pixel size: 3.1819 mm  
study date: 11.03.2021  
series time: 170401  
injection date: 11.03.2021  
radionuclide: 18<sup>F</sup>Fluorine  
half-life: 6586.2 seconds  
device: Biograph40\_mCT  
Post-recon filter FWHM: XYZ Gauss5.00 mm

Phantom, segmentation and RC boundaries configuration

6 lesions (1-10)

50 regiongrow thresh (%)

Show RC curve boundaries

RC\_max  RC\_A(thresh)

EARL\_2\_max EARL\_2\_A50

IEC Body Phantom

Experiment information

| sources                    |        | background              |        |
|----------------------------|--------|-------------------------|--------|
| activity (MBq)             | 57.06  | activity (MBq)          | 54.44  |
| time [hhmmss]              | 143100 | time [hhmmss]           | 143700 |
| residual activity (MBq)    | 0      | residual activity (MBq) | 0      |
| residual time [hhmmss]     | 143100 | residual time [hhmmss]  | 143700 |
| total dilution volume (ml) | 1000   | total volume (ml)       | 9800   |

Reset segmentation

Export results

ROI data

| roi   | mm | RC_max | RC_A50 |
|-------|----|--------|--------|
| roi 1 | 37 | 1.149  | 0.9393 |
| roi 2 | 28 | 1.1156 | 0.8879 |
| roi 3 | 22 | 1.1486 | 0.8773 |
| roi 4 | 17 | 1.1453 | 0.8622 |
| roi 5 | 13 | 1.0517 | 0.7667 |
| roi 6 | 10 | 0.7255 | 0.557  |

background real volume activity: 2195.4 Bq/ml

background measured volume activity: 2181.2 Bq/ml

background real / measured difference: -0.65 %

background COV: 0.9 %

## Uniformity\_analyzer

This code helps users to easily analyze the uniformity of reconstructed PET images of a phantom with a circular or elliptical shaped cross-section. It was mainly designed for a standard cylindrical shaped uniformity phantom. In addition to color coded uniformity analysis of each slice, the user gets information about the mean SUV in the imaged object, the difference between mean SUV in the whole phantom and individual slice mean SUV and individual slice coefficient of variation (COV). Within slice  $SUV_{max}$  and  $SUV_{min}$  is also displayed as well as the diameter of the ROI used for the uniformity calculation and the length of the VOI (selected phantom length).

The screenshot displays the 'Uniformity analyzer' software interface, which is divided into four main functional areas, each marked with a red number:

- 1 (Data frame):** Located in the top-left, it displays placeholder text for 'slice: ???', 'mean SUV: ???', 'diff SUV (%): ???', and 'COV (%): ???'. Below this, there are fields for 'SUV max: ???' and 'SUV min: ???'. At the bottom right of this frame, it shows 'ROI diameter: 000.0 mm' and 'VOI length: 000.0 mm'.
- 2 (DICOM info frame):** Located in the bottom-left, it contains a 'Load data, DICOM info' section with an 'Open data' button. Below this, there are input fields for 'Phantom volume: 6300 ml', 'Phantom activity: 0.000 MBq', 'Phantom injection time: 000000 h:mm:ss', and 'Phantom injection date: 000000 dd:mm:yyyy'.
- 3 (Uniformity check settings frame):** Located in the bottom-right, it contains various settings for the analysis, including 'Change ROI diameter by: 0.0 / 0 mm/px', a checkbox for 'Change also the ROI extent by the same amount of pixels?', 'Show outliers above -(blue) / +(red): ??? %', a checked checkbox for 'Show / hide color coding?', 'Phantom center threshold at: 50 %', 'Phantom end positions threshold at: ??? %', 'Calculated mean SUV:', 'Deviation from expected SUV=1: %', and 'Crop data to graph by: 0 slices'. It also features 'Calculate results' and 'Export results' buttons.
- 4 (Per slice deviation and COV frame):** Located in the top-right, it contains two vertically stacked line graphs. The top graph is titled 'per slice deviation' and the bottom graph is titled 'COV (%)'. Both graphs have 'diff (%)' and 'COV (%)' on the y-axis and 'slice #' on the x-axis. The x-axis for both graphs has multiple '0' labels, suggesting a range of slices.

The Uniformity\_analyzer window is divided into 4 frames that correspond with the steps needed to proceed with the analysis.

- 1) **Data** frame is used to display the phantom axial slices. It displays additional information about the particular slice, ROI and VOI. The ROI with a user modifiable diameter is drawn on the phantom slice. Once the analysis is complete, color coded positive/negative deviations over/under the user defined percentage threshold are shown. The user can scroll through the axial slices using the mouse scroll button. Using the scroll button together with Shift key pressed, a zoom (positive or negative depending on the scroll button's rotation direction) is applied on the image. The center point for the zoom function is the

current mouse cursor location. To reset the zoom the mouse scroll button must be pressed.

- 2) **Load data, DICOM info** frame contains an Open data icon. This is for selection of the directory containing data to be analyzed (only one series of PET attenuation corrected data). After all slices are loaded, brief information regarding the study is shown in this frame. Users can modify the phantom volume, activity and injection time/date should this differ from the information extracted from the DICOM header.
- 3) **Uniformity check settings** frame allows the user to select appropriate ROI and VOI for the analysis. It is recommended to use a two bed-position scan or a scan with sufficient extent in the longitudinal field of view to reduce the influence of the lower axial sensitivity in the end slices. The user can change the diameter of the automatically drawn ROI (based on center of mass calculation) to exclude peripheral voxels from the analysis. Also, the length of the VOI can be modified (by the same number of pixels as the diameter). This should be used only in situations where the phantom was centered, but not perfectly aligned with the longitudinal axis of the scanner. Phantom center and end point position thresholds can also be modified; however, 50 % default preset works well in most situations. Depending on the user's preference, the analysis can be made using different percentage tolerance values to calculate the outliers with 5 % being the initial setting. Calculated mean SUV and the deviation from the expected SUV = 1 is shown in this frame after the analysis is finished. Displayed graph data can be cropped by the user defined number of slices to suppress the influence of the lower axial sensitivity in the end slices on the graph scale. Results can be exported into .csv file using Export results button.
- 4) **Per slice deviation and COV** frame contains two graphs showing the calculated data in each slice and tools for graph manipulation and .png export.

### Uniformity analysis procedure

- Open the PET corrected data (frame 2). The ROI is automatically drawn on the axial phantom slice.
- Modify the phantom volume, activity and time of injection as required.
- User should adjust the ROI diameter to exclude any peripheral voxels that may distort the calculation. This is possible in multiples of pixel sizes. The user can also shorten the VOI used for the calculation by the same number of pixels.
- The default value of +/- 5 % for color coding the voxel outliers can be changed according to the user's preference.
- Thresholds for the phantom's center and extent can also be changed if the automatically generated ROI is incorrectly placed.
- Uniformity results are obtained after the Calculate results button is pressed. Any modification of the above stated parameters will appear only after the result is re-calculated.

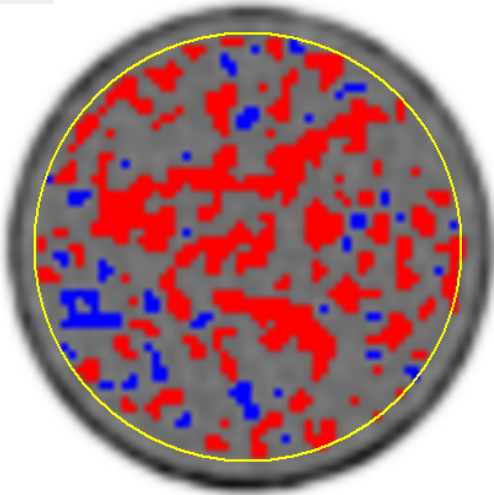


- After the analysis is done, the Export results button can be used to save a .csv file with the results.

Uniformity analyzer

**Data**

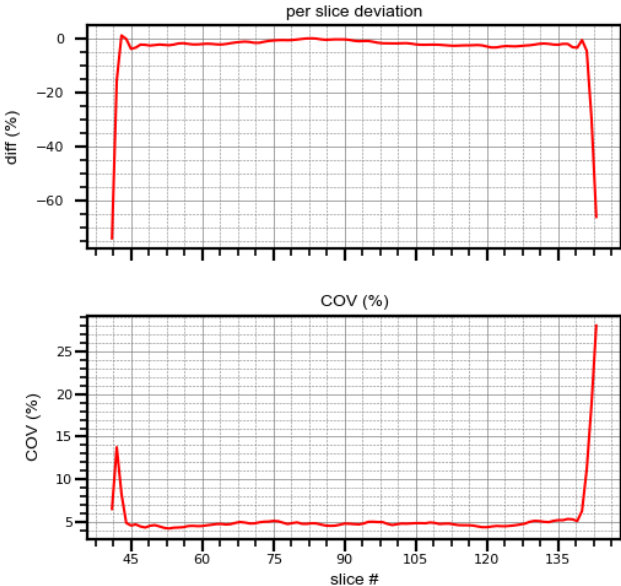
slice: 87  
 mean SUV: 0.996  
 diff SUV (%): -0.392  
 COV (%): 4.514



SUV max: 1.157  
 SUV min: 0.855

ROI diameter: 178.2 mm  
 VOI length: 204.0 mm

**Per slice deviation and COV**



**Load data, DICOM info**

Open data

rows: 256  
 columns: 256  
 slices: 174  
 slices thickness: 2 mm  
 pixel size: 3.1819 mm  
 study date: 04.05.2021  
 series date: 04.05.2021  
 series time: 162801  
 radionuclide: 18^Fluorine  
 half-life: 6586.2 seconds  
 device: Biograph40\_mCT  
 Post-recon filter FWHM: XYZ Gauss5.00 mm

Phantom volume: 6300 ml  
 Phantom activity: 115.48 MBq  
 Phantom injection time: 140500 h:mm:ss  
 Phantom injection date: 04052021 ddmmyyyy

**Uniformity check settings**

Change ROI diameter by: -12.73 / -4 mm/px    Change also the ROI extent by the same amount of pixels?

Show outliers above -(blue) / +(red): 5 %    Show / hide color coding?

Phantom center threshold at: 50 %

Phantom end positions threshold at: 50 %

Calculated mean SUV: 0.9713

Deviation from expected SUV=1: -2.87 %

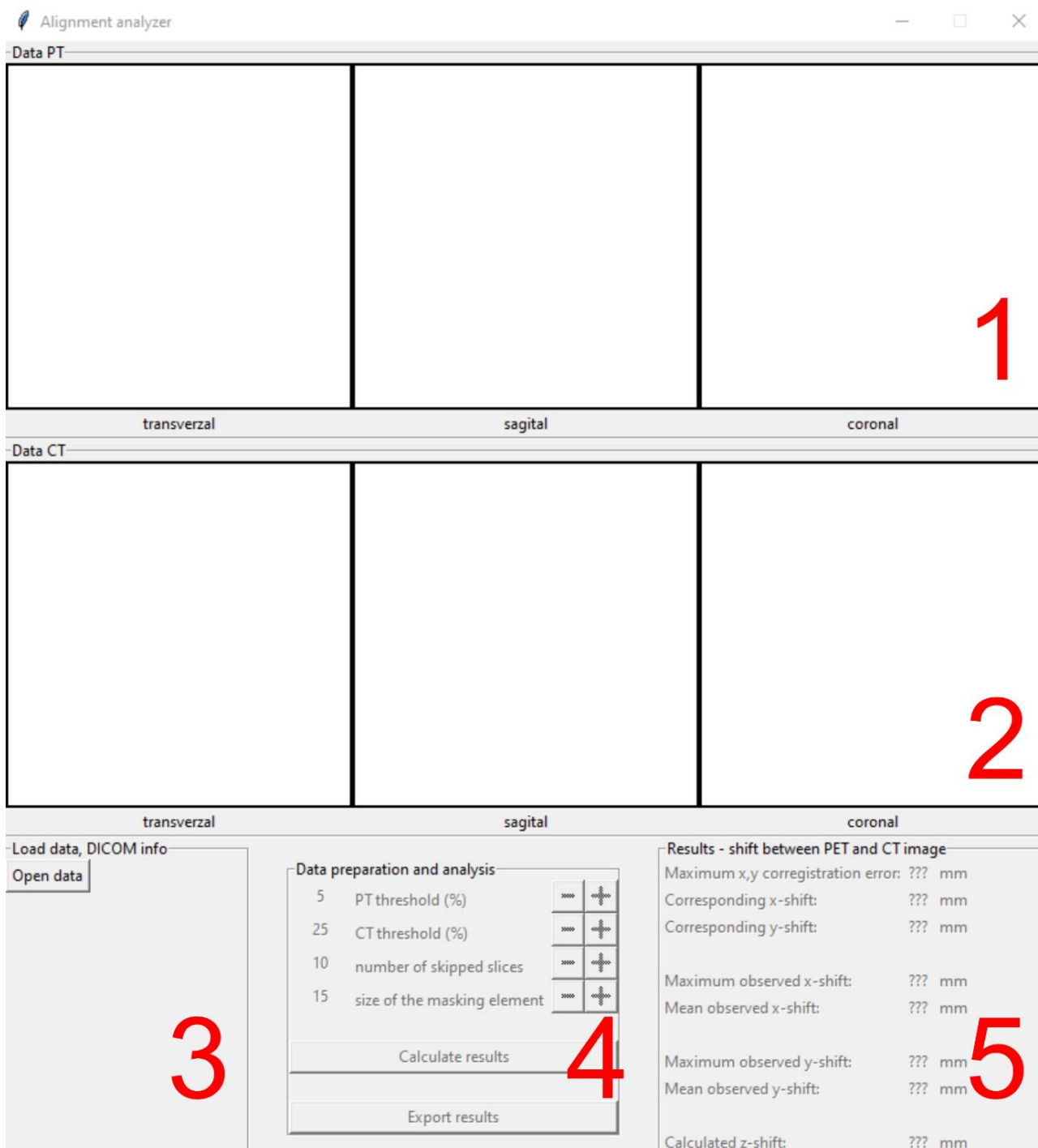
Crop data to graph by: 0 slices

\*In case of acquiring the data on the date different from the day phantom was filled, the activity has to be manually recalculated.

## Alignment\_analyzer

The Alignment analyzer code can be used to check the PET to CT gantry alignment independently from the vendor's procedure/phantom. The procedure is based on the calculation of the intersection of two straight line sources in one of the image planes (coronal or sagittal). The measuring device can be created from nearly anything with only four conditions: straight lines, clearly visible in PET and CT images, parallel in one of the image planes (coronal or sagittal), having an intersection in the other and extent over the axial length of the field of view.

The Alignment\_analyzer window is divided into 5 frames that correspond with the steps needed to proceed with the analysis.



The screenshot displays the 'Alignment analyzer' window, which is divided into five numbered frames:

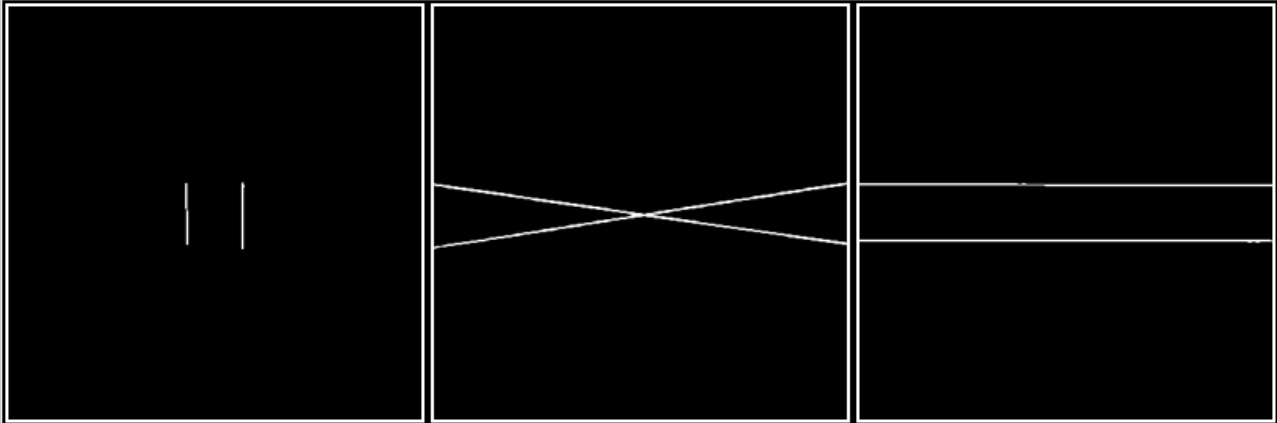
- 1**: 'Data PT' section, showing three empty image frames labeled 'transverzal', 'sagital', and 'coronal'.
- 2**: 'Data CT' section, showing three empty image frames labeled 'transverzal', 'sagital', and 'coronal'.
- 3**: 'Load data, DICOM info' section, containing an 'Open data' button.
- 4**: 'Data preparation and analysis' section, containing four input fields with sliders: 'PT threshold (%)' (value 5), 'CT threshold (%)' (value 25), 'number of skipped slices' (value 10), and 'size of the masking element' (value 15). Below these are 'Calculate results' and 'Export results' buttons.
- 5**: 'Results - shift between PET and CT image' section, displaying various registration metrics: 'Maximum x,y corregistration error: ??? mm', 'Corresponding x-shift: ??? mm', 'Corresponding y-shift: ??? mm', 'Maximum observed x-shift: ??? mm', 'Mean observed x-shift: ??? mm', 'Maximum observed y-shift: ??? mm', 'Mean observed y-shift: ??? mm', and 'Calculated z-shift: ??? mm'.

- 1) **Data PT** frame displays the PET corrected images of the phantom in all three image planes.
- 2) **Data CT** frame displays the CT images of the phantom in all three image planes.
- 3) **Load data, DICOM info** frame is for selection of the directory containing data to be analyzed (only one series of PET attenuation corrected data and a corresponding series of CT data). After all slices are loaded, brief information regarding the PET and CT studies is shown in this frame.
- 4) **Data preparation and analysis** frame allows users to select an appropriate threshold for the PET and CT data. The purpose of thresholding is to remove possible reconstruction artefacts and to make sure that only the line sources are visible on the CT images. A threshold of 5 % should be sufficient according to the NEMA NU 2-2018 publication. The utilized algorithm identifies the line sources on PET and CT transverse images. It starts with the first image to find the initial position and calculate the centroid of the first and second line source. It then follows the source on subsequent slices. The whole analysis can take some of time, so users can select number of subsequent slices to be skipped to speed up the computation time. It should be noted however, skipping slices will reduce the precision of the line source linear equation estimation. A masking element is used to find the particular line on the subsequent slice. The larger the number of skipped frames or the angle between the sources, the larger the masking element must be. After all parameters are set, the calculation is started by using the Calculate results button. Results can be exported into a .csv file using the Export results button.
- 5) **Results – shift between PET and CT image** frame only shows the calculated results. A maximum coregistration error and corresponding x, y shifts leading to this error. Maximum and mean shifts in x and y coordinates between line sources from all analyzed slices are also shown. A z-position shift is calculated based on difference between the position of the intersection of PET and CT image of the line sources.

### Alignment analysis procedure

- Open PET (corrected) and corresponding CT data (only those two series in a folder).
- If there are any other structures besides the line sources visible in PET or CT image, use the PT/CT thresholding to mask them.
- Proceed with the analysis using Calculate results button. A default setting of number of skipped slices and the size of a masking element is 10/15. Change these when appropriate or if the analysis fails. Different settings of the number of skipped slices give different results. This is caused by differences in the precision of the linear equation for line source estimation. The size of the masking element has no impact on the result. After switching to a different setting, the Calculate results button must be pressed again.
- After the analysis is done, the Export results button can be used to save a .csv file containing the results.

Data PT

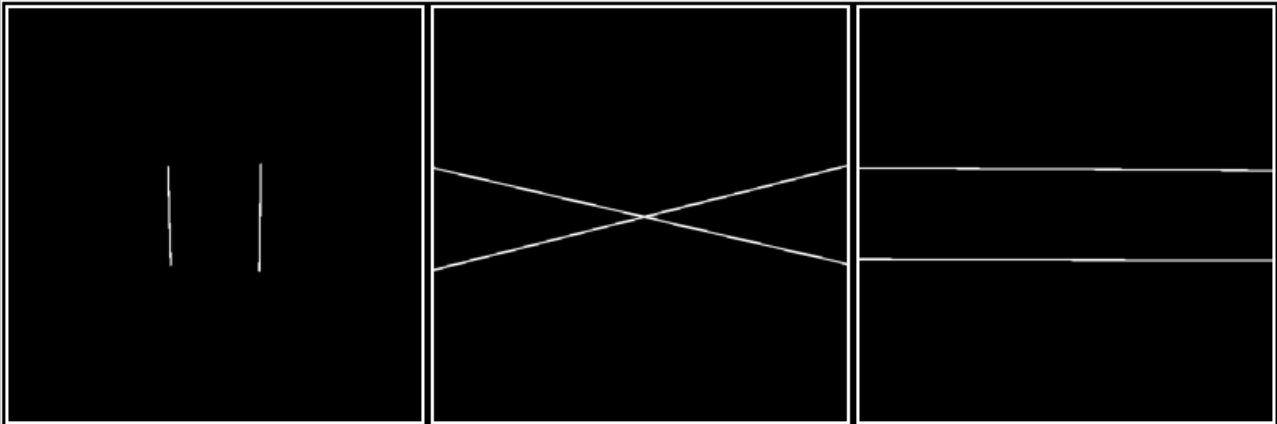


transverzal

sagital

coronal

Data CT



transverzal

sagital

coronal

Load data, DICOM info

Open data

PET  
 rows: 400  
 columns: 400  
 slices: 111  
 slices thickness: 2 mm  
 pixel size: ['2.03642', '2.03642'] mm  
 Post-recon filter FWHM: XYZ Gauss1.00 mm  
 CT  
 rows: 512  
 columns: 512  
 slices: 111  
 slices thickness: 2 mm  
 pixel size: ['0.9765625', '0.9765625'] mm  
 device: Biograph40\_mCT

Data preparation and analysis

- 5 PT threshold (%) - +
- 25 CT threshold (%) - +
- 10 number of skipped slices - +
- 15 size of the masking element - +

Calculate results

Export results

Results - shift between PET and CT image

|                                   |              |    |
|-----------------------------------|--------------|----|
| Maximum x,y coregistration error: | 0.742        | mm |
| Corresponding x-shift:            | 0.116        | mm |
| Corresponding y-shift:            | 0.733        | mm |
| Maximum observed x-shift:         | 0.733        | mm |
| Mean observed x-shift:            | 0.061±0.303  | mm |
| Maximum observed y-shift:         | -0.492       | mm |
| Mean observed y-shift:            | -0.013±0.222 | mm |
| Calculated z-shift:               | 0.154        | mm |