

User guide

Local Image Features **Extraction** — **LIFEx** —

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Part I
LIFEx

Chapter 1

Introduction

1.1 What is LIFEx?

LIFEx is a medical software that reads (DICOM, Nifti, png, tiff, bmp, jpg, ...) images locally or over a network using a DICOM browser (only for DICOM images) and includes a powerful 3D reconstruction based slice viewer.

LIFEx runs on Windows10, Windows11, MacOS (Mojave, Catalina, Big Sur, Monterey, Ventura, Sonoma (available on M1 or M2 ARM processors)) and Linux/Ubuntu, Debian, Fedora distributions (.rpm, .tar, .deb). It is distributed with examples and includes tutorials.

User support is offered ([Contact link](#)).

LIFEx has already been distributed to research labs, nuclear medicine departments and radiology departments ([LIFEx accounts link](#)) for investigating different tumor types

1.2 Acknowledgements

(gliomas, cervix, lung, breast, and colorectal tumors), and has been very positively received ([Journal papers link](#)).

The intuitive interface associated with the tutorials make it fast to master for staff, and allowed us to start building databases of normal textural values in brain (white and grey matter), breast, liver, lung, fat, and muscles for various imaging equipment and protocols in US, PET and CT, while MR data are currently being collected and processed. Such data enable an accurate characterisation of the variability of different textural indices in a given imaging modality as a function of the scanner and the imaging protocol. New indices are being implemented based on users requests as the software is intended to evolve over time based on advances in the field.

1.2 Acknowledgements

We would like to take this opportunity to thank all LIFEx users for their feedback and relevant suggestions. The software highly benefits from your feedback and suggestions.

Do not hesitate to download this new release and replace your old LIFEx version. Your feedback will always be welcome.

1.3 Help us to keep it free

LIFEx is free of charge. Please help us to keep it free by always quoting the LIFEx reference:

C Nioche, F Orhac, S Boughdad, S Reuze, J Goya-Outi, C Robert, C Pellot-Barakat, M Soussan, F Frouin, and I Buvat. LIFEx: a freeware for radiomic feature calculation in multimodality imaging to accelerate advances in the characterization of tumor heterogeneity. *Cancer Research* 2018; 78(16):4786-4789

1.4 Popular Features

LIFEx reads DICOM images locally or over a network using a DICOM browser, is compatible with Osirix and includes a powerful 3D reconstruction-based slice viewer.

LIFEx reads Nifti, png, tiff, jpg, bmp images from local hard disk.

Volumes of interest (VOI) or Region of interest (ROI) can be either imported from previously created files or drawn and manipulated using LIFEx. Results are exported in "csv" format files.

It is distributed with examples ([examples link](#)) and includes tutorials ([documentation link](#)).

User support is available. Users can optionally contribute to the gathering of index values measured in different tissue types and different images as a public data bank of reference values is currently being built and integrated in the software for assisting the users with the interpretation of their results.

1.5 Main application windows

The application presents three types of windows:

- on the left of the screen, the main control window called "LIFEx" displays the basic control functions. This window also includes dialog boxes attached to the current image series (see chapter 2.1 p.28);
- the window "ROI" on the right includes all tools needed to create and modify ROI (see chapter 5.1 p.48);
- the third window is dedicated of the management of image display, once image is selected in the three space planes (see chapter 3.1 p.36).

1.6 Working space and directory tree

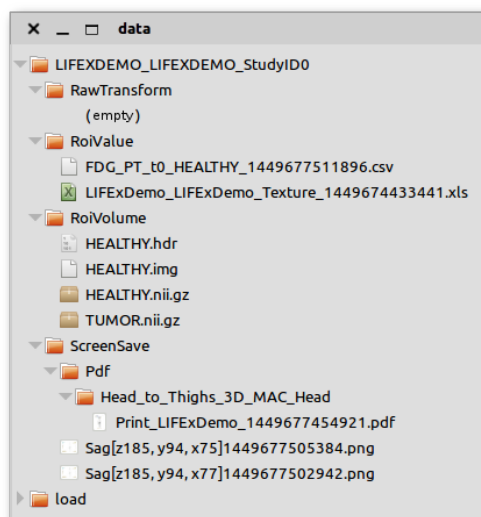


Figure 1.1 Display of the directory tree

Directory tree. This application manages the organization of directories, sub-directories and files in which all data related to a scan are stored. The highest directory level corresponds to the patient name, patient ID, study ID, and this directory includes:

- RawVolume : volumes recorded at your request using one of the supported formats (.dcm, .nii) with sub-directories depending on the file format;
- RawTransform : transformation matrices recorded automatically when performing image volume registration;
- ROIVolume : volumes of the recorded ROI using the supported formats: the loss-less compressed NIfTI (.nii.gz) or (.nii);
- ROIValue : result files (.csv ou .xls) including the indices calculated from the ROI on specific image series.

1.6 Working space and directory tree

- ScreenSave : image files recorded at your request;
- ScreenSave/pdf : pdf files recorded at your request.

Directory path. Directory named "data" in which data are saved can be changed by the user in preference frame.

Files. When saving a file, the file names are set automatically for you. If needed, you can change file names later in the file manager of your system (without special rules).

Chapter 2

Protocols of LIFEx

What are the *LIFEx* protocols ?

The application can be seen as a set of functions. The different functions are sorted and arranged as a function of the choice that you make when starting a session. A specific group of functions is what we call a protocol (see Fig.2.1, p.14).

2.1 Viewer protocol

• Purpose, What is Viewer protocol?

Viewer protocol includes core functions. It lists all the functions of a radiological or nuclear medicine image viewer. Examples of core functions are:

- image reading;
- snapshot (*filmer*) and creation of a pdf;

2.2 Texture

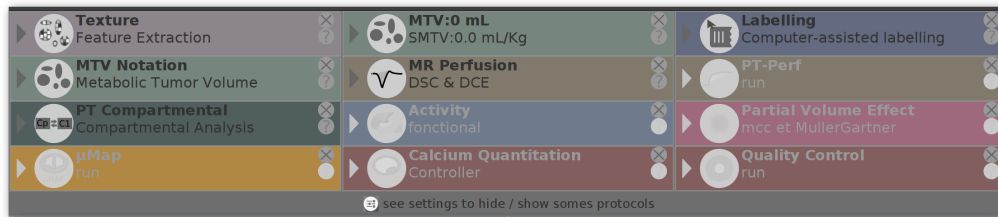


Figure 2.1 Display of the available protocols

- display of an image volume as a *panel* showing slices in the sagittal, transaxial, and coronal planes;
- management of regions of interest (ROI) including drawing, addition, edition, saving;
- management and stacking of different layers corresponding to different image series.

2.2 Textural analysis protocol

• What is Texture?

Various image analysis approaches can be used to characterize tumor heterogeneity. In PET, CT, MR and US, the 2 most frequent approaches are the methods based on the analysis of the histogram of the voxel values within the tumor and the methods accounting for the spatial arrangement of voxel values.

In the histogram-based methods, the heterogeneity descriptors (HDs) disregard the inherent spatial relationship between voxel values, only reflecting the voxel-value frequency distribution. They include the mean, SD, median, skewness, kurtosis, entropy, and energy and are called first-order statistics (FOS).

The second approach accounts for the spatial arrangement of the voxel values within the tumor using higher-order statistics by first calculating a 2-dimensional matrix describing this spatial organization. This matrix is often the gray-level cooccurrence matrix, giving the probability of observing a pair of voxel values at a given distance in a given direction. Several other matrices are also used, among which are the neighborhood gray-tone difference matrix, which provides information regarding how each voxel value differs from the neighbor voxel values; the gray-level run length matrix, which stores the number of voxels with identical values in each direction; and the gray-level size zone matrix, which stores the size of the 3-dimensional region that includes a given voxel value. All these matrices capture some spatial relationship between voxel values, and each matrix enables the calculation of several HDs, therefore yielding several dozen HDs

• What is the Texture protocol?

Texture protocol is thus a protocol dedicated to the extraction of advanced image features. All the matrices mentioned above are calculated in this protocol.

- **Scripting procedure**

Purpose. Scripting procedure for texture calculation without user interaction.

Rationale. When you have a large number of ROI and/or a large number of patients in which you want to calculate whatever features, it can be convenient to run a script that will do all the calculations for you without any user interaction. ROI have to be prepared beforehand, only once. You can then run the script many times if you want to perform the calculations using different sets of parameters.

See scripting example in the "Texture User Guide" ([link](#)).

- **Read more**

The technical and bibliographical aspects of textural analysis and radiomics features are defined in the "Texture User Guide" ([link](#)).

2.3 (Total) Metabolic Tumor Volume protocol

- **What is MTV?**

In PET, beyond SUV, other metrics for analysis of tumor FDG uptake include the (total) metabolic tumor volume (MTV) and an index called total lesion glycolysis (*TLG*). MTV measures the volume of FDG-avid disease, for which three-dimensional regions of interest are drawn (typically by autosegmentation using LIFEx, with some manual adjustment by the user) around individual lesions. Volumes for all lesions are then added to derive the total body metabolic tumor volume. *TLG* additionally accounts for the intensity of FDG uptake in each disease site ($TLG = MTV * mean\ SUV$ within the lesion).

- **What is the MTV protocol?**

MTV protocol is a protocol dedicated to the extraction of (total) metabolic tumor volume *MTV* and total lesion glycolysis *TLG* in FDG PET modality.

- **Read more**

If you want to read more see section "MTV Protocol Tutorials How To Extract TLG, MTV, total MTV and standardised MTV (pdf)" in the documentation specific to the MTV protocol ([link](#)).

2.4 Dynamic Susceptibility Contrast or DSC

- **What is DSC-MR?**

Dynamic Susceptibility Contrast or DSC is a method for measuring cerebral blood flow, ie blood flow to the brain. The technique requires intravenous contrast delivered through an automated power injector attached to an IV. The scanner creates an image reflecting multiple cerebral perfusion parameters including cerebral blood flow (CBF), mean transit time (MTT), and negative enhancement integral or cerebral blood volume (rCBV). These techniques are most beneficial to patients with vascular stenosis, stroke, and brain tumors.

2.5 Labeling

- **What is the DSC-MR protocol?**

DSC – MR protocol is a protocol dedicated to the extraction of in rCBV, CBF, MTT maps in MR modality.

- **Read more**

If you want to read more see section "Dynamic Susceptibility Contrast (pdf)" in the documentation specific to the DSC-MR protocol ([link](#)).

2.5 Labeling application

- **What is the Labeling application?**

The labeling protocol allows users to easily annotate images and associated regions.

It is a generic module that makes it possible to define pre-established questions/answers for application-specific annotation and to fill in a database. This database can then be exploited for machine learning or deep learning purposes.

The questions (and possible answers) are pre-defined in a script built beforehand by the user. In the script all information necessary for the annotation task is specified. The execution of the script is then a repetition of the tasks in an automatic way with automated loading of the images and of all menus needed for the annotation. The filling in of the annotation tasks is followed by a controller that monitors and displays the progress of the script. The user can thus know at any time the progress of his work.

- **What is the Labeling application protocol?**

The protocol consists of 3 panels that are open in the LIFEx application in three different places:

1. the controller in the master panel of the protocol (blue window at the top with the other protocols);
2. the patient selector (blue window on the left in the panel dedicated to patients);
3. the property input panel (blue window on the right next to the panel dedicated to ROI).

- **Read more**

If you want to read more see section "Labeling protocol (pdf)" in the documentation specific to the Labeling protocol ([link](#)).

2.6 Quality Control

- **What is the Quality Control application?**

Goal. This Quality Control protocol allows for the assessment of the quantification accuracy and the uniformity of a cylindrical phantom filled with an uniform activity concentration. It has been designed by the PET working group of the French Society of Medical Physics (SFPM).

- **What is the Quality Control protocol?**

QualityControl protocol is a protocol dedicated to the Quality Control in PET modality.

- **Read more**

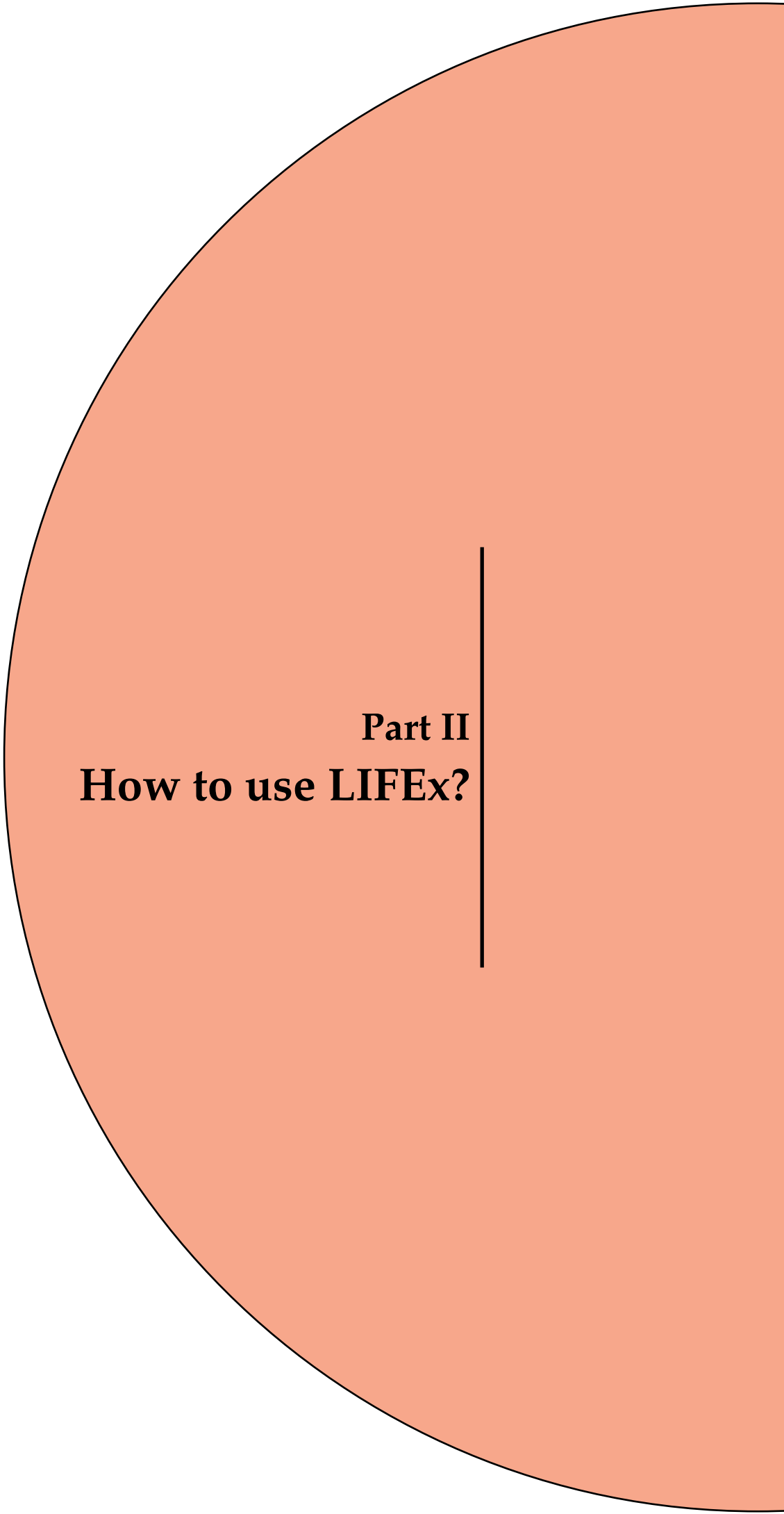
If you want to read more see section "Quality protocol (pdf)" in the documentation specific to the Quality protocol ([link](#)).

Protocols of
LIFEx

2.7 Scripting LIFEx

Scripting procedure for calculation without user interaction is available on LIFEX.

A special user guide is available under the name LIFEx-Script. You can consult it on the website in the documentation section ([link](#)). The protocols of Texture and MTV, Labeling are fully automatic with scripts. As well as many other features such as image format conversion.



Part II
How to use LIFE_x?

Chapter 1
**loading and saving
image files**

1.1 DICOM browser

The reading of images using the DICOM format is performed using the *DICOM series loading* interface ; See LIFEx tutorial: "How to open and view Dicom images? ([Tutorial link](#)).

Loading, saving image files

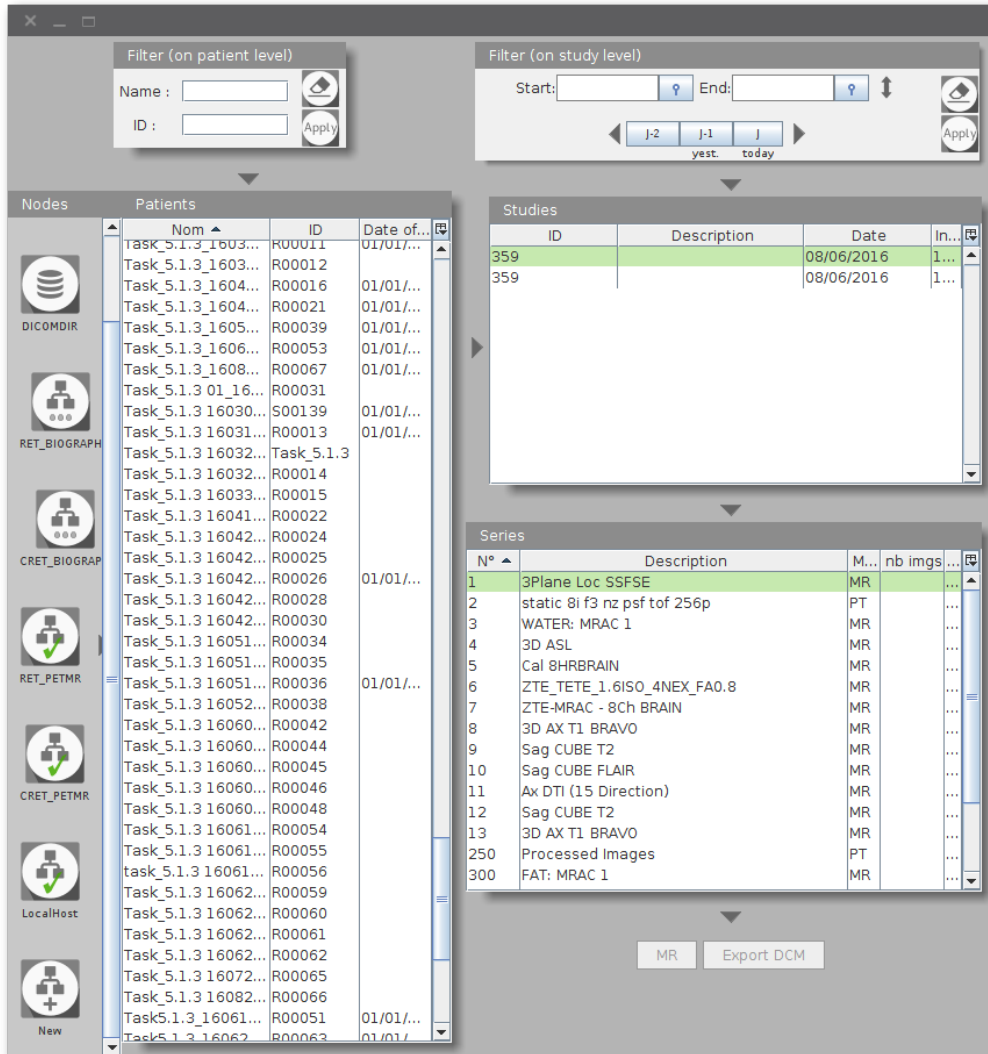


Figure 1.1 Selection of patient/scan/series

This interface supports two main functions:

- reading image files through a network connection to the distant network: The application makes a *C – GET* request to the DICOM server. This type of request does not necessitate any declaration on the distant node but is often not permitted for security reasons. If this transfer mode fails, the application then sends a *C – MOVE* request. The declaration of the two nodes in the network is needed for processing the *C – MOVE* request. The IP address, (*Internet Protocol*), AET

(*Application Entity Title*) and listening port of the distant station then need to be filled in.

Locally, adding a supplementary node in the communication interface is needed to perform *C – QUERY* request of patient lists. Click on the *Add new node* button in the node list and fill in the fields corresponding to the distant station. If you do not know these fields, please ask the software management of your facility.

The definition of the local node called "LocalHost" should be checked. The "Local-Host" hostname is set, but the default parameters AET=LIFEX and port=4006 can be changed. You should check that the IP address corresponds to the one of your network card.

In addition, you should check that:

- the ports are open on the server side but also on your local machine in which LIFEX is installed.
- the LIFEX node on your server is properly declared.

Loading, saving image files

You can open image files from your local hard disk or from a DICOMDIR simply by using a drag and drop in the main application window (the one with the LIFEX vX.Y header). Wait for a green frame around the deposit panel to appear before dropping.

The connection to the OsiriX application has to be seen as an additional DICOM node that you have to define using the parameters of the Osiris DICOM receptor of your computer (cf. OsiriX / Preferences / Receptor).

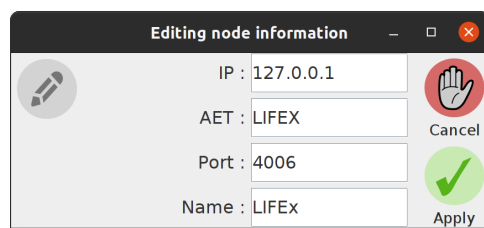


Figure 1.2 Settings of a DICOM node

- local reading of files located on the disk of your computer, or a USB memory stick, or on any file system mounting (NFS, HFS...). To do so, click on the *local Disk* button and browse your files to select one of the images of the image series you would like to read (the image number (*instanceNumber*) does not matter). The application manages all files in the directory as the whole image series corresponding to a scan.

1.2 Patient / studies / series / images selection

Patient selection. The *browser* shows the list of patients in the left part of the *Patients* window. The patient selection is performed by selecting the appropriate row in the table. When a row is selected, the application looks for the corresponding scans and displays them.

Scan selection. The list of the scan associated with the selected patient is displayed in the *Study* window. The selection of a given scan is performed by clicking on the corresponding row. When a row is selected, the application looks for the corresponding image series and display them.

Selection of an image series. The list of image series associated with a scan is displayed in the *Series* window. The selection of a series is performed by clicking on the corresponding row.

Selection of an image. The application does not enable the selection of a subset of images in a whole image set. All DICOM files are selected. Non DICOM files are ignored. The *DICOM DIRFILE* and *DICOMDIR* files do not disturb the loading of a series.

Reading several image series To read several image series, each series has to be read one after the other. Loading several series simultaneously after selecting multiple rows is not supported. The reason is that the order in which series are loaded can be important, as each new series is stacked on the previous one as a new layer. The order in which the series are acquired is often different from the order the user wants to display them. Please see section Warning 1 p.30.

The application consists of the following windows:

- the left hand side window (image management dialog box) also called main control window as the protocol header and includes the following operations: file reading, series stacking, addition of views, *filmer*, *panel*, preference interface, and application exit;
- the central windows are the display windows, corresponding to the axial, coronal and sagittal views;
- the right hand side window is the ROI/mask manager.

1.3 Saving images

Saving images Images loaded in the application can be saved using one export button (nii). This button is at the bottom of the image management dialog box.

Choice of the series to be saved When several image series have been loaded, please select the image management dialog box corresponding to the image layer you want to save using the export button.

File format Supported format: Nifti-1 (.nii extension). If the file is compressed, the file name ends by .gz.

Save units The user can choose the units in which the file is saved. The units are defined the same way as the TAC units when plotting curves or as the units used for displaying values using the cursor. For instance in PET, if the values are displayed in SUV units, the file will be saved in SUV units as well. The setting of the slope/intercept values associated with the file content is automatically managed. Supported units are SUV, Cps/vx, kBq/mL, or native(#) and the corresponding file names include "SUV", "Cps_vx", "kBq_mL" or "#".

Reading previously saved image series The application can re-read the saved images: the units will be automatically determined based on the file name and displayed accordingly.

1.4 Dicom registration file (DICOM-REG)

Loading, saving image files

Scope and Field of DICOM-REG: The Spatial Registration instance defines a transformation from its own local Reference Coordinate System (Patient, image B) to that of the reference image (image A)

Multi-Modality Fusion: A software registers images from independent acquisition modalities PET, CT, MR, NM, and US or from multiple series. The software stores the registration parameters for subsequent visualization and image processing. Such visualization may include side-by-side synchronized display, or overlay (fusion) of one image on the other. LIFEx can handle the images and corresponding registration file so as to properly display the realigned images.

Dataset Fusion, step by step:

- load series A: this will be the reference series ;
- load series B: to be registered on series A ;
- load the DICOM-REG file exactly as if you were loading an image.

Be careful: you must have loaded the two series to be registered in the application before loading the DICOM-REG file.

Proceeding step: Reading this DICOM-REG file will generate the following actions:

- reading the unique reference information of the two series A (reference) and B ;
- reading the transformation matrix to convert coordinates of series B into coordinates of reference series A ;
- extraction of transformation matrix to convert coordinates of series B into coordinates of reference series A ;
- checking that series A and B are loaded in LIFEx ;
- application of the transformation matrix to image B (rotation + translation) so as to align it with reference image A ;
- update ROI statistics results if some are already displayed.

Chapter 2
Main control window

2.1 Presentation of the main control window

2.1 Presentation of the main control window

The control window includes the following elements (cf. fig. 2.1):

- an upper toolbar (see "Patient button" in fig. 2.1 and sections below) ;
- a middle toolbar (see Applied to selected series in fig. 2.1 and sections below) ;
- dialog boxes corresponding to the loaded image series (see "ref:PT..." in fig. 2.1, and sections below) ;
- a bottom toolbar (see "Help" in fig. 2.1 and sections below) ;

Main control window

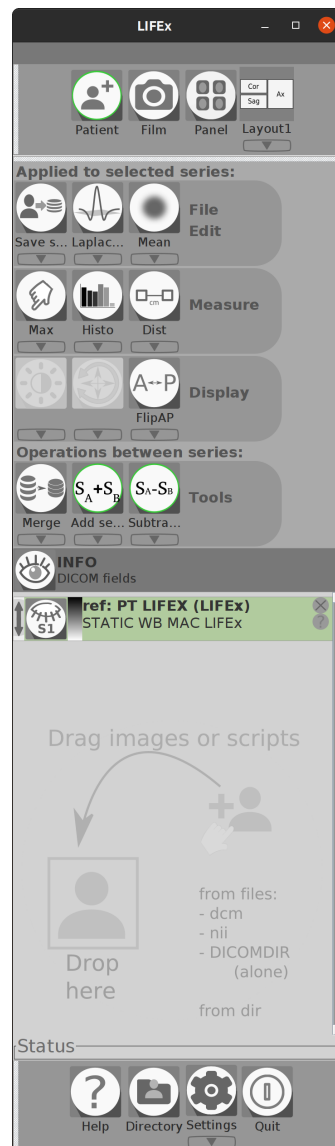


Figure 2.1 Presentation of the control window

2.2 Control window toolbar

Upper toolbar. The functions of this toolbar are as follows:

- reading a new image series using the *Series loading* frame;
- building a pdf booklet including screenshots that you perform any time during your work session;
- displaying a window including all slices in a given orientation;
- 6 display options (template Layer 1 (L1) to Layer 9 (L9)).

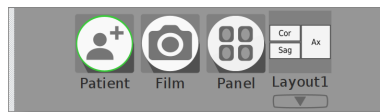


Figure 2.2 Top toolbar

Bottom toolbar. The functions of this toolbar are as follows:

- accessing the help panel of LIFEx;
- accessing the local directory of your computer;
- accessing the preferences of your applications; for instance, you can change the path of data saved, the name of your institution, the department and the corresponding address. The created pdf files will therefore be customized.
- Application exit.

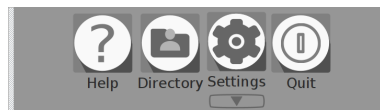


Figure 2.3 Bottom toolbar

Main control window

2.3 Management of volumes (of series)

Definition of a series layer. A layer is the display interface of an image series. Each display window is a stack of layers with an image series in each layer. The layer transparency can be managed by varying the *alpha* opacity parameter (cf. alpha parameter, p.31 et 54).

Definition of the reference image series. The first series that is read is called the reference series. This reading operation opens a new work session, and the settings used for this series will also be used for all other subsequent series and for the regions of interest (*Region Of Interest, ROI*). New image series are then displayed as new layers on the reference series. The ROIs are open using the matrix format of the reference image series. .

2.4 Reordering image series with layers

Warning 1. If you have several image series to be read, it is recommended that you open first the one that you want to be overlaid with any other one. It often corresponds to the 3D MR or to the CT when you open a PET/MR or a PET/CT study for instance. All registration information and ROI-related information (for instance if you draw a new ROI) will be associated with this reference series.

Warning 2. In a longitudinal study, the order of the image series of the first study should be carefully chosen. When you read a subsequent study, the same order as that used for the initial study should be used. Using a different order might mixed up ROIs and registration parameters.

Warning 3. In textural analysis, the ROIs should be drawn from the reference series.

However, it is possible to calculate textural features in the ROIs from a different series than the reference one.

Main control window

2.4 Reordering image series with layers

It is possible to change the layers order of the series after loading them. For example, it is possible to display the MR-DIFFUSION series before the BR_CTAC_TOTAL-PT series (see fig. 2.6). To do it, just click on the left border of the title (It easier when the dialog box is not developed).



Figure 2.4 Reordering image series with layers

Important note: The position (=layer) of the reference series can also be changed as that of the other series. Nevertheless, this series will always remain the reference series for drawing ROI and will be called "← ROI Reference".

Additional note: It is needed to adapt the alpha coefficient of transparency assigned to each layer when changing the layers order for an appropriate image rendering.

2.5 Volume management

Management of the stacked volumes. The volume of the reference series is always displayed as the background. The additional volumes are stacked onto that volume, and transparency (the vertical cursor alpha%, showed right on the image) can be tuned using the vertical slider on the right hand side that sets the alpha transparency value; a 0% value corresponds to a full transparency of the image, meaning that is not displayed. A 100% value corresponds to an image that is fully displayed without any transparency, so that the images behind cannot be seen. The order of the different layers in the stack can be changed.

Selection of the active image series. When you load more than one image series, the selection of a specific series makes it active, while all other series are inactive. Only one series can be active at a given time. The active series can be recognized through the green background in the header of the corresponding dialog box. When running a function, this function will affect only the selected image series, while the other series will remain unchanged. For instance, if you load 3 image series and select the second one, and then want to get the maximum value in a ROI using the dedicated button in the toolbox, the maximum value will be calculated in series number 2, and the 3D pointer will be located in the corresponding voxel of series 2.

Main control window



Figure 2.5 Example of dialog box associated with the reference series (note the green background of the header)

Tools associated with the volumes. Some tools associated with the series are within the corresponding dialog box of each series. For instance, the DICOM *header* information, which depend on the series and not on a given ROI, is shown by clicking on the question mark in the series dialog box.

2.6 Volume registration

Volume registration. Image registration can be performed. These registration operations are needed when new loaded series have not been acquired during the same scanning session as the reference series, for instance in longitudinal studies, or when a patient has moved during a given imaging session.

2.6 Volume registration

The reference series is fixed. The other series should be registered to this reference series.

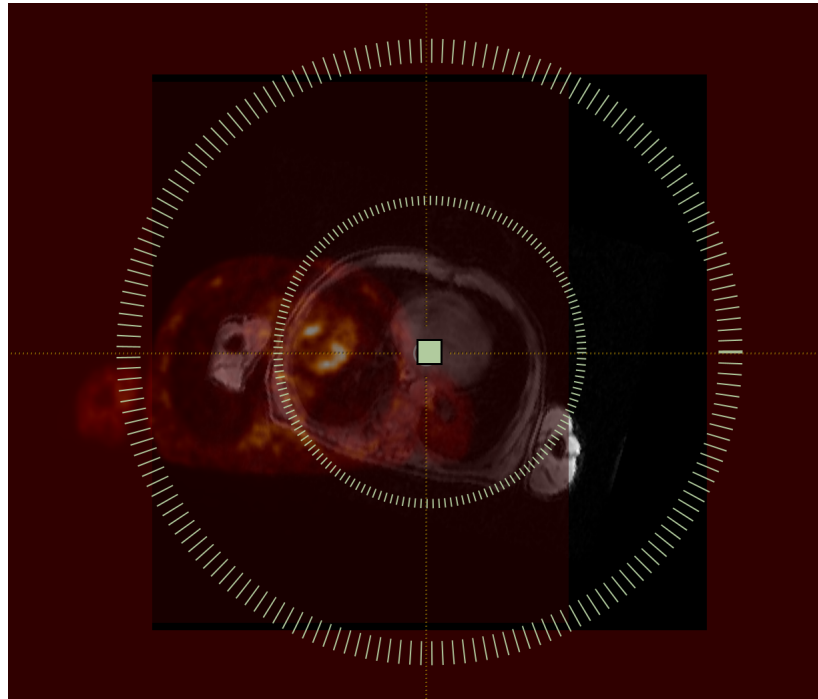


Figure 2.6 Reordering image series with layers

If needed, you can use the *Trans/Rot* button, and run the manual translation and rotation operation.

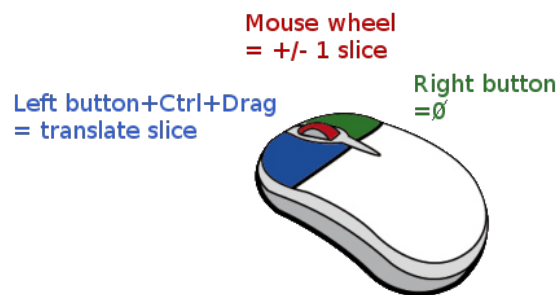


Figure 2.7 Manual translation of image series using the mouse

Manual translation. After clicking on the translation/rotation (*Trans/Rot*) button, press the *Ctrl* key and translate the images in the appropriate center using the **left button mouse**. The volume can be translated with the little green square in the three plans successively. Once the translation gives a visually satisfactory result, it can be applied on the image volume by clicking on the *Apply* button. All statistics regarding the ROI are then updated.

2.6 Volume registration

Manual rotation. After clicking on the translation/rotation (*Trans/Rot*) button, press the *Ctrl* key and rotate the images in the appropriate angle using the **left button mouse**. The rotation center corresponds to the actual center of the image. The volume can be oriented in the three plans successively. Once the rotation gives a visually satisfactory result, it can be applied on the image volume by clicking on the *Apply* button.

**Main control
window**

Chapter 3
Display windows

3.1 Main principles

3.1 Main principles

Manual positioning of the display windows. The application keeps in memory the position and size of the 3 main windows when you exit the application. From one session to another, these windows will therefore appear identically.

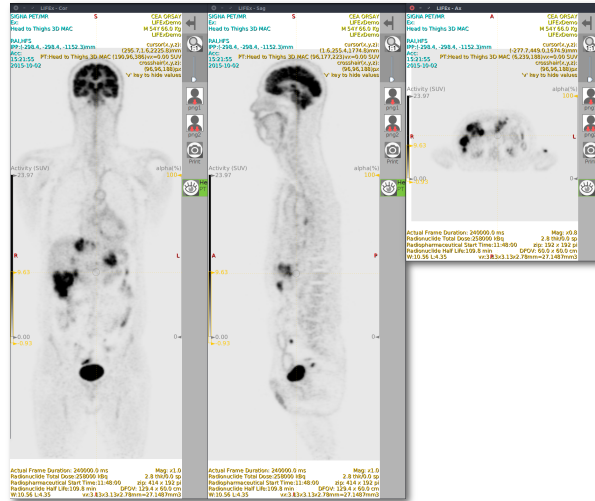


Figure 3.1 (Whole Body) display

Display windows

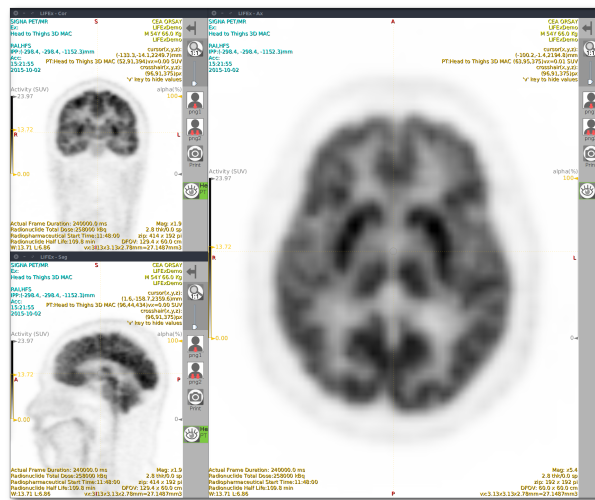


Figure 3.2 Square (Square) arrangement of the display windows

Automatic positioning of the display windows. Many templates positioning of windows are available. For example:

- *Whole Body* - The template layer number 5 (L5) button automatically restores the initial positioning of all the application windows. The window arrangement has been designed so as to facilitate the display of a whole-body scan (see fig. 3.1 p.36).

- *Square* - The template layer number 4 (L4) button automatically restores the initial positioning of all the application windows. The window arrangement has been designed so as to facilitate the display of the three views in the three sagittal, transaxial and coronal plans of a scan, for instance a brain scan (see fig. 3.2, p.36).

3.2 Presentation of the composition of the display

The figure 3.3, p.37 shows an example of windows showing a coronal view.

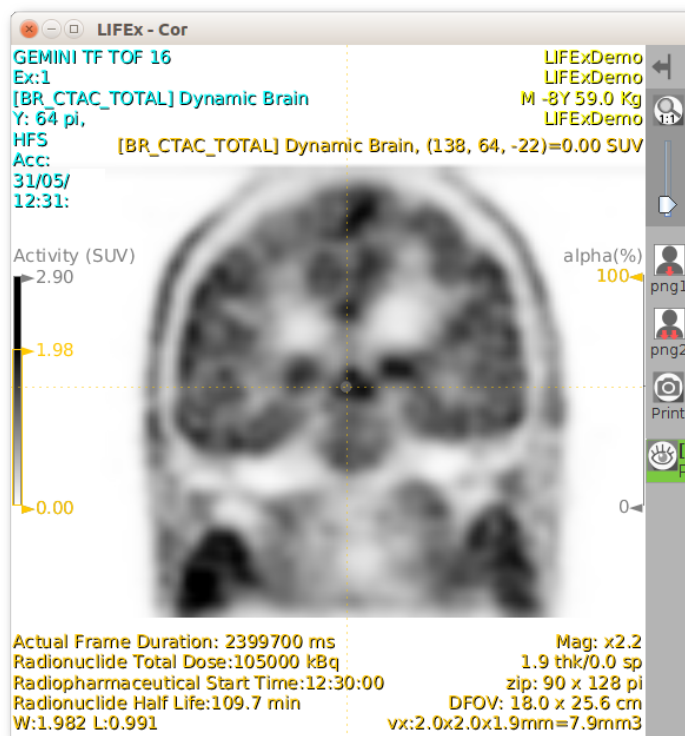


Figure 3.3 Example of a display window showing a coronal view

Display windows

3.3 Moving through an image volume

Moving through an image volume. The 3D display in the 3 orientations (sagittal, coronal and axial) makes it possible to navigate through the image volume. To navigate through the volume, the user can use three methods:

- move the **mouse wheel** up or down; the slices move one by one (1 step corresponds to +/- 1 slice) ;
- if there is no mouse, after selecting the appropriate window, the keyboard arrows can be used to move through the slices (1 click = +/- 1 slice);
- using the pointer (cross within a circle) after selecting it using the **left button mouse** and sliding it at the target position;

3.3 Moving through an image volume

- using click on the **left button mouse** directly at the target position with *Shift* key down (no need to use the 3D pointer).

The volumes are always aligned with the workspace associated with the reference series. If you navigate through a given image series, all stacked series will be affected so that all images remained realigned. Figure 3.4 p.38 indicate the main commands for volume display accessible through the mouse.

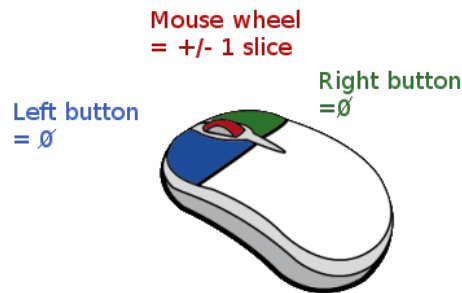


Figure 3.4 Management of the volumes using the mouse

Image display and associated functions. The image is displayed and centered within the window. Several actions are available:

- as a general rule, pressing the *Shift* together with another function assigns this function to all open windows;
- moving the view: using the *Ctrl* + **left button of the mouse** + moving the mouse;
- applying a zoom : using the *Ctrl* + **mouse wheel** to adjust the zoom level;
- tuning the image windowing: using the **middle button of the mouse** and moving the mouse: horizontally for the level (*WL window leveling*) and vertically for the width (*WW window width*) ; the windowing is always applied to all windows simultaneously;
- changing the color scale. The color scale can be changed using a **left click** on the color scale shown on the left of the image. Successive clicks allow one to go from one color scale to another among the 6 predefined color scales (monochromatic, inverse monochromatic, rainbow, inverse rainbow, hot, inverse hot). An additional click makes it possible to get back to the initial color scale (monochromatic).

Composition of the toolbar. This toolbar is related to the display window content only and does not affect the rest of the application (figure 3.5 p.39) . It consists of:

- The management of this dialog box is the same as the management of the command window except that all actions will be applied only to the selected window. When you add some windows and some series, this allows you to have additional views (for instance two axial views), to display one series in one window and another series in a second window in the same plane. This function is especially useful for multimodality imaging. All windows are always spatially synchronized.
- a zoom button and slider ; the button performs a 1 : 1 zoom to get back to the default zoom ; the slider starts zooming in one direction or another. To zoom all windows simultaneously, the *Shift* key should be pressed when zooming;

3.3 Moving through an image volume


- buttons to save screen snapshots in the working directory. You can capture a slice or as many slices as contained in the view.
- print button that allows to transfer screenshot of display into a booklet;
- the stacking of layers (eye) and alpha blending (slider) of layer of image.



Figure 3.5 Composition of the toolbar of image panel

Display windows

Chapter 4
Image filters



4.1 General caution

Caution on texture protocol, the intensity bounds of the image change when applying this filter and the new values must be taken into account for setting the discretization parameters in the texture.

4.2 Boundary conditions

These boundary conditions are defined in IBSI2 documentation available here: [IBSI2-filters](#): Constant Value Padding / Nearest Value Padding / Periodisation / Mirror. Please feel free to consult this more complete documentation.

4.3 Bounding box conditions

- on whole body: no ROI required. The filter is performed on the whole image.
- on bounding box without padding: on the exact bounding box of the activated ROI without additional padding (the boundary conditions are applied)
- on bounding box with padding: on the bounding box of the activated ROI with an extra padding to avoid edge effect. If the ROI location allows it, otherwise the boundary conditions are applied.

4.4 Mean/Laws/Gaussian/Laplacian of Gaussian filter/Wavelet filters

Mean, Laws, Laplacian of Gaussian, Wavelet filters from the version v6.9.0.

Gaussian filter from the version v7.2.0.

The documentation of these filters is included in the IBSI2 documentation available here: [IBSI2-filters](#). These filters of LIFEx are Image Biomarker Standardisation Initiative (IBSI) compliant with consortium requirements.

4.5 Series tool

4.5.1 Series Random tool (v>=7.6.2)

Main principles. The series random function is used to create a new series from the selected series. This new series will be the result of moving the position of the voxels according to a random sequence. The statistical results will therefore be identical in value (same min, max, mean or stdev value). However, features such as the peak (1st order) or the texture (second order) will be modified in their results.

How to activate the tool. To validate the tool, select one series and one ROI. Only the voxels in this ROI will determine which voxels in the series will be randomly moved.

Warning. Each time you use this function, you will get a different result.

4.5.2 Series Merger tool

Series merger tool. The "Series merger" tool allows you to create a new series that will contain several other series. The new series can be saved in dcm and nii formats among others.

This tool can be used when the examination is composed of several acquisitions (when the InstanceNumber field is different) in order to create a single series of images.

Some remarks about this tool:

- the merge will include all the series visible during the action. If you don't want a series to be included, just make it invisible (disable the viewing eye);
- the field of view (FOV) of the new series shall be calculated to include all FOVs of each series taken separately;
- the resolution (Z, Y, X spacing) of the new series will have the resolution of the series selected before run the action.

Step by step explanation(see tutorial video):

- load all the series in the application;
- choose and select the series to be used as reference (output resolution);
- click on the "Series Merger" button;
- possibility to save the new series with the "nii" or "dcm" buttons.

Image filters

4.6 CT Patient Table Eraser

CT Patient Table Eraser (v6.0.0) - Tools dedicated to CT images. Although 3D-slice display of x-ray CT with patient table is routine it is desirable to remove the table for some subsequent image display and analysis.

Figure 4.1 p.44 shows patient tables from Philips, General Electric, and Siemens PET/CT as well as CT scanners. Considering the availability of other scanners and vendors, the variation is even higher.

GUI in LIFEx. For advanced 3D display and visualization, as MIP (fig. 4.2), it is necessary to remove the patient table from 3D CT slices. There are two techniques that can be used for that purpose in LIFEx: (fig. 4.4):

- Fully automated table removal with no interactive operation required
- Manual deletion of CT table from a single axial ROI.

4.6 CT Patient Table Eraser

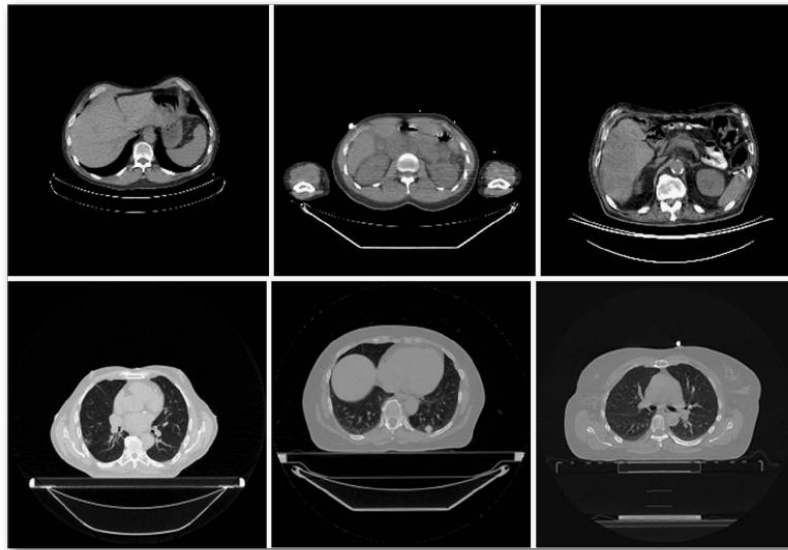


Figure 4.1 CT acquired on Philips, General Electric, and Siemens PET/CT scanners (top row) and their CT scanners (bottom row). Ref: Automatic Patient Table Removal in CT Images, Yang-Ming Zhu, Steven M. Cochoff and Ronald Sukalac, J Digit Imaging. 2012 Aug; 25(4): 480-485

Fully automated table removal with no interactive operation required. A robust, automated, table identification and removal method is independent of table characteristics is implemented in LIFE_x. The tools used are morphological tools (open, close, keep one of center object).

This algorithm works in 99% of cases. A possible error occurs when there is more than one "object" on the table. For example, if a field of view includes only the 2 legs, it is complicated to find a single object in the image.

Manual deletion of the CT table with a single transaxial ROI. In cases where the automatic mode does not work, it is possible to manually remove the table using an axial ROI roughly centered in the volume to be deleted. Draw a ROI that completely encompasses the table (ie the region you want to get rid of) in a transaxial slice. This volume will be repeated on all z (see fig. 2.3-B).

This method therefore only works when the axis of the table is parallel to the central line of the sagittal plan.

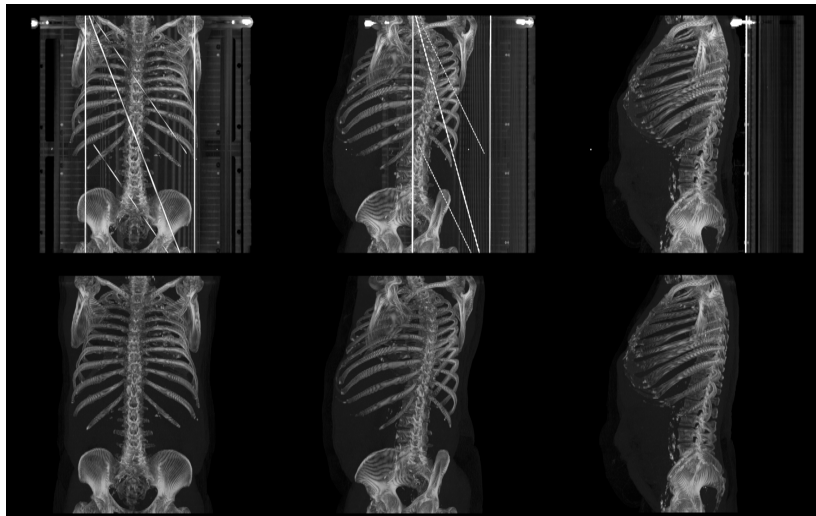


Figure 4.2 MIP view produced with LIFEx with patient table (top row) and without table patient (bottom row).

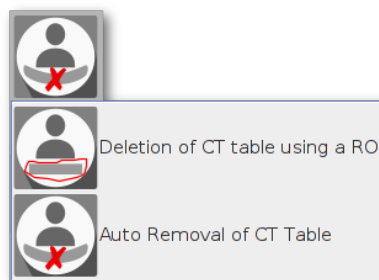


Figure 4.3 Graphic user interface including the two options for removing the table in CT scans.

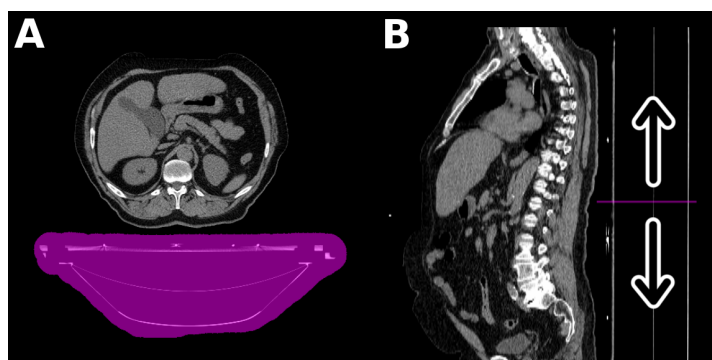


Figure 4.4 Manual deletion of CT table using a ROI drawn on a single transaxial slice

Chapter 5
Window for ROI control

5.1 Main principles

Background. The command window for ROI management includes two parts: one includes the different tools while the other includes the dialog boxes associated with each ROI.

5.2 Description of the tools

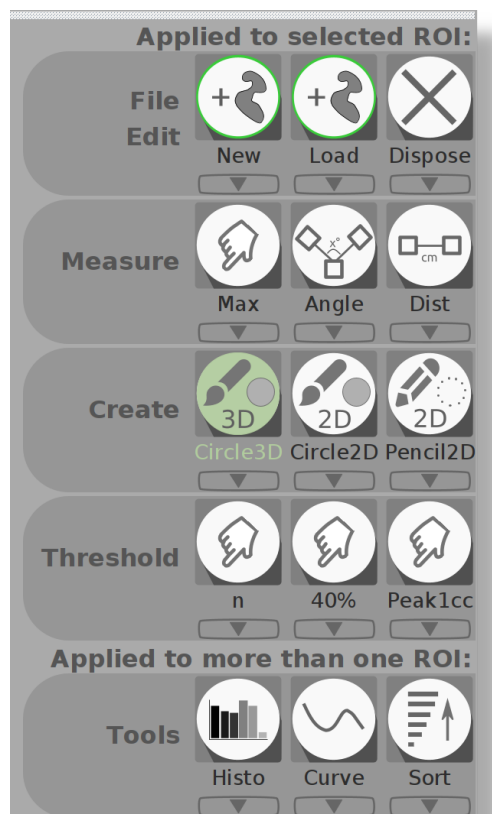


Figure 5.1 ROI toolbox

The toolbox includes several functions (see figure 5.1):

- loading series in *NIfTI* (.nii extension) format, loading RTSTRUCT object from DICOM-RTSTRUCT file;
- erase full content of selected ROI;
- hide/show buttons for all ROIs: this is equivalent to changing all ROI layers using the eye button simultaneously;
- creating a new ROI: creates a new dialog box corresponding to a specific image layer. The drawing can be performed directly on the image;

- copying a ROI: copies the active ROI and creates the corresponding dialog box;
- creating the union of ROIs including all selected ROI (using the eye button). This operation also creates a new dialog box corresponding to the resulting ROI;
- ROI interpolation: You must have selected at least two non contiguous 2D axial slices on same ROI to calculate the intermediate volume at these two slices; This tool is available only on axial slices.
- creating a mirror ROI with respect to the sagittal plan and the corresponding dialog box;
- split a ROI: The basic idea of region splitting is to break the ROI into a set of disjoint regions. Disjointed areas that do not have at least 4 voxels are eliminated.
- keep one cluster (locate under cursor) tool; In order for the tool to work correctly, you must first adjust the crosshair on the area to be kept.
- eroding a ROI in 3D using an erosion with a spherical structure element de n voxels in diameter;
- dilating a ROI in 3D using a dilatation with a spherical structure element de n voxels in diameter;
- closing a ROI in 3D using a dilatation followed by an erosion with a spherical structure element of 10 voxels in diameter;
- modifying a ROI using a 2D disk or 3D sphere (*Shift*+left click using the mouse to draw, *Shift*+right click using the mouse to erase);
- modifying the ROI using a filling tool in 2D / 3D (*Shift*+wheel upward for positive values + wheel downward for negative values);
- modifying the ROI using a snake tool in 2D / 3D, see section 5.3.7 p.53 ;
- filter definition as a function of the maximum value in the ROI, see section 5.3.5 p.51;
- filter definition using absolute (tool n) or relative values (tool n%), see section 5.3.6 p.51;
- ring dilatation (to the outer edges)
- V40% creation of a ROI defined using a 40% threshold with respect to the maximum value in the ROI. The lower values are not included in the ROI.
- V70% ; same as 40% but using a 70% threshold;
- Nestle segmentation, see section 5.3.3 p.50;
- CBM, Contrast Based Method;
- drawing a so-called Vpeak (0.5 mL or 1 mL) spherical region; the 3D pointer is then located on the maximum value of the resulting ROI.
- drawing a so-called Vmax region ; the 3D pointer is then located on this maximum value.
- definition of a ROI using the method by Nestle;

5.3 Segmentation tools

- The "click and draw" method (specially designed for PET images), see section 5.3.1 p.50;
- display curve plot of ROI, "curve" tool;
- translating of ROI on images, "move" tool;

5.3 Segmentation tools

5.3.1 Click (and draw)

The "click (and draw)" method (specially designed for PET images) creates a VOI from the initial point that is clicked using the following approach:

- reading of the intensity (I) of the point the user clicked on
- $SegF$ = 3D flood filler algorithm stopped at $I * 70/100$
- if $volume(SegF) > 500\text{cm}^3$ = error "Out of allowed size"
- I_{max} = maximum intensity in $SegF$
- $SegN$ = Nestle formula (with $\beta = 0.3$ and I_{max}) yields the so-called Nestle threshold ($ThresN$)
- $SegResult$ = 3D flood filler algorithm stopped at $ThresN$

The result might be similar to that obtained using 40% thresholding but will be more robust to the background signal surrounding the tumor area. This click and draw method is part of the adaptive threshold menu.

5.3.2 Click40

The "click40" method is a variant of the tools "Click and draw". The step $SegF$ is made with $I * 40/100$ instead of $I * 70/100$.

5.3.3 Nestle Segmentation

The Nestle volume is automatically delineated using the approach described by Nestle et al [Nestle2005] for PET imaging where the threshold (T_{nestle}) is defined by: $T_{nestle} = \beta * I_{70} + I_{bgd}$. The mean tumor uptake I_{70} is the mean uptake value in a contour containing all voxels with an uptake greater than 70% of the maximum uptake. I_{bgd} is defined as the mean uptake in a shell of 4 mm thickness located 12 mm away from the region used to calculate I_{70} . Voxels with uptake greater than 2.5 SUV units are excluded from the calculation of I_{bgd} .

The β parameter depends on the acquisition device and acquisition and reconstruction protocols. It can be estimated using phantom experiments. A convenient phantom is one including spheres of different known radii (for instance the NEMA phantom including 6 spheres) in which the sphere to background activity ratios are typical of those encountered in real patients. The β parameter that make the V_{nestle} volumes closest to the known sphere volumes should be used. This β value can be obtained by plotting or graphical fit.

As an example, a β value of 0.237 was found optimal using a FDOPA-PET acquisition with a Philips Gemini TF (Philips Healthcare, Cleveland, Ohio) based on 3 acquisitions of a NEMA quality image phantom including 6 spheres of 0.52, 1.15, 2.57, 5.57, 11.49 and 26.52 mL, with sphere to background activity ratios varying from 8.4:1 in the first acquisition, 5.06:1 in the second, and 2.59:1 in the third, when the images were reconstructed using a RAMLA algorithm without regularization parameter and 2 iterations.

Ref:

- value **0.15 of beta**: Nestle U, Kremp S, Schaefer-Schuler A, Sebastian-Welsch C, Hellwig D, Rube C, Kirsch CM. Comparison of different methods for delineation of 18F-FDG PET-positive tissue for target volume definition in radiotherapy of patients with non-Small cell lung cancer. *J Nucl Med.* 2005 Aug;46(8):1342-8
- value **0.30 of beta**: Maisonobe JA, Garcia CA, Necib H, Vanderlinden B, Hendlisz A, Flamen P, Buvat I. Comparison of PET metabolic indices for the early assessment of tumour response in metastatic colorectal cancer patients treated by poly-chemotherapy. *Eur J Nucl Med Mol Imaging.* 2013 Jan;40(2):166-71

5.3.4 Contrast Based Threshold of segmentation

The Contrast Based (CB) volume is automatically delineated using the approach of contrast vs background for PET imaging where the threshold (T_{CB}) is defined by: $T_{CB} = 0.5 * SUV_{peak} + SUV_{bgd}$.

The SUV_{peak} is a (1 mL) spherical region located on the maximum value of the ROI. If the volume is less than 1 mL, a 0.5 mL sphere is used instead. This threshold is not computed. If the initial region doesn't encompass a 0.5 mL spherical region this threshold is not computed.

The mean background uptake SUV_{bgd} is defined as the mean uptake in a 3D shell of 1 vx thickness located 2 cm away from the region corresponding to all voxels with a value greater than 70% of SUV_{max} . Voxels with uptake greater than 4 SUV units are excluded from the calculation of SUV_{bgd} .

The resulting ROI includes all voxels of the initial region with an uptake greater than or equal to T_{CB} .

ROI control

5.3.5 Filter definition as a function of the maximum value in the ROI

This segmentation corresponds to using a percent threshold of the maximum value in the selected ROI (ie the selected ROI) to define a new ROI. The voxels with values strictly lower than the threshold are out of the resulting ROI. The threshold is defined in the dialog box (fig. 5.2) that appears when a segmentation is requested (tool n%).

This segmentation method automatically creates a new ROI as a function of the initially selected ROI and of the threshold. This new ROI can be renamed by double-clicking on the ROI window header.

5.3 Segmentation tools

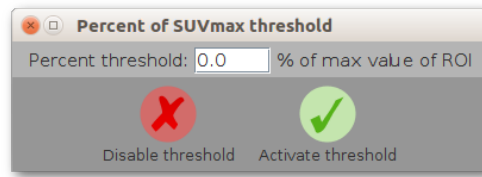


Figure 5.2 Dialog box of filter definition as a function of the maximum value in the ROI

5.3.6 Filter definition using absolute or relative values

A filter using absolute or relative values can be combined with the *DRAW 2D* or *DRAW 3D* tools. This filter can be activated using the *activate filter (on selected ROI)* button, and can be de-activated using the *unactivate filter* button of the dialog box, figure 5.3 p52. When using this filter, the minimum and maximum values setting the range of values defining the ROI should be filled in.

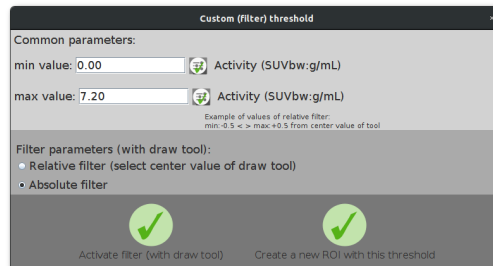


Figure 5.3 Dialog box of filter definition using absolute or relative values

"Relative filter". When using a so-called relative filter, this select the values from the *DRAW 2D* or *DRAW 3D* tool as a function of the value of the central voxel of the initial ROI (ie current layer) in the selected image. When you move the ROI drawing tool, the value of the central voxel changes and the filter result is readjusted to account for that change.

ROI control

The minimal and maximal bounds to be defined in the dialog box should have a negative sign for the lower bound (*minValue* field) and expressed in the unit in which the image is expressed. This unit appears in the dialog box (1st row).

Beware: the filter result depends on:

- the initial value in the current image;
- the minimum and maximum bounds of the filter;
- the selected ROI layer;
- the position of the ROI drawing tool.

"Absolute filter". For using a filter expressed in absolute values, the result will be calculated from the current position of the *DRAW 2D* or *DRAW 3D* tool as a function of the range bounds defined in the dialog box. These bounds have to be expressed in the unit in which the selected image is displayed. This unit appears in the dialog box (1st row).

The absolute filter can be applied using two methods:

- the first method is identical to that used for the relative filter. Please use the *activate filter (on selected ROI)* button and use that filter before the ROI drawing. The ROI drawing will then be in line of the filter parameters.
- the second method consists in applying the filter after the ROI drawing using the *run threshold and create a new ROI* button. This action will add an extra ROI layer that will be named after the original ROI and the bounds. The initial ROI will not be changed and the result will of the filter will define the new ROI corresponding to that new layer.

5.3.7 Use of (2D, 3D) snake tools

1. First set an initial point by clicking the left mouse button + shift key and KEEP down this left button and shift key till the end of action.
2. Then, just do 1 step of rotation (to top direction) of mouse wheel, wait for the processing to visualize the change, and repeat this step if necessary. If one wheel step produces a too large change, just do one inverse step of rotation, and wait for the processing to visualize the result.

The processing time depends on your processor. The snake tool is one of the most time consuming tools.

3. When you have finished your segmentation, release the left button and shift key.

5.4 ROI dialog box

This dialog box includes all dialog boxes corresponding to the different ROIs and associated layers. For each layer, there is a corresponding dialog box, and conversely.

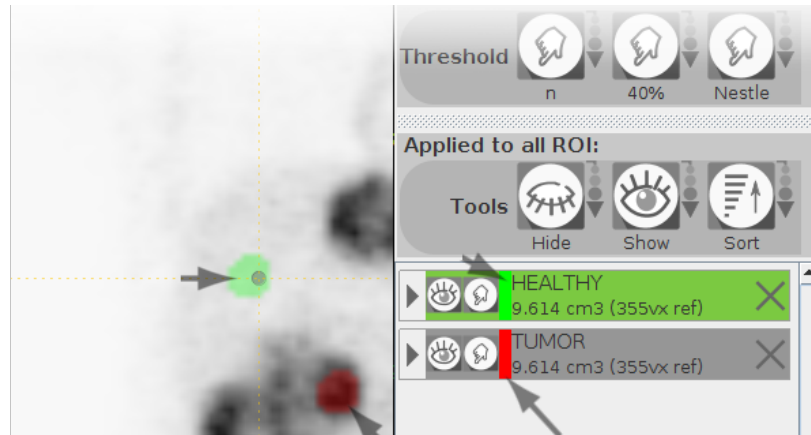


Figure 5.4 Examples of ROI layers: a ROI corresponding to the healthy tissue (*Healthy*) is selected while the ROI corresponding to the tumor tissue (*TUMOR*) is not.

The dialog box includes two parts (cf. fig. 5.5):

- a header (cf. top of fig. 5.5) :
 - the visibility of the ROI (cf. eyes in fig. 5.5) with a possible action on the eye to display or not the corresponding layer.
 - the marking of the ROI max value : move image to this location value
 - changing the ROI color on the layer (cf. color rectangle in fig. 5.5).
 - ROI name (cf. title in fig. 5.5) that can be changed using a double left click.
 - closing the ROI, (cf. close button): The corresponding file is not removed.
- an option area (cf. end of fig. 5.5) :
 - alpha tuning in the corresponding layer (cf. Blending in fig. 5.5);
 - expanding the information zone (arrow in fig. 5.5);
 - information zone displaying the statistics associated with the ROI (bottom of fig. 5.5);

5.5 Special case of ROI RTSTRUCT

The RTSTRUCT *radiotherapy structure set* object is supported by the application. It makes it possible to read regions of interest (ROI) that have been created and stored using a different software. This RTSTRUCT file can include multiple ROI. They will all be read and appear in the dialog box as additional layers.

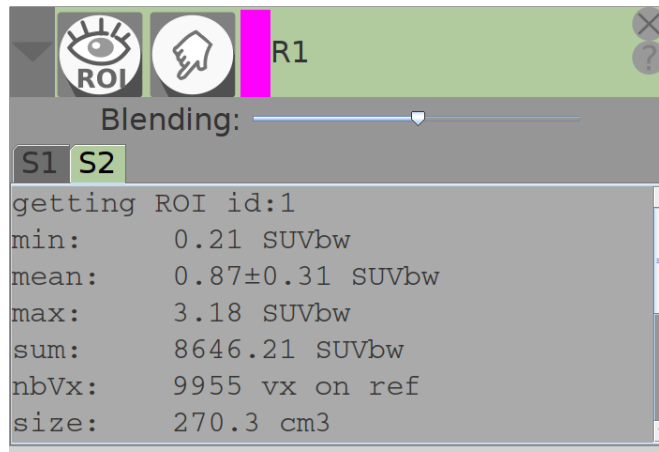


Figure 5.5 ROI dialog box

Be careful! a RTSTRUCT file must be read after reading the reference series it applies to, and this reference series should be the one used to create the ROI stored in the RTSTRUCT file. The reference series of RTSTRUCT may be different from the first series loaded in LIFE_x (Remember to activate the correct series before reading RTSTRUCT). Otherwise a warning will be displayed and the corresponding ROI may be truncated.