LIFEx v6.00
Announcement
— LIFEx —

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BioMaps

Inserm
La science pour la santé
From science to health

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What is new?

LIFEx version 6.00
Last update of document: 2020/04/30

Acknowledgements

Dear LIFEx users,

We are pleased to announce the release of LIFEx v6.00. Do not hesitate to download this new release and replace your old LIFEx version.

We would like to take this opportunity to thank all 3.000 LIFEx users for their feedback and relevant suggestions. We took into account your comments to enhance the software and produce this version. We hope you will enjoy it.

Your feedback will always be welcome.

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

Please note that the correct reference to be cited is:
C Nioche, F Orlhac, S Boughdad, S Reuzé, 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

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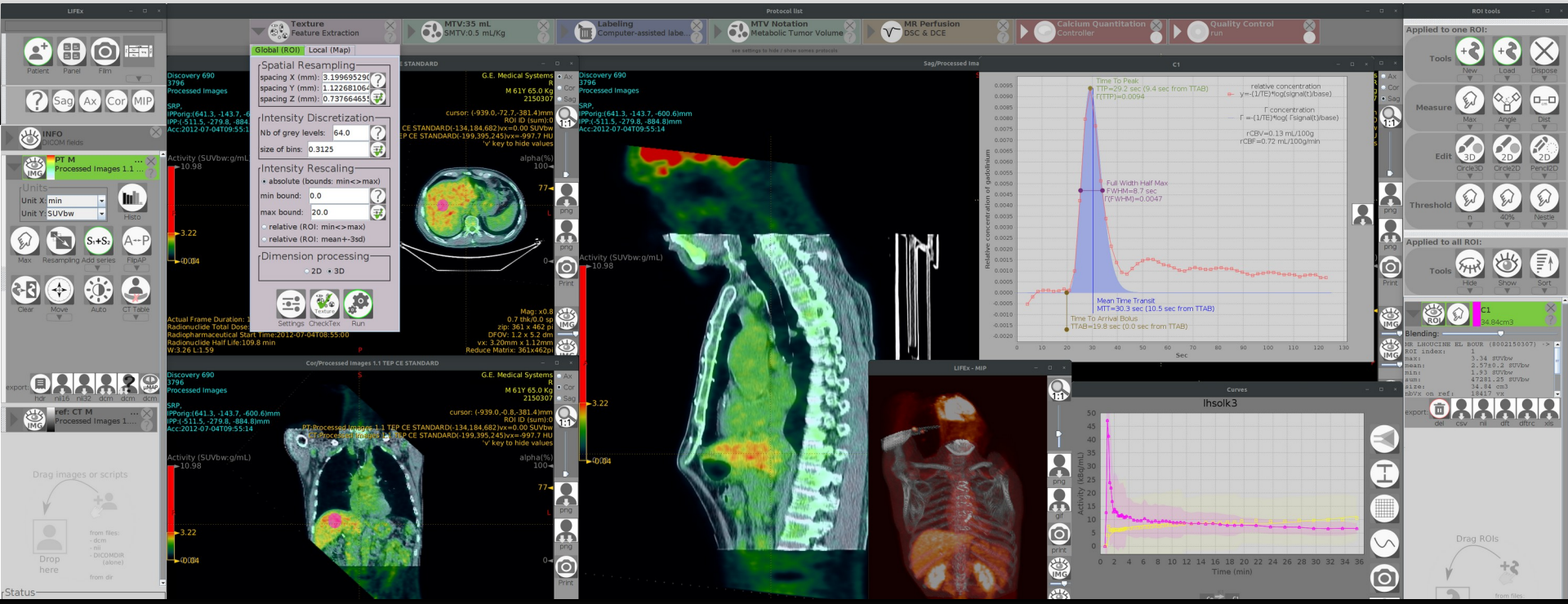
Interface screenshot



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- Main update
- Texture update
- New Labeling protocol
- New DSC-MR protocol

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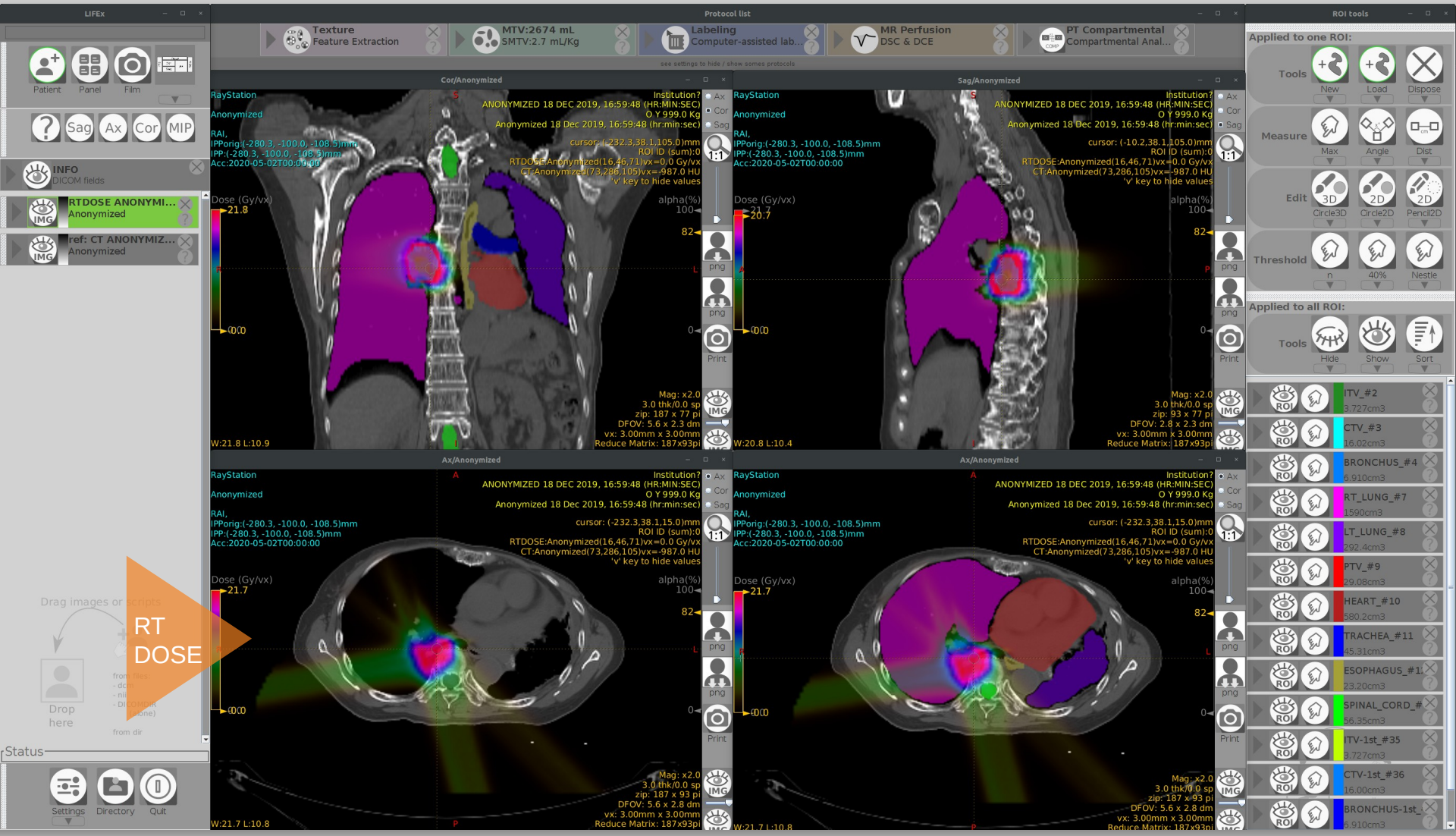
Main updates

C. Nioche

Implementation of DICOM-RT Dose Module



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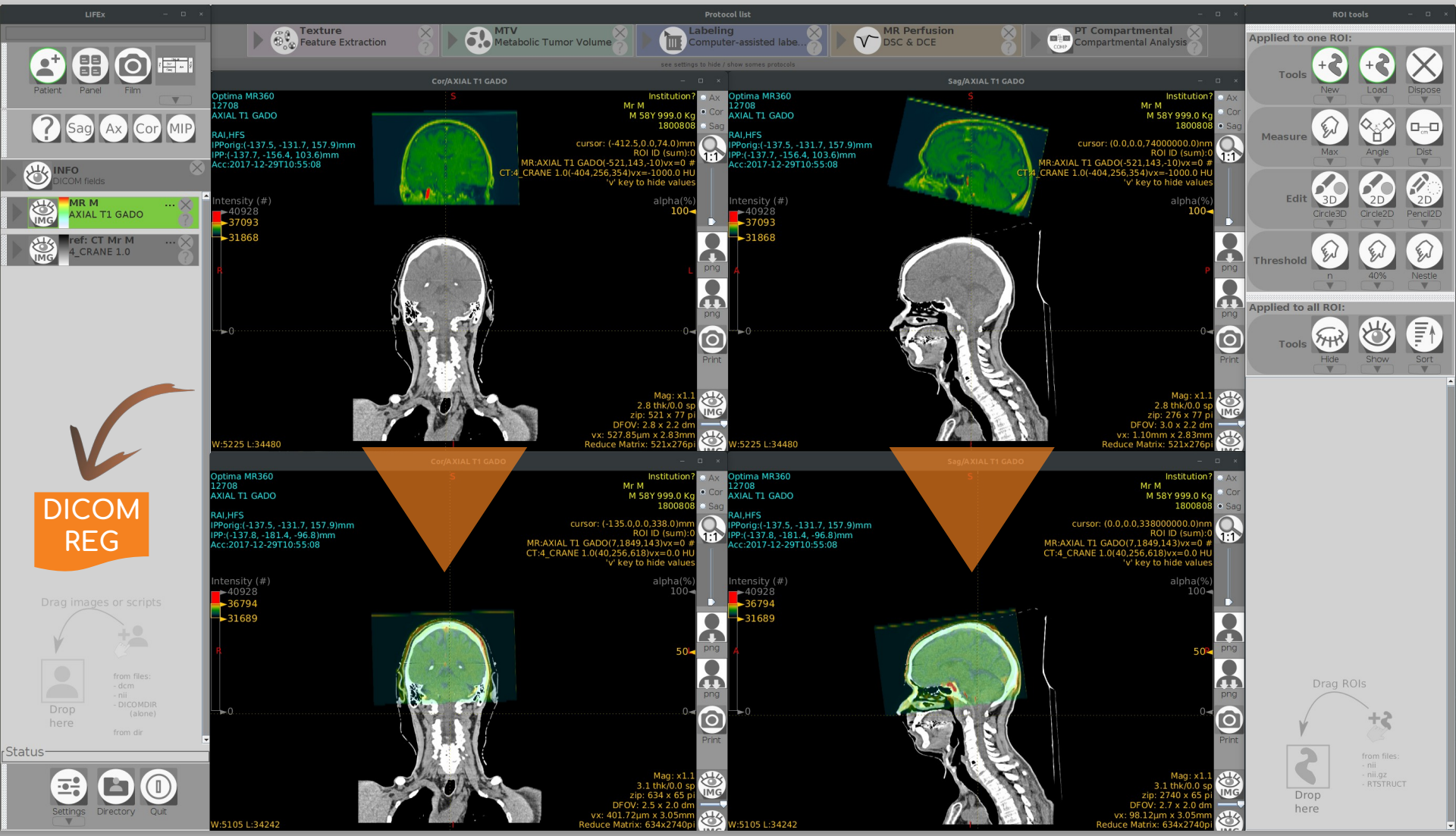
Main updates

C. Nioche

Implementation of DICOM-REG (registration file between 2 series)



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Main updates

C. Nioche

Automatic removal of CT patient table

Main updates

C. Nioche

Added / Improved / Fixed

Added

- quick orientation (Axial, Coronal, Sagittal) is available in each frame
- display only border of ROI with border/fill button added to ROI tool menu
- implementation of 3D, 4D enhanced dicom format (Enhanced ClassStorage)
- implementation of decoder for Philips DICOM (JP2) images
- implementation of spatial resampling
- contrast-based method for ROI delination (CBM ROI tool)

Improved

- nifti ROI can be floating numbers (cast in integer ROI is implemented)
- list of protocols is now in a single frame (and not integrated under series GUI)
- if slices in RTStruct are not adjacent then interpolation between slices is performed
- diameter of circle3D and circle2D tools is displayed when tool size is changed
- color palette is now unique for each frame.

Fixed issue

- multiple acquisitionNumber in one study
- application of orientation volume when loading from DICOMDIR

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Texture updates

C. Nioche, F. Orlhac, I. Buvat

Added / Improved

Added

- 2D or 3D processing setting
- 4D or temporal 3D of local texture (map) is available
- 2D processing of GLCM features in coronal and sagittal views

Improved

- "sessionXls" is changed into "SessionCsv" in script files
- result file is changed to *.csv instead of *.xls (too many problems with excel files)
- "check ROI for texture" is moved from ROI tools to Texture GUI
- checking the number of voxels compatible with textural feature calculations (64 for 3D ROI, 16 for 2D ROI) has moved after voxel resampling
- processing of GLZLM matrix and SUVpeak is faster
- remove all hash and space characters on column title in csv ouput file
- "NaN" values in result file when these values are not calculated
- the session result file has its name set automatically and fixed; It is created and appended automatically
- time frame is calculated in texture calculation, time column is added to the result file

Texture updates

C. Nioche, F. Orlhac, I. Buvat

Added / Updated

Add new features

- SHAPE_surface
- CONVENTIONAL_AgatstonScore,
- DISCRETIZED_min, _mean, _std, _max,
- DISCRETIZED_Q1, _Q2, _Q3
- DISCRETIZED_Skewness, _Kurtosis, _ExcessKurtosis,
- DISCRETIZED_peakSphere0.5mL, _peakSphere1mL,
- DISCRETIZED_AgatstonScore,
- DISCRETIZED_TLG(mL),
- DISCRETIZED_RIM_min, _RIM_mean, _RIM_stdev, _RIM_max, _RIM_sum
- DISCRETIZED_HISTO_Skewness
- DISCRETIZED_HISTO_Kurtosis
- DISCRETIZED_HISTO_ExcessKurtosis

Update features

- SHAPE_sphericity
- SHAPE_compacity

Rename former

- HISTO_Skewness feature into CONVENTIONAL_Skewness feature
- HISTO_Kurtosis feature into CONVENTIONAL_Kurtosis feature
- HISTO_ExcessKurtosis feature into CONVENTIONAL_ExcessKurtosis
- HISTO_Entropy_log10 feature into DISCRETIZED_HISTO_Entropy_log10
- HISTO_Entropy_log2 feature into DISCRETIZED_HISTO_Entropy_log2
- HISTO_Energy feature into DISCRETIZED_HISTO_Energy

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New labeling protocol

C. Nioche, F. Orlhac, I. Buvat

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.

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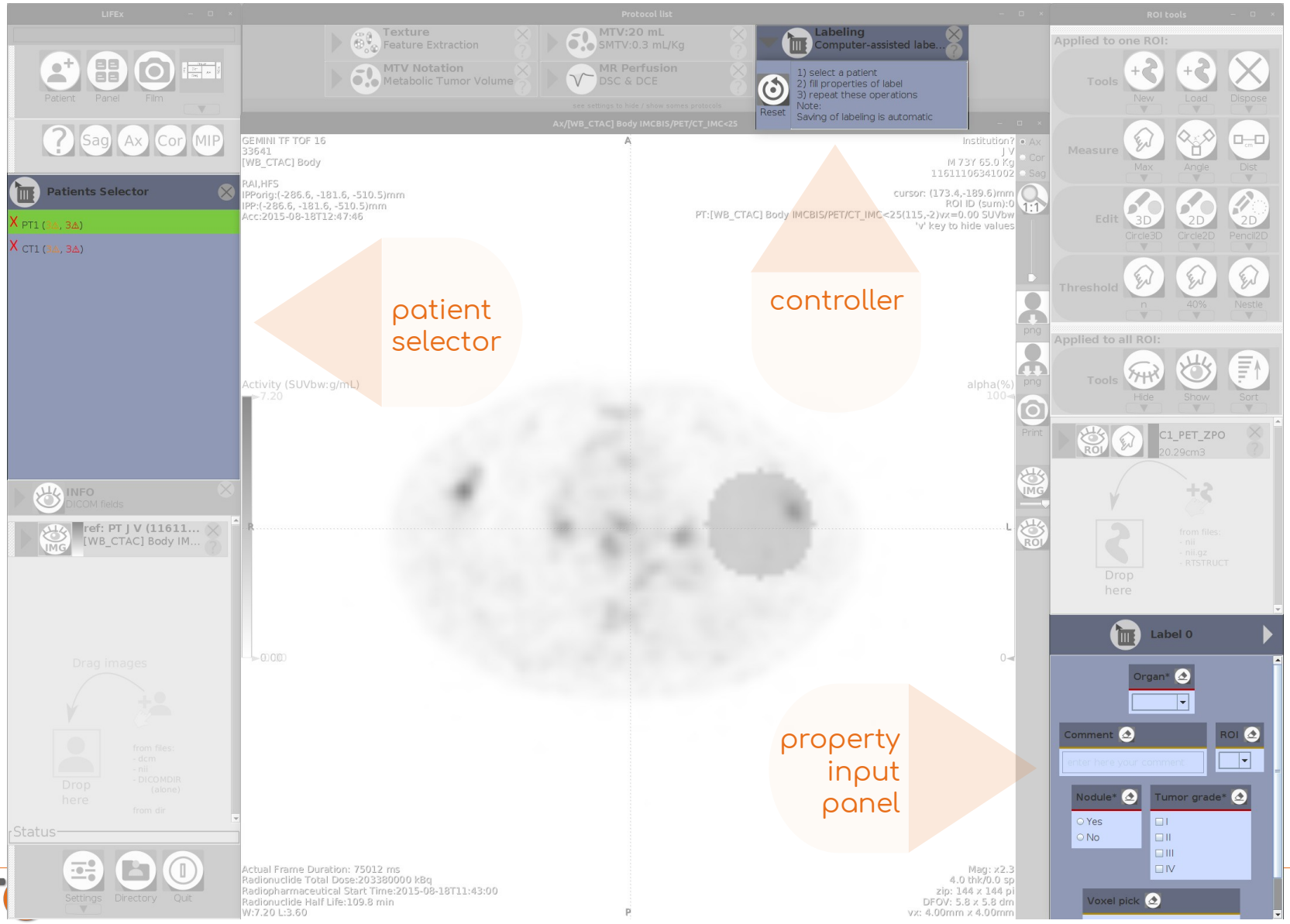

New labeling protocol

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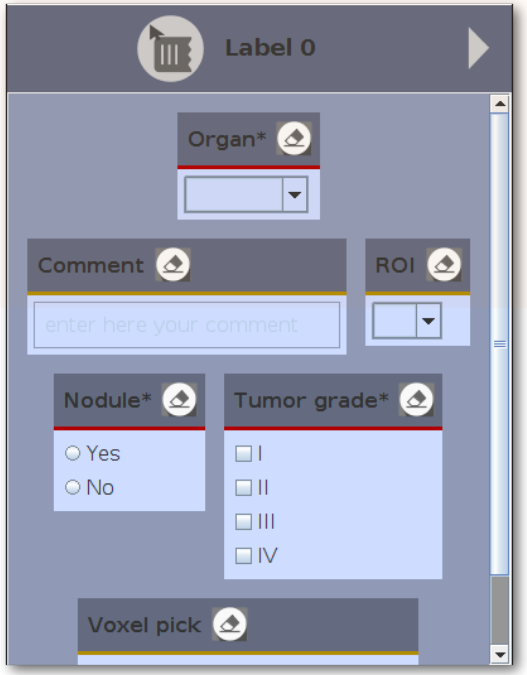
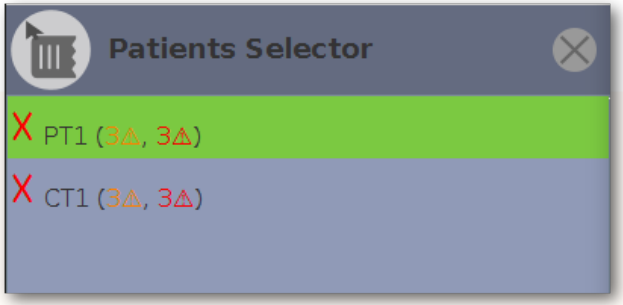


Properties form

The property entry form is built from the definitions given in the script. Each definition will be associated with a property and thus a dialog box.

Patient Selector

Patient Selector shows the patients that still need to be annotated



New labeling protocol

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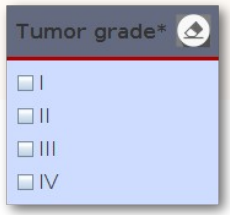
Several types of fields are available to define a complete form.

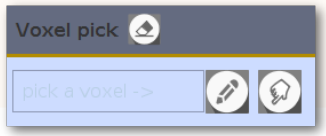


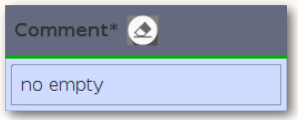
Checkbox

property#.type=checkbox

Voxel pick

property#.type=voxelpick



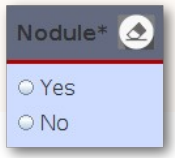


Textfield

property#.type=textfield

ROI pick

property#.type=roipick

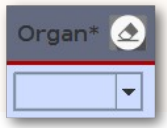


Radiobutton

property#.type=radiobutton

Dropdown

property#.type=dropdown



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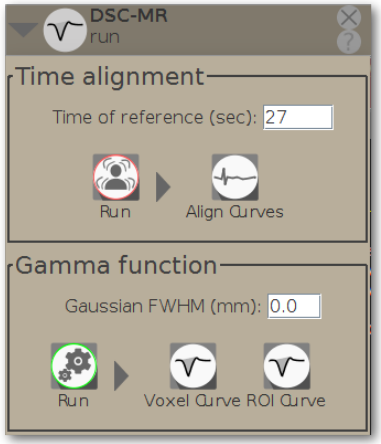
DSC-MR protocol

C. Nioche, S. Desmidt, F. Frouin, I. Buvat

→ The DSC-MR protocol of LIFEx derives perfusion-related parameters using gadolinium-based dynamic image series methods.



This technique is the use of an exogenous, intravascular, nondiffusible contrast agent, usually a gadolinium-based contrast agent, that enhances the susceptibility effects on the echo signal, in first-pass dynamic susceptibility contrast-enhanced (DSC) MR imaging.

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rCVB result after DSC-MR perfusion calculation