

LIFEx v7.2.0

Announcement

— LIFEx —

C. Nioche, O. Lamer, I. Buvat

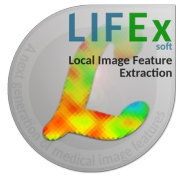


What is new?



LIFEx version 7.2.0

Last update of document: 2022/03/21



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- Series update
- Protocol update
- ROI update



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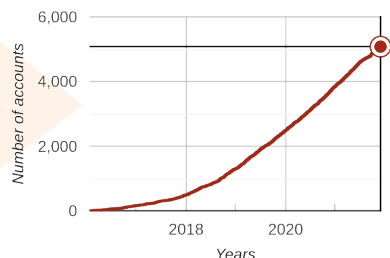
Acknowledgements

Dear LIFEx users,

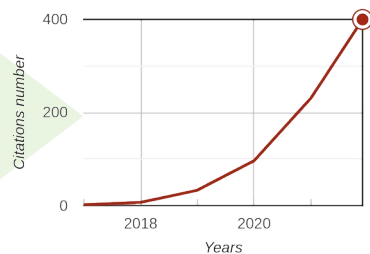
We are pleased to announce the release of **LIFEx v7.2.0**

We would like to take this opportunity [to thank all 5.000 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.

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



Evolution of the number of accounts
(from our site web)



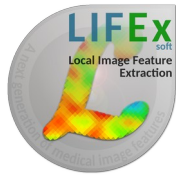
Evolution of the number of citing
LIFEx
(from PubMed)

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

The screenshot displays the LIFEx v7.2.0 software interface, which is used for PET/CT image analysis. The interface is divided into several main sections:

- Top Panel:** Contains tabs for different analysis modes: **Texture** (Feature Extraction), **MTV:135 mL** (SMTV:1.8 mL/Kg), **Labelling** (Computer-assisted labelling), and **MR Perfusion** (DSC & DCE).
- Left Panel:** A toolbar with various icons for file operations (Film, Panel, Layout1), applied series (File, Edit, Measure, Display), operations between series (Merge, Add se..., Subtra...), and status (Help, Directory, Settings, Quit).
- Central Panel:** Displays PET/CT scans in multiple views (Coronal, Axial, Sagittal). A yellow ROI is visible on the PET scan, and a purple ROI is visible on the CT scan. The interface shows various parameters like activity (SUVbw:g/mL) and alpha(%).
- Right Panel:** A control panel for ROIs, including buttons for File (New, Load, Dispose), Measure (Max, Angle, Dist), Create (Circle3D, Circle2D, Pencil2D), Threshold (n, 40%, Nestle), and Tools (Histo, Curve, Sort). It also shows a list of applied ROIs (R1, R2) and a histogram for the selected ROI.
- Bottom Panel:** A status bar showing the current ROI (R1, R2) and a histogram of the selected ROI's activity values.



The Laboratory of Translational Imaging in Oncology is a mixed research unit supported by Inserm (=French NIH) and Institut Curie, the 1st cancer center in France.



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Main updates

C. Nioche

Series:

- added: reading of the RT-Struct with the DICOM browser

The screenshot shows the 'Series loading' window with the following components:

- Filter (on patient level):** Name: A*, ID: [empty], Apply button.
- Filter (on study level):** Start: 29/11/2021, End: 29/11/2021, Apply button, and navigation buttons (J-2, J-1, J).
- Nodes:** A sidebar with icons for Disk, DICOMDIR, localhost, 3DSlicer, and New remote.
- Patients table:**

Nom -	ID	Date of birth
RMpz2	002	
- Studies table:**

ID	Description	Date	InstanceUID
	StudyDescription		1.2.246.352.221.57...
- Series table:**

N° -	Description	Modality	nb imgs	InstanceUID
0	SeriesDescription	RTSTRUCT	1	1.2.246.352.2...
4	SeriesDescription	MR	50	1.2.246.352.2...
- Buttons:** A 'load RTSTRUCT' button is located at the bottom center.





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Series updates

C. Nioche

Series:

added: loading more than one series (in nifti format) using a single "drag and drop"

The screenshot displays the LIFEx software interface. On the left, a file explorer shows a list of files including 'IMG_1mm.nii.gz', 'LabelingResults.props', and several 'main_U-Net_Scratch_WL' files. A large orange arrow points from this list towards the central software window. The central window features a control panel with sections for 'Operations between series' (containing 'Merge', 'Add se...', 'Subtra...', 'SA+SB', and 'SA-SB' buttons) and 'INFO' (containing 'DICOM fields'). Below this is a series list with icons for 'S4', 'S3', 'S2', and 'S1'. The right side of the interface shows a multi-planar view of a CT scan with axial, sagittal, and coronal slices. Technical parameters like 'Mag: x2.7', '1.0 thk/0.0 sp', 'zip: 419 x 196 pi', 'DFOV: 4.2 x 2.0 dm', 'vx: 1.00mm x 1.00mm', and 'Reduce Matrix: 419x419pi' are visible. A 'Time (#)' dropdown menu is also present.

Attention, we recommend that the loading of the 1st series is done with only 1 series in order to set the reference series.



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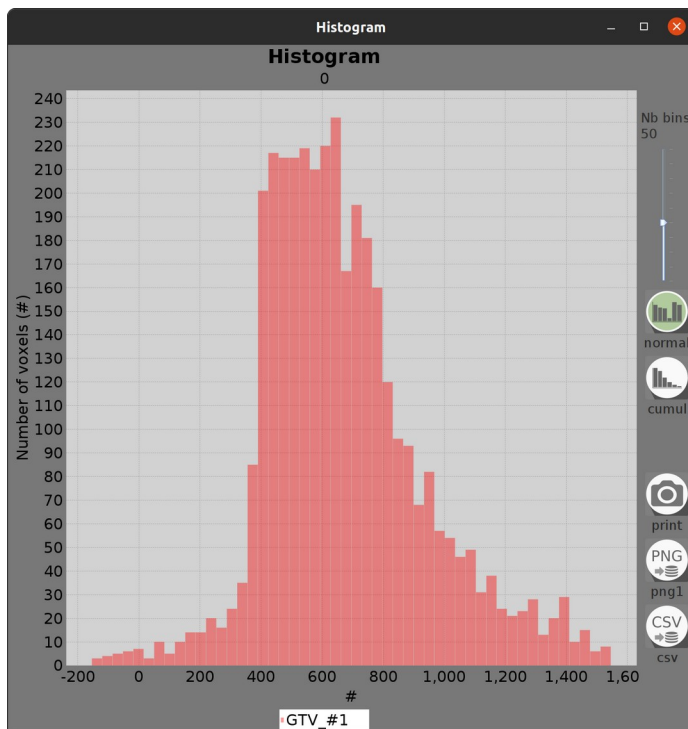
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Main updates

C. Nioche

Series:

- added: saving of histogram data in .csv format



A	B
GTV_#1	
-137.501846313477	3
-103.501846313477	4
-69.5018463134766	5
-35.5018463134766	6
-1.50184631347656	7
32.4981536865234	3
66.4981536865234	10
100.498153686523	5
134.498153686523	10
168.498153686523	14
202.498153686523	14
236.498153686523	20
270.498153686523	16
304.498153686523	24
338.498153686523	35
372.498153686523	85
406.498153686523	201
440.498153686523	217
474.498153686523	215
508.498153686523	215
542.498153686524	219
576.498153686523	210
610.498153686523	220
644.498153686523	232
678.498153686523	167
712.498153686523	195
746.498153686524	181
780.498153686523	160
814.498153686523	120
848.498153686523	96
882.498153686523	93
916.498153686523	68
950.498153686523	82
984.498153686523	57
1018.49815368652	54
1052.49815368652	46
1086.49815368652	49
1120.49815368652	31
1154.49815368652	38
1188.49815368652	24
1222.49815368652	21
1256.49815368652	23
1290.49815368652	28
1324.49815368652	13
1358.49815368652	20
1392.49815368652	29
1426.49815368652	10
1460.49815368652	15
1494.49815368652	6
1528.49815368652	8



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Series updates

C. Nioche

Series:

- changed: SUV is not required for Nuclear Medicine images (avoids the warning SUV conversion error)
- added: SUV property form to modify SUV calculation values

SUV Properties

Changing these values directly impacts the SUV calculation.
Please use them with great care.

Patient:

Patient's Weight: 54.0 kg

Patient's Size: 1.58 m

Series:

Series (date and time (T)): 2018-04-13 12:00:26

Acquisition/Instance:

Acquisition (date and time (T)): 2018-04-13 12:23:56

Corrected Image: AT DTIM RANSNG DCAL SLESENS NORM

RadioPharmaceutical:

Decay Correction: START

Units: BQML

Radiopharmaceutical start (date and time (T)): 2018-04-13 10:15:00

Radionuclide Total Dose: 2.2E8 Bq

Radionuclide Half Life: 6586.200195312 seconds

Cancel Apply SUV



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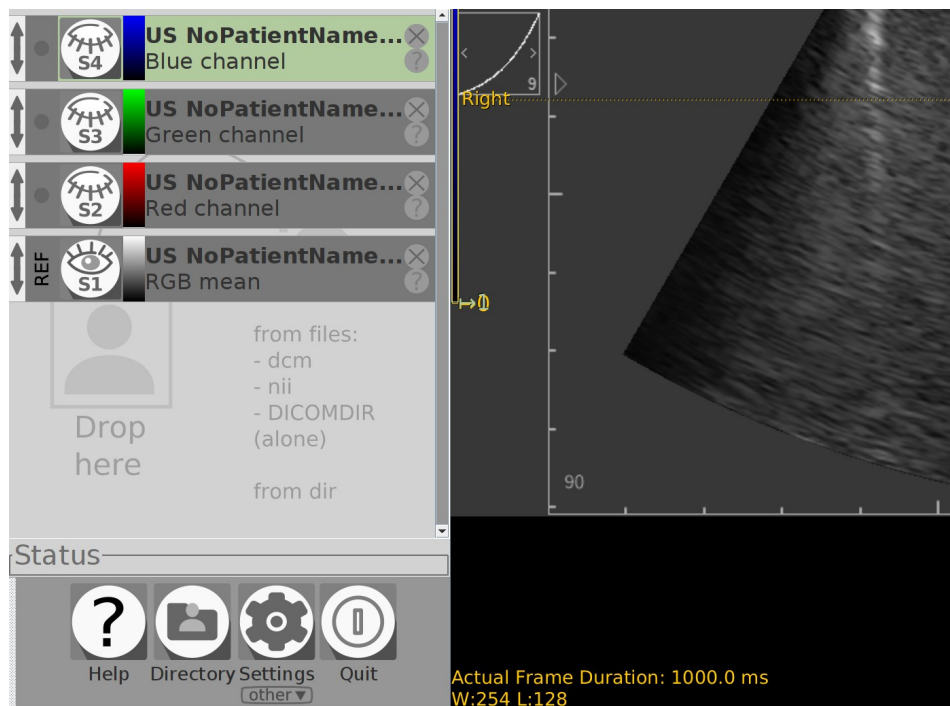
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Series updates

C. Nioche

Series:

- added red, green and blue channel decomposition from US modalities





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Series updates

C. Nioche

Series:

- added: de-synchronization of the MIP colour palette versus 2D colour palettes



MIP with gray colour palette



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Series updates

C. Nioche

Series:

- added: Script loading-saving of Series



or how to convert dicom to nifti (Dcm2Nii)

Name of script

LIFEx.Type=ScriptLoadingSavingOfSeries

#####

Output part

Output directory (keep empty, for keep same input directory)

LIFEx.Output.Directory=/Users/outputDirectory

format of output files [nii]

LIFEx.Output.FileFormat=nii

type of output files [int16 || float32]

LIFEx.Output.FileType=int16

dimension of output images [tzyx=4D || zyx=3D || yx=2D]

LIFEx.Output.Run0=tzyx

LIFEx.Output.Run1=zyx

LIFEx.Output.Run2=yx

#####

Input part

Image orientation patient: [enable || disable]

LIFEx.Input.IOP = disable

Image position patient: [enable || disable]

LIFEx.Input.IPP = enable

reading file (or directory that include images)

LIFEx.Input.Img0=/Users/inputDirectory



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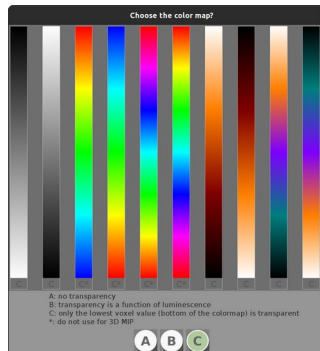
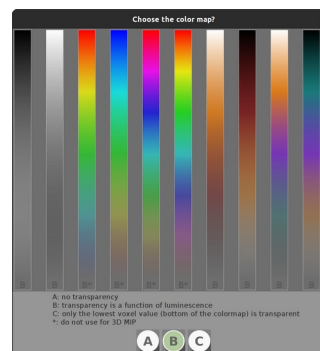
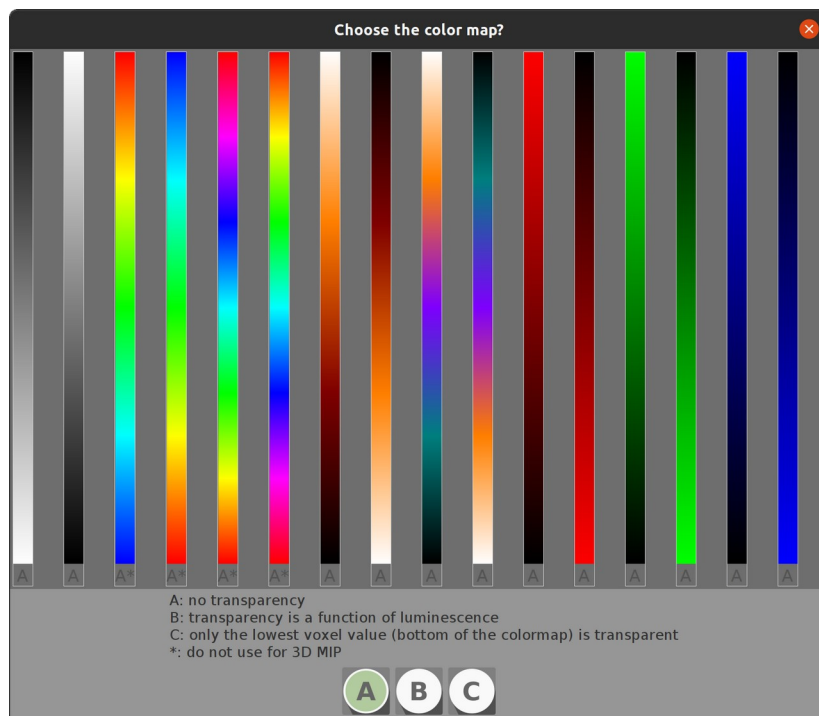
Series updates

C. Nioche

Series:

- changed: color map selector frame
- added: Warm Metal, red, green, blue color maps on series

Warm Metal





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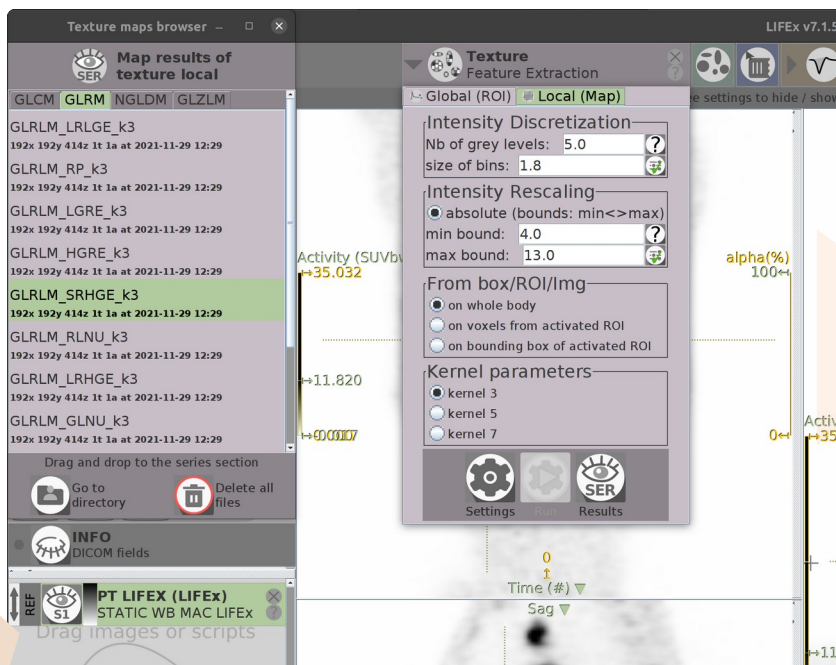
— LIFEx —

Protocol updates

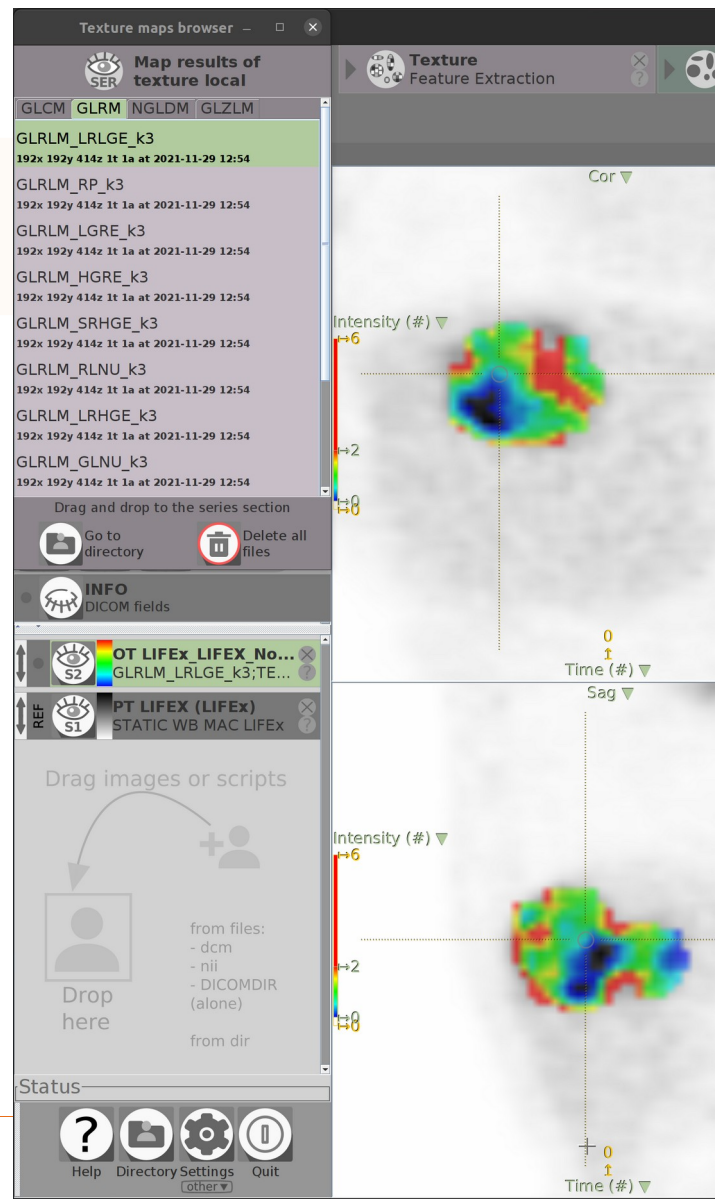
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Texture protocol:

- new GUI for management of texture local (map) results
- new texture local (map) results : GLCM, GLRM, NGDLM



Drag and drop





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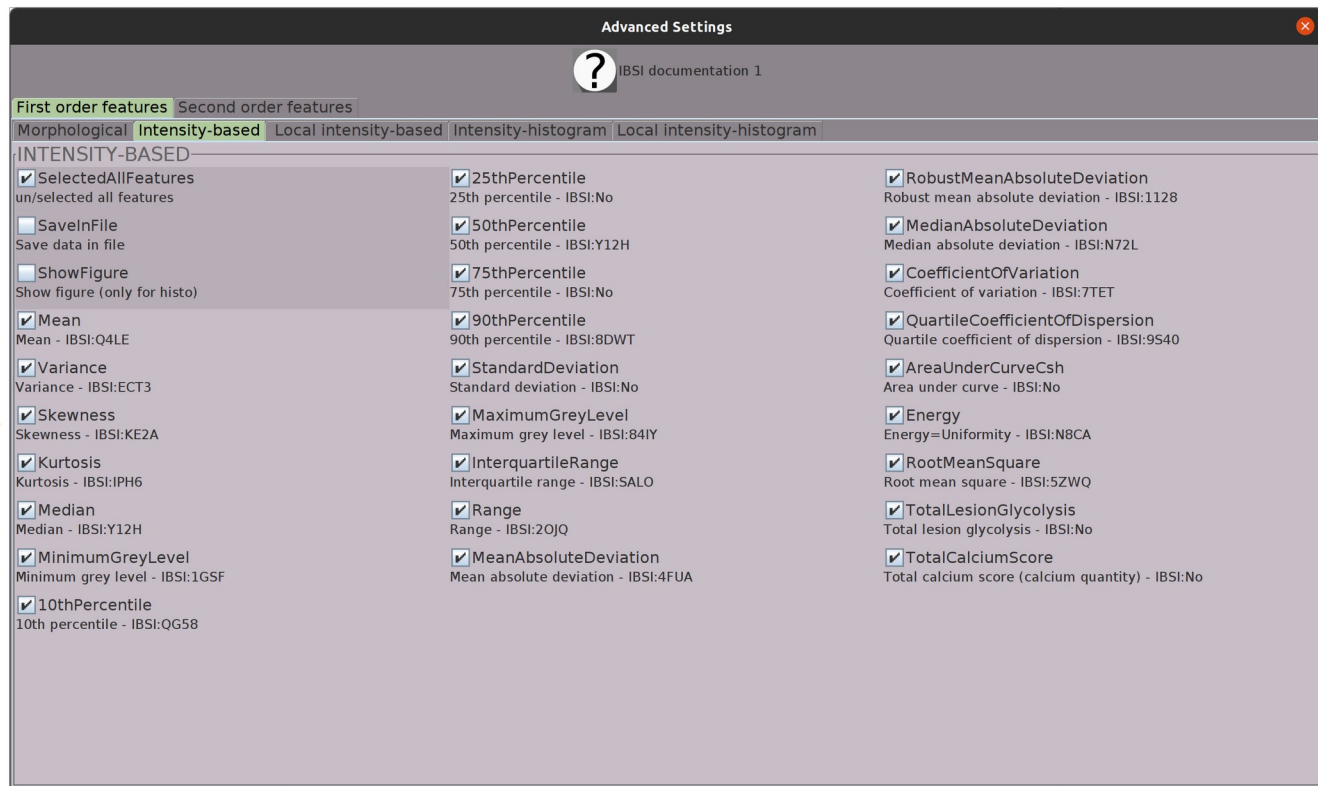
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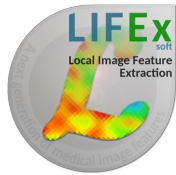
Protocol updates

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Texture protocol:

- new Advanced Settings (simplified version)





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Protocol updates

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Texture protocol:

- reduced processing time of GLCM map
- reduced time processing for RIM features

time / 20
time / 50

Changed namming :

Added IBSI code on feature : example IBSI_Q4LE

- GLCM_EntropyLog → GLCM_JointEntropyLog
- CONVENTIONAL/DISCRETIZED_meanValue → CONVENTIONAL/DISCRETIZED_MeanIntensity(IBSI_Q4LE, ...)
- CONVENTIONAL/DISCRETIZED_stdValue → CONVENTIONAL/DISCRETIZED_IntensityStandardDeviation(IBSI_No)
- CONVENTIONAL/DISCRETIZED_Skewness → CONVENTIONAL/DISCRETIZED_IntensitySkewness(IBSI_KE2A, ...)
- CONVENTIONAL/DISCRETIZED_minValue → CONVENTIONAL/DISCRETIZED_MinimumIntensity(IBSI_1GSF, ...)
- CONVENTIONAL/DISCRETIZED_maxValue → CONVENTIONAL/DISCRETIZED_MaximumIntensity(IBSI_84IY, ...)
- CONVENTIONAL/DISCRETIZED_excessKurtosis → CONVENTIONAL/DISCRETIZED_ExcessIntensityKurtosis(IBSI_No)
- CONVENTIONAL/DISCRETIZED_Kurtosis → CONVENTIONAL/DISCRETIZED_IntensityKurtosis(IBSI_IPH6, ...)
- SHAPE_Volume_mL → MORPHOLOGICAL_ApproximateVolume(IBSI_YEKZ)
- SHAPE_* → MORPHOLOGICAL_*
- NGLDM_* → NGTDM_*
- GLZLM_* become GLSZM_*
- GLZLM_ZLNU → GLSZM_ZSNU(IBSI_4JP3)
- GLCM_Energy → GLCM_AngularSecondMoment(IBSI_8ZQL)
- GLCM_Homogeneity → GLCM_InverseDifferenceMoment(IBSI_WF0Z)
- See News on web to learn more

Added features :

- GLCM_JointMaximum(IBSI_GYBY)
- GLCM_JointAverage(IBSI_60VM)
- GLCM_JointVariance(IBSI_UR99)
- MORPHOLOGICAL_surfaceToVolumeRatio(IBSI_2PR5)
- MORPHOLOGICAL_Compactness1(IBSI_SKGS)
- MORPHOLOGICAL_Compactness2(IBSI_BQWJ)
- MORPHOLOGICAL_SphericalDisproportion(IBSI_KRCK)
- See News on web to learn more



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Protocol updates

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Script of texture:

- added line : LIFEx.check=true||false
- added line : LIFEx.cluster=true||false

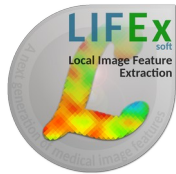
LIFEx.cluster=true

> clusters are not searched
(available only is
chek=true)

LIFEx.check=true

> Only these features are calculated (very quick):

INFO_PatientName	CONVENTIONAL_min
INFO_PatientID	CONVENTIONAL_mean
INFO_ProcessDateOfTexture	CONVENTIONAL_std
INFO_SeriesDate	CONVENTIONAL_max
INFO_Series	SHAPE_Volume(mL)
INFO_ActualFrameDuration	SHAPE_Volume(vx)
INFO_NameOfRoi	
INFO_TimePosition	
INFO_zLocation	



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ROI updates

C. Nioche

ROI:

- added: uint8 format on nifti saved ROI
- changed : naming of
 - SaveAllInAll into Save-S (separate files)
 - SaveAllInOne into Save-M

M	Merge
S	Separate (or single)
8	uint8
16	uint16
Save-M-8	Merge all ROIs in a single file [uint8] (=n ROI -> 1 file)
Save-M-16	Merge all ROIs in a single file [uint16] (=n ROI -> 1 file)
Save-S-8	Separate all ROIs in many files [uint8] (=1 ROI / file)
Save-S-16	Separate all ROIs in many files [uint16] (=1 ROI / file)

Applied to more than one ROI:

The screenshot shows a 'File Edit' menu with the following options:

- Histo (other)
- Curve (other)
- Sort (other)

The main menu is divided into four sections: File, Edit/reformat, Advanced, and Display. The 'File' section includes:

- Save-M-16 (1nii)
- Save-M-8 (1nii)
- Save-S-16 (4nii)
- Save-S-8 (4nii)
- Save-M-dcm (1dcm)
- Delete
- Dispose

The 'Edit/reformat' section includes Union and Subtract. The 'Advanced' section includes Histo, Curve, Compare, Quarter, and Labelling. The 'Display' section includes Show, Hide, Invert, Sort, and Border/Fill.



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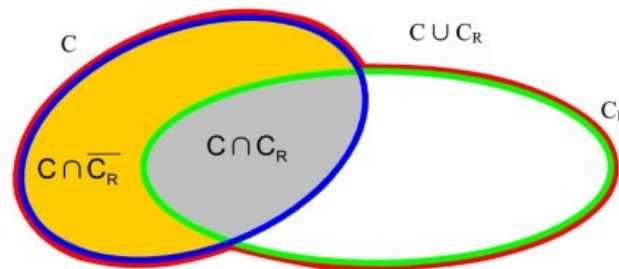
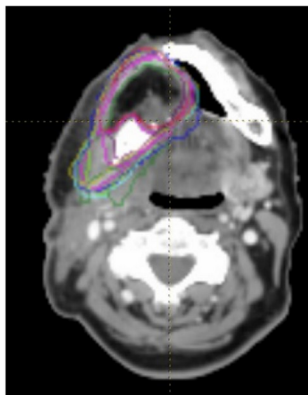
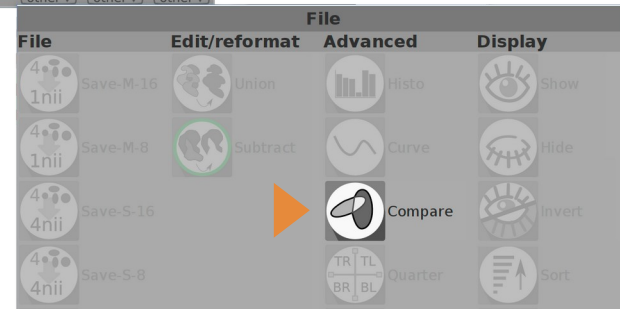
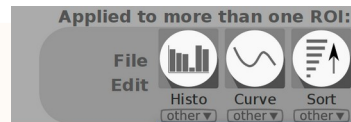
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ROI updates

C. Nioche

ROI compare tool (C vs C_R):

- C intersection with C_R
- C union with C_R
- C intersection not C_R
- Volume Ratio C / C_R
- Common Delineated Volume = fraction of C_R overlapped by C
- Additional Delineated Volume = fraction of C not overlapping with C_R
- DICE Similarity Coefficient DSC
- Overlap Index
- Hausdorff distance



C_R: Reference Contour
C: Contour to compare

Volume Ratio	$VR = C/C_R$	Optimum: 1
Common Delineated Volume	$CDV = (C \cap C_R) / C_R$	Optimum: 100%
Additional Delineated Volume	$ADV = (C \cap \bar{C}_R) / C$	Optimum: 0%
Kappa Index	$KI = 2 \times (C \cap C_R) / (C + C_R)$	Optimum: 1
Overlap Index	$OV = (C \cap C_R) / (C \cup C_R)$	Optimum: 1



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LIFEx is still evolving

Other functionalities are being added every week.
Stay tuned !
We hope you go on enjoying LIFEx !



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