



LIFEx v7.3.0

Announcement

— LIFEx —

C. Nioche, F. Orlhac, I. Buvat



What is new?



LIFEx version 7.3.0

Last update of document: 2022/09/20



LIFEx v7.3.0

Annoucement

— LIFEx —

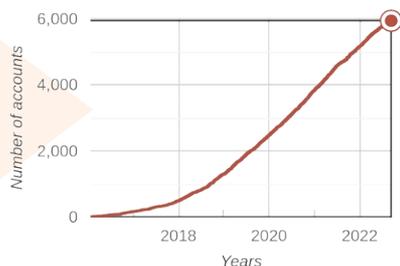
Acknowledgements

Dear LIFEx users,

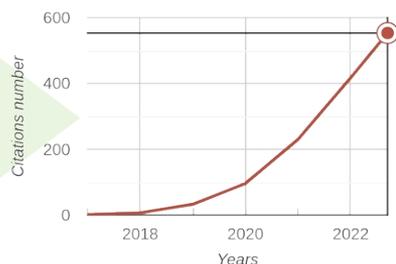
We are pleased to announce the release of **LIFEx v7.3.0**

We would like to take this opportunity [to thank all 6.000 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 Orhac, 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



LIFEx v7.3.0

Annoucement

— LIFEx —

Interface screenshot

The screenshot displays the LIFEx v7.3.0 software interface, which is used for PET/CT image analysis. The interface is divided into several main sections:

- Top Panel:** Contains tabs for different processing modes: **Texture** (Feature Extraction), **MTV:135 mL** (SMTV:1.8 mL/Kg), **Labelling** (Computer-assisted labelling), and **MR Perfusion** (DSC & DCE).
- Left Panel:** A vertical toolbar with various icons for file operations (Film, Panel, Layout1), applied series (Patien..., Laplac..., Mean), measure (Max, Histo, Dist), display (Auto, Trans..., FlipAP), and operations (Merge, Add se..., Subtra...). It also includes an **INFO** section for DICOM fields and a **Reorder Layers** section with 'top layer' and 'bottom layer' buttons.
- Central Area:** Shows a 3D PET/CT scan of a human torso. A yellow ROI is visible on the right side of the chest. The interface includes a **Global (ROI) / Local (Map)** selection dropdown and a **see settings to hide / show some protocols** link.
- Right Panel:** Displays detailed data for the selected ROI, including:
 - Activity (SUVbw:g/mL):** 69.41
 - Actual Frame Duration:** 180000.0 ms
 - Radiopharmaceutical Total Dose:** 314000000 Bq
 - Radiopharmaceutical Start Time:** 2018-04-13T09:03:38
 - Radiopharmaceutical Half Life:** 109.8 min
 - W:3.09 L:4.50**
 - Mag: x2.0**
 - 3.0 thk/0.0 sp**
 - zip: 168 x 168 pi**
 - DFOV: 6.8 x 6.8 dm**
 - vx: 4.07mm x 4.07mm**
- Bottom Right Panel:** Shows a **Histogram** plot for the selected ROI, with a yellow peak on the left and a pink peak on the right. The histogram is titled **Histogram 2006_PET TAP 618SG5 LIFEx**.
- Far Right Panel:** A control panel for ROIs, including **Applied to selected ROI:** (File, Edit, Measure, Create, Threshold), **Applied to more than one ROI:** (Tools), and **Blending:** (S1, S2) options.





LIFEx v7.3.0

Annoucement

— LIFEx —

CONTENTS

- 
- Series update
 - Protocol update
 - ROI update



LIFEx v7.3.0

Annoucement
— LIFEx —

Series updates

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MIP Series:

Series Selection (LMB+Ctrl):

→ retrieves in 3D the coordinates of the voxel pointed in the MIP and centers the sagittal, coronal and transaxial views on that coordinate.

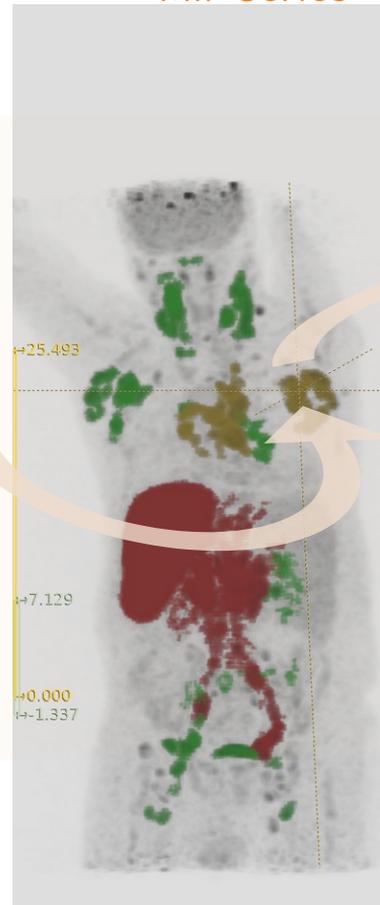
ROI Selection (LMB+Shift):

→ retrieves in 3D the ROI to which the voxel pointed in the MIP belongs to and locates the sagittal, coronal and transaxial views on the max Value coordinate of the ROI.

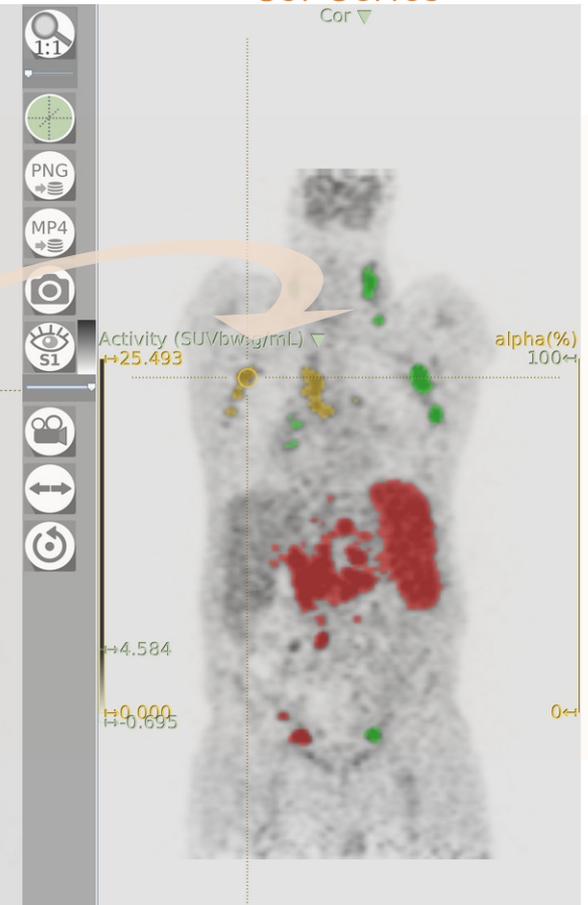
remove ROI (RMB+Shift)

→ retrieves in 3D the ROI to which the voxel pointed in the MIP belongs to and removes this ROI.

MIP Series



Cor Series



The MTV volume is automatically recalculated



LIFEx v7.3.0

Annoucement

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Protocol updates

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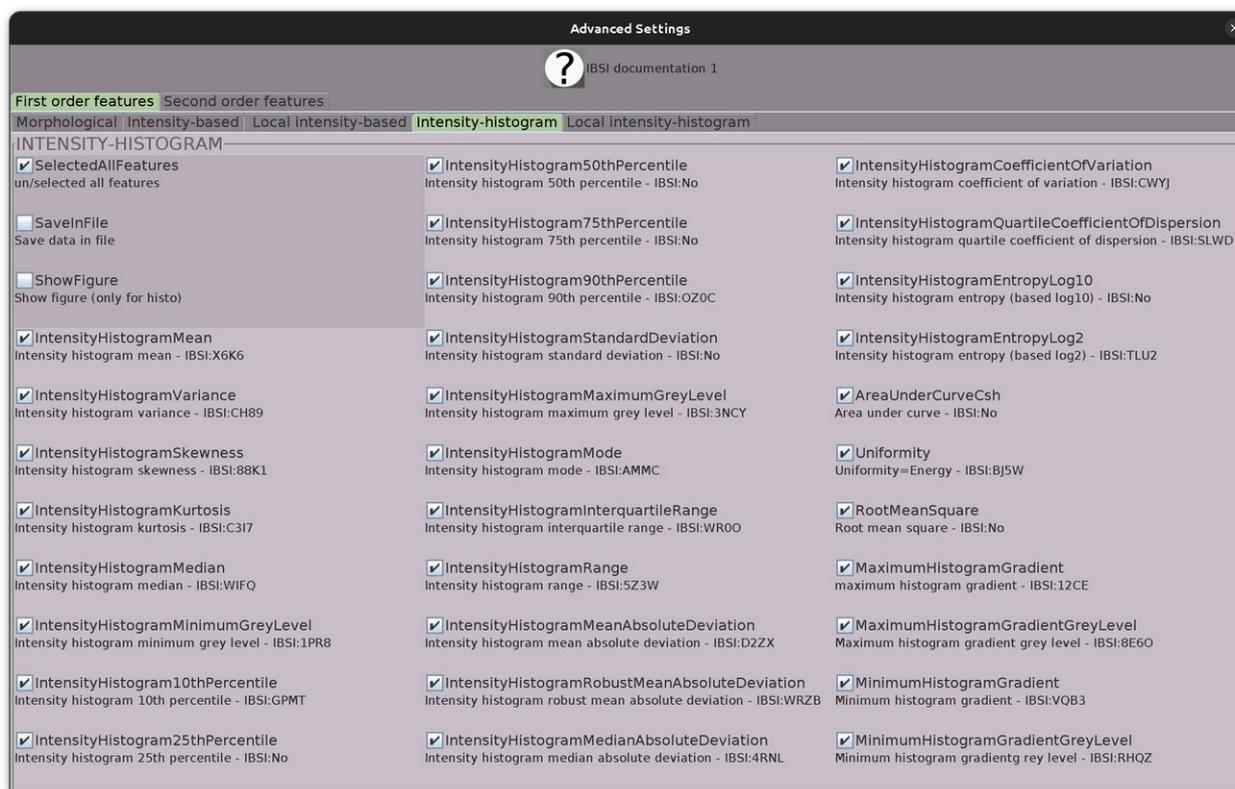
Texture protocol:

- changed: approximateVolume (number of voxels in the VOI as per IBSI definition) instead of volume (mesh-based volume calculation as per IBSI definition) into MORPHOLOGICAL_NormalizedHocRadiusSphere(IBSI:No) and MORPHOLOGICAL_NormalizedCentreOfMassShiftRadiusSphere(IBSI:No) features (the volume (mesh calculation) is too sensitive to the resampling variation)
- changed: MORPHOLOGICAL_compacity(IBSI:No)
 - is now $=\text{pow}(\text{surfaceArea}, 3/2)/\text{volume}$
 - it was before: $=\text{volume}/\text{surfaceArea}$
- changed: name changed of HOC(IBSI:No) into HOCMax(IBSI:No), private feature
- added: all feature HOCPeak0.5mL, HOCPeak1mL (IBSI:No), private feature
- added: "private" tag in place of "NaN" when features are not public
- improved: calculate the texture in the orientation of the primary slices (coronal and sagittal, in addition to the axial view)
- improved: mesh volume corrected
- many little others corrections...



Texture protocol:

- new feature names according to IBSI





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Annoucement

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Protocol updates

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Script for TMTV calculation:

- added: scripts are available

```
#####  
# Common  
#####  
# fixed information on script -> mandatory  
LIFEx.MTV.script = MTV  
LIFEx.MTV.script.version = 1.0  
  
# result file -> mandatory  
LIFEx.MTV.output.file={}/script/MTV_results.csv  
  
#####  
#           patients / ROI           #  
#####  
LIFEx.MTV.Session0.lmg0={}/script/PT  
LIFEx.MTV.Session0.Roi0={}/script/R1.uint8.nii.gz  
LIFEx.MTV.Session0.Roi1={}/script/R2.uint8.nii.gz  
LIFEx.MTV.Session0.Roi2={}/script/R4.uint8.nii.gz  
  
LIFEx.MTV.Session1.lmg0={}/script/PT  
LIFEx.MTV.Session1.Roi0={}/script/R1.uint8.nii.gz  
LIFEx.MTV.Session1.Roi1={}/script/R2.uint8.nii.gz  
LIFEx.MTV.Session1.Roi2={}/script/R4.uint8.nii.gz
```



LIFEx v7.3.0
Annoucement
— LIFEx —

ROI updates

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ROI:
undo action on last ROI deletion

The screenshot displays the LIFEx software interface. On the left, there are two axial (Ax) and sagittal (Sag) views of a brain scan. The top view shows a green ROI on a brain slice. The right side of the interface features a toolbar with various tools categorized into 'Applied to selected ROI:' and 'Applied to more than one ROI:'. The 'Applied to selected ROI:' section includes 'File Edit' (New, Load), 'Measure' (Angle, Dist), and 'Create' (3D, 2D, 2D). The 'Applied to more than one ROI:' section includes 'File Edit' (Sort, Curve, Sort). Below the toolbar is the 'ROIs sorting' panel, which contains a list of ROIs. A button labeled 'undo the last ROI deletion' is highlighted with an orange arrow. The ROI list includes:

ROI ID	MTV	TLG
R32	1639cm ³	0
R10	116cm ³	440
R12	74cm ³	296
R14	56cm ³	225



LIFEx v7.3.0

Annoucement

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LIFEx is still evolving

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



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C Nioche, F Orhac, 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



LIFEx v7.3.0

Annoucement

— LIFEx —

All updates

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What has been added, changed or updated in this new release?

Here is a list of the most significant additions, changes or updates in LIFEx v7.3.0:

Main:

- improved: removal of all problematic characters * in filename (for windows system)
- improved: the number of images is now correct when displaying the DICOMDIR list
- improved: construction of a DICOMDIR when at least two directories are read at the same time
- corrected: special character < and > are not accepted by Windows in filename -> they are replaced by (and)
- improved: Selection of the layout according to the FOV of the read images (whole body (cor view), brain (square view))
- added: undo action on last ROI deletion
- improved: namefile of logfile become LIFExn.n.n_yyyyMMdd_HHmss.log instead of LIFExn.n.n.log (n.n.n is the version number)

MIP:

- improved: Selection in the MIP view is now possible with three functions:
 - LMB+Ctrl (corresponds to Series MIP Selection): This action retrieves in 3D the coordinates of the voxel pointed in the MIP and centers the sagittal, coronal and transaxial views on that coordinate
 - LMB+Shift (corresponds to ROI Selection): This action retrieves in 3D the ROI to which the voxel pointed in the MIP belongs to and locates the sagittal, coronal and transaxial views on the coordinate of the maxVal in that ROI
 - RMB+Shift (corresponds to remove ROI): This action retrieves in 3D the ROI to which the voxel pointed in the MIP belongs to and removes this ROI
- improved: crosshair on 3D MIP is available
- improved: selection of MIP color palette is simplified with the display of the only compatible palette
- improved: changing the window/levelling on the planar slices no longer affects the MIP view

Series:

- changed: implementation of the Gaussian filter (sum of kernel = 1); result values are changed
- added: 2D calculation for Mean filter
- added: BoundingBoxMethod of filter
- added: series ECAT7 reader
- improved: statistics are now updated after filters are applied
- improved: crosshair scrolling is based on the series with the lowest resolution
- deleted : resampling with NO_INTERPLATION, NEAREST_NEIGHBOR
- corrected: US (Bmode+Elasto+Quality) loading



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Here is a list of the most significant additions, changes or updates in LIFEx v7.3.0:

ROI:

- corrected: close function on 2D slices
- changed: close function is renamed close3D function
- added: close2D function
- corrected: sDmax renamed into wDmax (weighted Dmax) as from the wCom
- improved: acceleration of "slice interpolation" tool
- added: fill2D (1 and n slices) function: to fill the inside of 2D contour on axial slices only

Texture protocol:

- changed: approximateVolume (number of voxels in the VOI as per IBSI definition) instead of volume (mesh-based volume calculation as per IBSI definition) into MORPHOLOGICAL_NormalizedHocRadiusSphere(IBSI:No) and MORPHOLOGICAL_NormalizedCentreOfMassShiftRadiusSphere(IBSI:No) features (the volume (mesh calculation) is too sensitive to the resampling variation)
- changed: MORPHOLOGICAL_compacity(IBSI:No) is now $=\text{pow}(\text{surfaceArea}, 3/2)/\text{volume}$. (it was before: $=\text{volume}/\text{surfaceArea}$)
- changed: name changed of HOC(IBSI:No) into HOCMax(IBSI:No)
- added: "private" tag in place of "NaN" when features are not public
- added: features HOCPeak05mL(IBSI:No) and HOCpeak1mL(IBSI:No)
- improved: deletion of all spaces of properties values from script file
- improved: calculate the texture in the orientation of the primary slices (coronal and sagittal, in addition to the axial view)
- improved: mesh volume corrected

PT Compartmental analysis protocol:

- added: export in .csv file of fitted data, Vd, K1, k2, k3, k4, and Vp%

MTV-protocol:

- added: added: scripting MTV calculation (cf. MTV_script.txt)