



LIFEx v7.4.0

Announcement
— LIFEx —

C. Nioche, F. Orlhac, I. Buvat



What is new?



LIFEx version 7.4.0

Last update of document: 2022/11/28

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Statistics of the latest version
Main / Series updates
Protocols updates
ROI updates



CONTENTS

Statistics of the latest version

This part will be removed from the next new version campaign.



LIFEx v7.3.0

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Compagnes Email

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Sending:
300 mails / 20 days

ID	NOM	DESTINATAIRES	OUVERTS	CLIQUE	DÉSINSCRITS	PLAINTES	BOUNCES	DATE D'ENVOI
#20	★ LIFEx v7.3.0 now available	275 100%	88 32,08% Détails	11 4%	0 0%	1 0,36%	0 0%	09 Oct, 2022 15:30
#19	★ LIFEx v7.3.0 now available	300 100%	89 30,28% Détails	6 2,03%	1 0,34%	0 0%	5 1,67%	08 Oct, 2022 15:31
#18	★ LIFEx v7.3.0 now available	300 100%	96 32,27% Détails	5 1,69%	2 0,68%	0 0%	4 1,33%	07 Oct, 2022 15:31
#17	★ LIFEx v7.3.0 now available	300 100%	125 42,57% Détails	12 4,08%	0 0%	0 0%	6 2%	06 Oct, 2022 15:32
#16	★ LIFEx v7.3.0 now available	300 100%	115 38,82% Détails	5 1,69%	2 0,68%	0 0%	7 2,33%	05 Oct, 2022 15:31
#15	★ LIFEx v7.3.0 now available	300 100%	109 36,72% Détails	11 3,72%	5 1,69%	0 0%	4 1,33%	04 Oct, 2022 15:31
#14	★ LIFEx v7.3.0 now available	300 100%	120 41,63% Détails	13 4,50%	3 1,04%	0 0%	11 3,67%	03 Oct, 2022 15:31
#13	★ LIFEx v7.3.0 now available	300 100%	112 37,96% Détails	10 3,38%	3 1,01%	0 0%	4 1,33%	02 Oct, 2022 15:31
#12	★ LIFEx v7.3.0 now available	300 100%	112 38,68% Détails	7 2,42%	0 0%	0 0%	11 3,67%	01 Oct, 2022 15:30
#11	★ LIFEx v7.3.0 now available	300 100%	86 29,55% Détails	9 3,09%	2 0,69%	0 0%	9 3%	30 Sep, 2022 15:31
#10	★ LIFEx v7.3.0 now available	300 100%	112 38,49% Détails	5 1,72%	3 1,03%	0 0%	9 3%	29 Sep, 2022 15:31
#9	★ LIFEx v7.3.0 now available	300 100%	97 33,20% Détails	8 2,73%	1 0,34%	0 0%	7 2,33%	28 Sep, 2022 15:30
#8	★ LIFEx v7.3.0 now available	300 100%	111 38,11% Détails	6 2,07%	1 0,34%	0 0%	10 3,33%	27 Sep, 2022 15:32
#7	★ LIFEx v7.3.0 now available	300 100%	98 33,87% Détails	13 4,48%	2 0,69%	0 0%	10 3,33%	26 Sep, 2022 15:31



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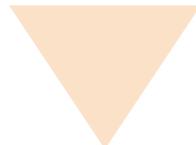
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Mardi.20-09-2022

Dimanche.09-10-2022

[Voir les statistiques](#)

◀ Septembre, 2022 ▶

LU	MA	ME	JE	VE	SA	DI
29	30	31	1	2	3	4
5	6	7	8	9	10	11
12	13	14	15	16	17	18
19	20	21	22	23	24	25
26	27	28	29	30	1	2
3	4	5	6	7	8	9

◀ Octobre, 2022 ▶

LU	MA	ME	JE	VE	SA	DI
26	27	28	29	30	1	2
3	4	5	6	7	8	9
10	11	12	13	14	15	16
17	18	19	20	21	22	23
24	25	26	27	28	29	30
31	1	2	3	4	5	6

Total d'envois 20

Total destinataires 5 975

Total ouvertures 1 723

Total clics 175

Total désinscrits 45

Total Répondus 0

Total Soft + Hard Bounces 157

Taux d'ouverture

35,39% [Détails](#)

Taux de clics

3,01%

Taux de désinscription

0,77%



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Users testimonials

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POLITECNICO DI TORINO

Corso di Laurea in Ingegneria Biomedica
Tesi di Laurea Magistrale

Analisi radiomica di tumori cerebrali studiati
con 18 F-DOPA PET/CT

Relatori:

Prof. Gianni Coppa

Prof.ssa Désirée Deandrea

Dott.ssa Michela Zotta

Candidata

Ambra Maria Torre

Ottobre 2022

Capitolo 4

Discussioni

4.1 Considerazioni finali

Per essere largamente applicabile, un modello scaturito dalle features radiomiche deve basarsi su una definizione univoca delle espressioni delle features, del ricampionamento spaziale e della discretizzazione dei livelli di intensità. L'uso di free software come LIFEx ha rappresentato un enorme passo in avanti nella possibilità di validare i modelli in coorti indipendenti tra di loro, dal momento che ha comportato un certo grado di standardizzazione. Infatti in LIFEx buona parte delle features estratte seguono le formule standardizzate proposte da IBSI (Image Biomarker Standardization Initiative). La scelta del ricampionamento spaziale e della discretizzazione dei livelli di intensità ha una ricaduta fondamentale sulla robustezza dei risultati dato che le features radiomiche possono dare dei risultati molto sensibili agli artefatti da movimento e al rumore. Si è deciso di attuare una discretizzazione assoluta usando 64 livelli tra 0 e 20 SUV, come suggerito nell'ambito della PET nella guida per l'utente di LIFEx, proprio per ottenere risultati maggiormente robusti.

In order to be widely applicable, a model derived from radiomic features must be based on an unambiguous definition of feature expressions, spatial resampling and discretization of intensity levels. The use of free software such as LIFEx represented a huge step forward in the possibility of validating models in independent cohorts, since it entailed a certain degree of standardisation.

In fact, in LIFEx most of the features extracted follow the standardised formulae proposed by IBSI (Image Biomarker Standardisation Initiative). The choice of spatial resampling and discretisation of intensity levels has a fundamental impact on the robustness of the results, given that radiomic features can be very sensitive to motion artefacts and noise. It was decided to implement absolute discretisation using 64 levels between 0 and 20 SUVs, as suggested in the PET user's guide of LIFEx, precisely to obtain more robust results.



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Users testimonials

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Hannequin P, Decroisette C, Kermanach P, Berardi G, Bourbonne V. **FDG PET and CT radiomics in diagnosis and prognosis of non-small-cell lung cancer.** *Transl Lung Cancer Res* 2022;11(10):2051-2063. doi: 10.21037/tlcr-22- 158

Translational Lung Cancer Research, Vol 11, No 10 October 2022

training/testing procedure. Whatever the practical impact of presenting negative results must be considered (39). The differences of findings between several institutions could be explained by specificities of populations: ethnics and social status of patients as well as kind and level of medical care, this confusion bias being rarely taken into account in available data. Technical development of PET-CT devices must also be taken into account as well as specificities of the radiomics software and the way to handle it. For information, LifeX (22) team has a project to develop an application that will enables the evaluation, in a multicenter way, of radiomics and\or AI models proposed for the management of lung cancer patients. Multicenter validation of models remains indeed essential to consider for their clinical use. Several studies focused on the lack of harmonization of radiomics (38,39) while others (10-12,40,41) underscore more sophisticated methodology such as principal components analysis (PCA), artificial intelligence (AI), multiblock discriminant analysis (42). However these techniques can be explored in research centers but are not suited for a clinical use which needs simple and robust procedures. Nowadays, one should be cautious in applying results obtained by others and the creation of one's own survival analysis seems necessary, before calculating the optimal local suited radiomics signature.



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Next release v7.4.0



LIFEx v7.4.0

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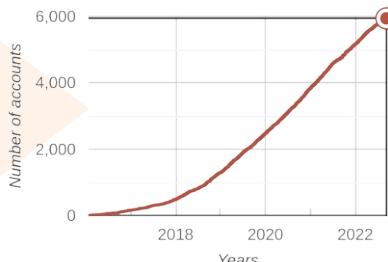
Acknowledgements

Dear LIFEx users,

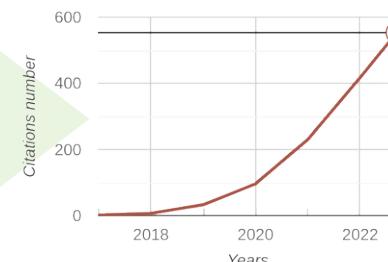
We are pleased to announce the release of **LIFEx v7.4.0**

We would like to take this opportunity [to thank all 6.700 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 Pellet-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



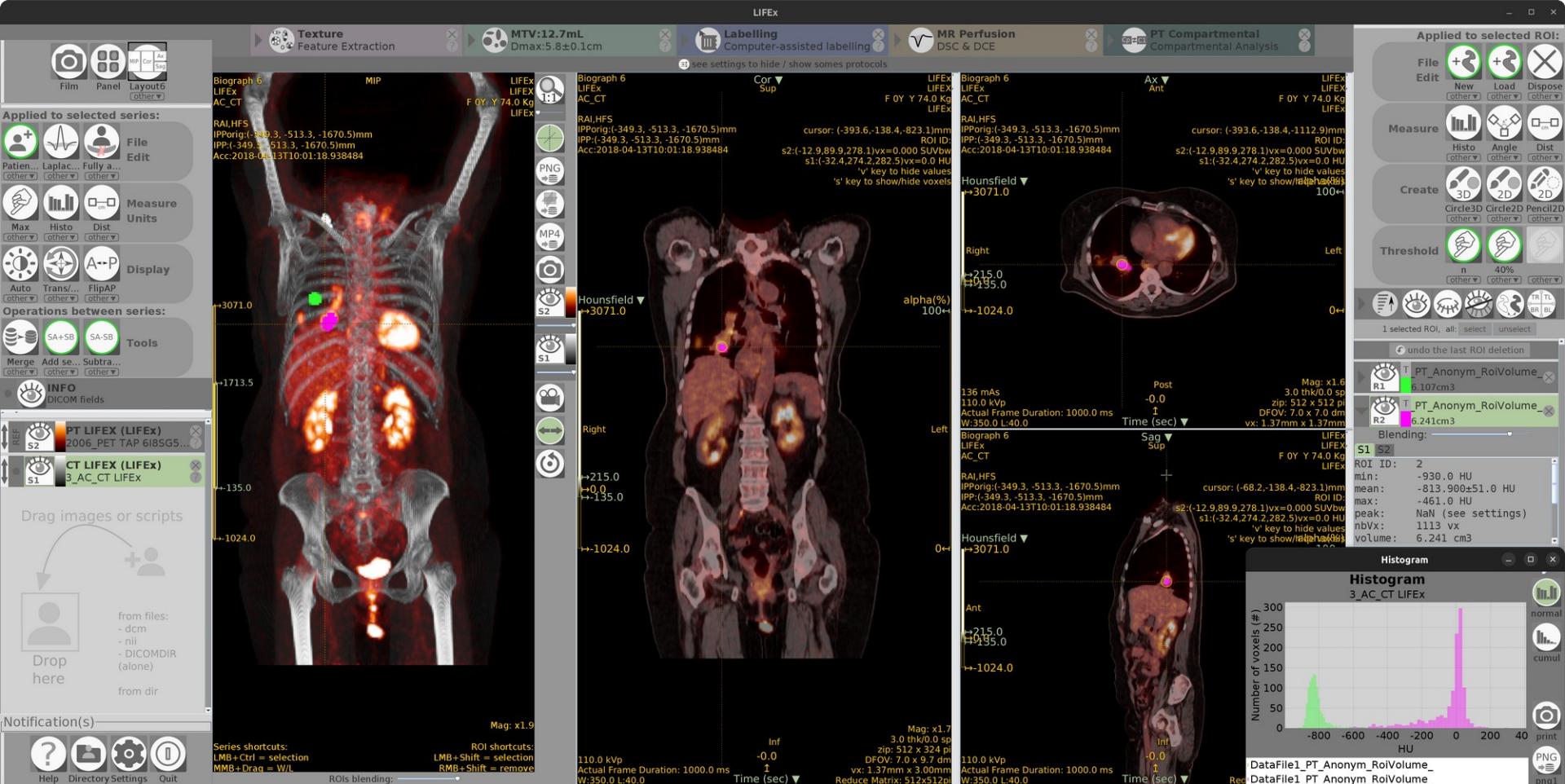
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Interface screenshot

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Main / Series updates

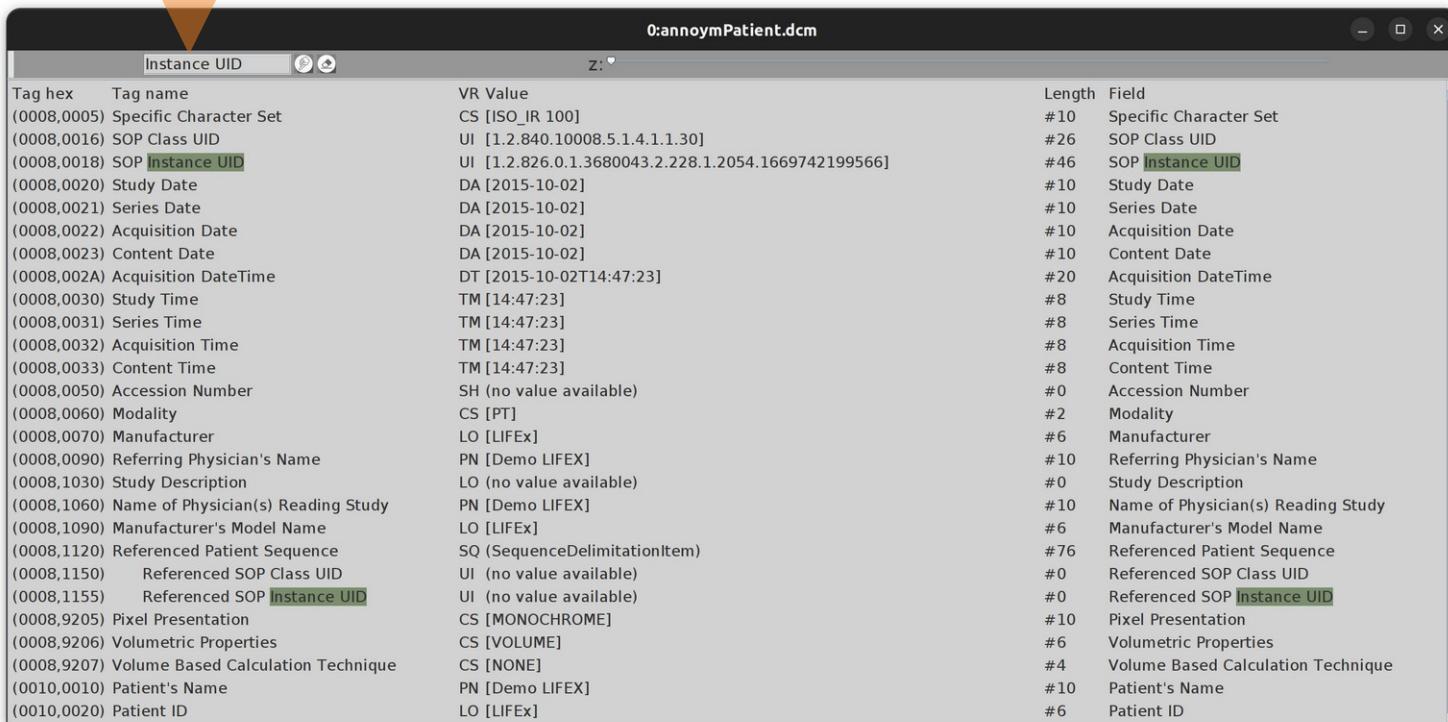


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Main:

- added: search field in DICOM viewer
- fixed: (group, item) of DICOM tag in viewer DICOM



Tag hex	Tag name	VR Value	Length	Field
(0008,0005)	Specific Character Set	CS [ISO_IR 100]	#10	Specific Character Set
(0008,0016)	SOP Class UID	UI [1.2.840.10008.5.1.4.1.1.30]	#26	SOP Class UID
(0008,0018)	SOP Instance UID	UI [1.2.826.0.1.3680043.2.228.1.2054.1669742199566]	#46	SOP Instance UID
(0008,0020)	Study Date	DA [2015-10-02]	#10	Study Date
(0008,0021)	Series Date	DA [2015-10-02]	#10	Series Date
(0008,0022)	Acquisition Date	DA [2015-10-02]	#10	Acquisition Date
(0008,0023)	Content Date	DA [2015-10-02]	#10	Content Date
(0008,002A)	Acquisition DateTime	DT [2015-10-02T14:47:23]	#20	Acquisition DateTime
(0008,0030)	Study Time	TM [14:47:23]	#8	Study Time
(0008,0031)	Series Time	TM [14:47:23]	#8	Series Time
(0008,0032)	Acquisition Time	TM [14:47:23]	#8	Acquisition Time
(0008,0033)	Content Time	TM [14:47:23]	#8	Content Time
(0008,0050)	Accession Number	SH (no value available)	#0	Accession Number
(0008,0060)	Modality	CS [PT]	#2	Modality
(0008,0070)	Manufacturer	LO [LIFEx]	#6	Manufacturer
(0008,0090)	Referring Physician's Name	PN [Demo LIFEx]	#10	Referring Physician's Name
(0008,1030)	Study Description	LO (no value available)	#0	Study Description
(0008,1060)	Name of Physician(s) Reading Study	PN [Demo LIFEx]	#10	Name of Physician(s) Reading Study
(0008,1090)	Manufacturer's Model Name	LO [LIFEx]	#6	Manufacturer's Model Name
(0008,1120)	Referenced Patient Sequence	SQ (SequenceDelimitationItem)	#76	Referenced Patient Sequence
(0008,1150)	Referenced SOP Class UID	UI (no value available)	#0	Referenced SOP Class UID
(0008,1155)	Referenced SOP Instance UID	UI (no value available)	#0	Referenced SOP Instance UID
(0008,9205)	Pixel Presentation	CS [MONOCHROME]	#10	Pixel Presentation
(0008,9206)	Volumetric Properties	CS [VOLUME]	#6	Volumetric Properties
(0008,9207)	Volume Based Calculation Technique	CS [NONE]	#4	Volume Based Calculation Technique
(0010,0010)	Patient's Name	PN [Demo LIFEx]	#10	Patient's Name
(0010,0020)	Patient ID	LO [LIFEx]	#6	Patient ID



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Main / Series 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 v7.4.0

Main:

- added: new layout (MIP Ax Cor Sag)

MIP:

- improved: window blocking under heavy use
- improved: increase default alpha blending of ROI on MIP frame
- fixed: mouse button operations are available on MacOS system
- improved: add "Click" and "Click40" tools on MIP frame with Shift+LMB
- improved: remove ROI on MIP frame with Shift+RMB

Series:

- added: shift of slice location with Ctrl+Mouse move (with takes into account the mouse displacement to calculate the shift location)
- fixed: ROIs don't disappear anymore after a screenshot of all view frames (.png)
- fixed: when binary file with orientation (ROI for example) is read to add a series, then the NEAREST_NEIGHBOR interpolation is chosen instead of the QUINTIC_LAGRANGIAN interpolation
- fixed: a bug prevented the series sorting from being done correctly

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Protocols updates



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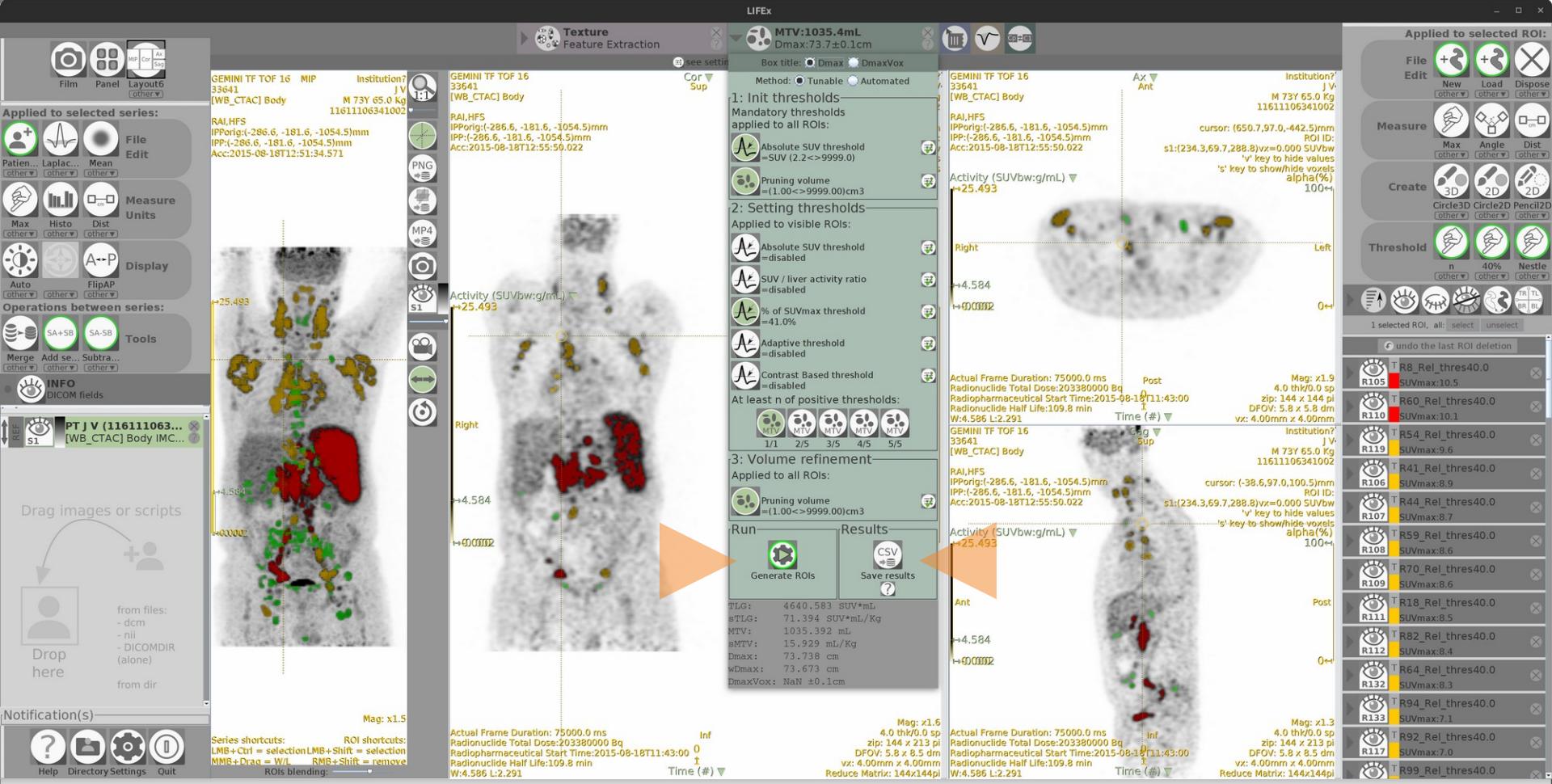
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MTV updates

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The MTV results has become independent of the generation of ROIs
→ i.e. it can therefore now be saved with already existing ROIs



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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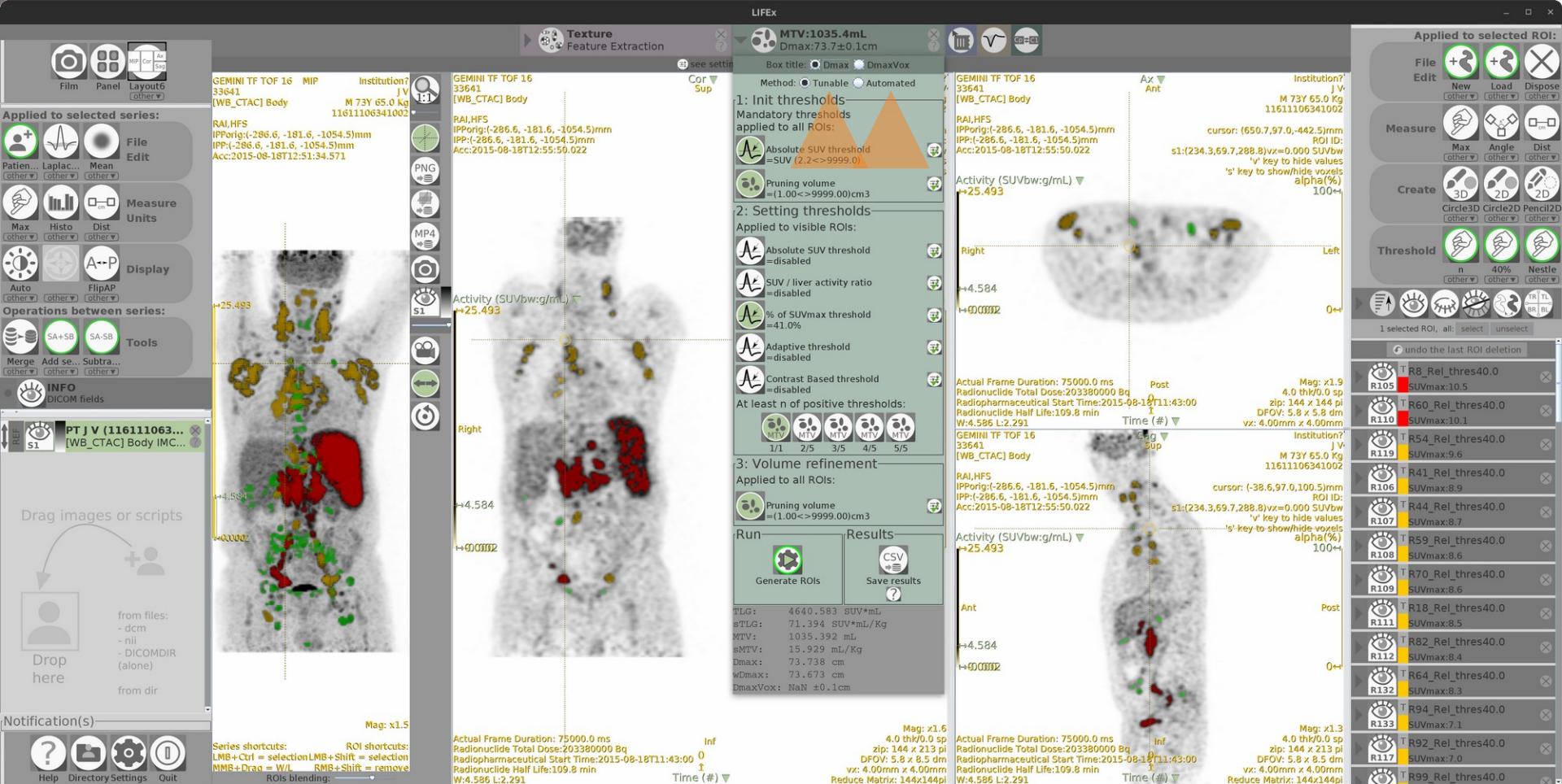
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MTV updates

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New automated method (without input parameters) to generating ROIs



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.

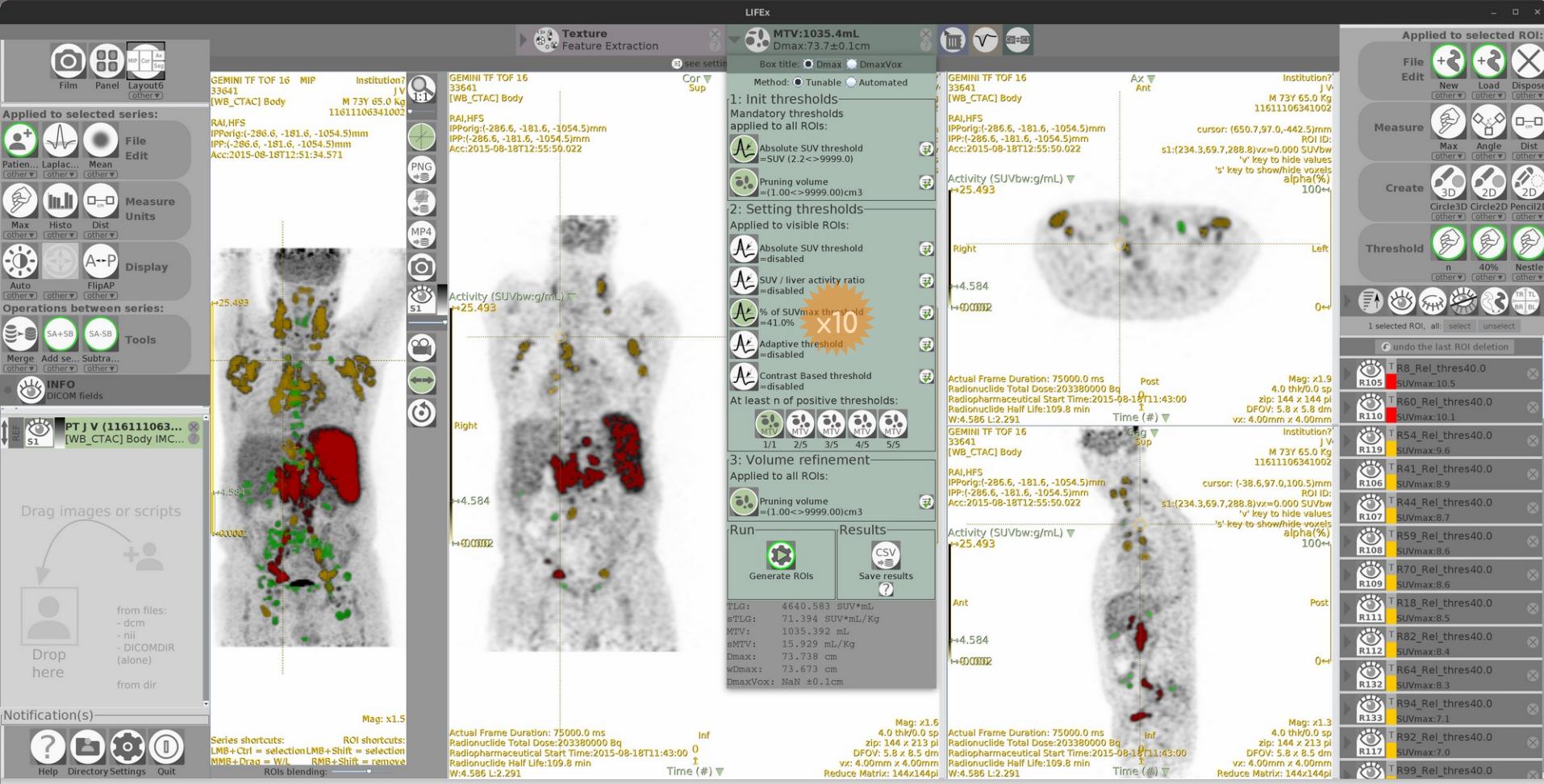


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Annoucement

MTV updates

Acceleration (x10) of the tunable segmentation process





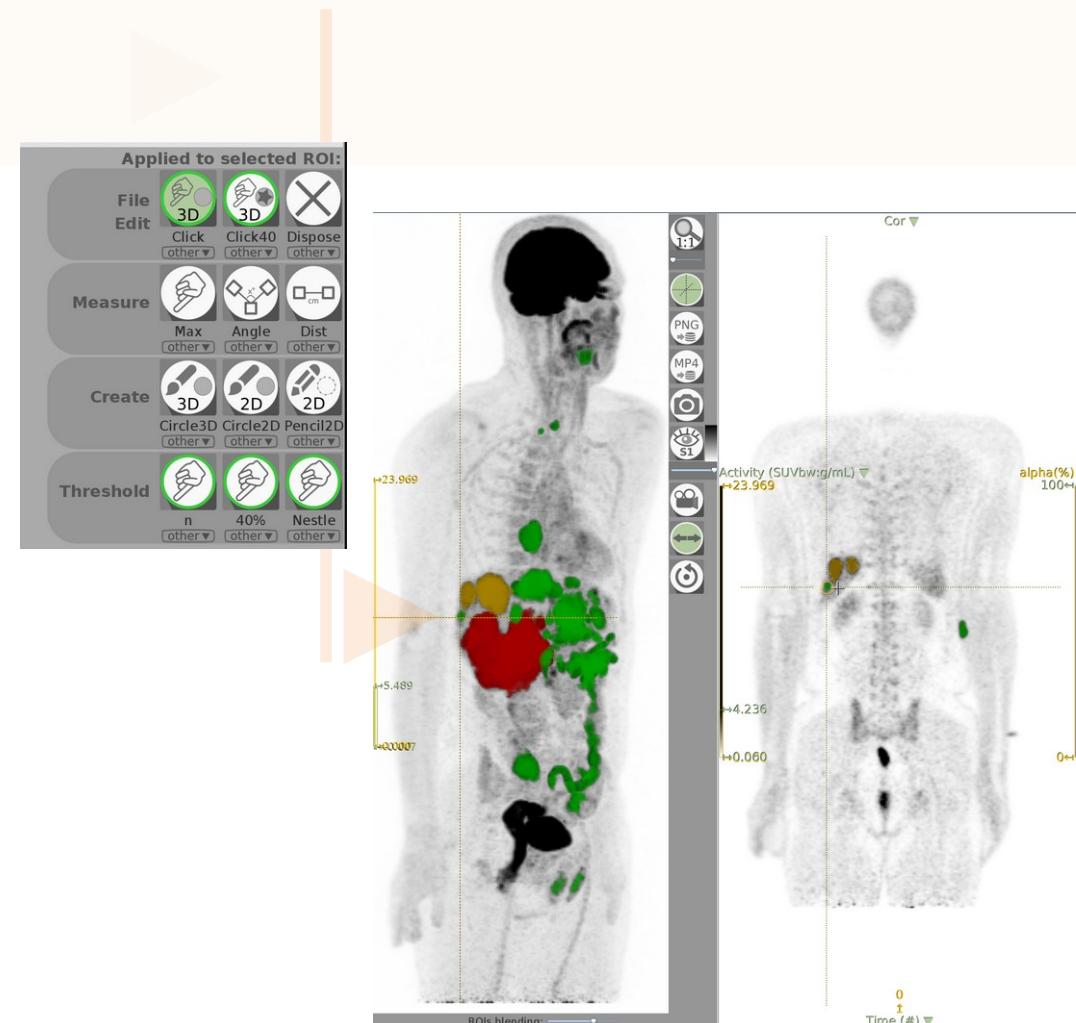
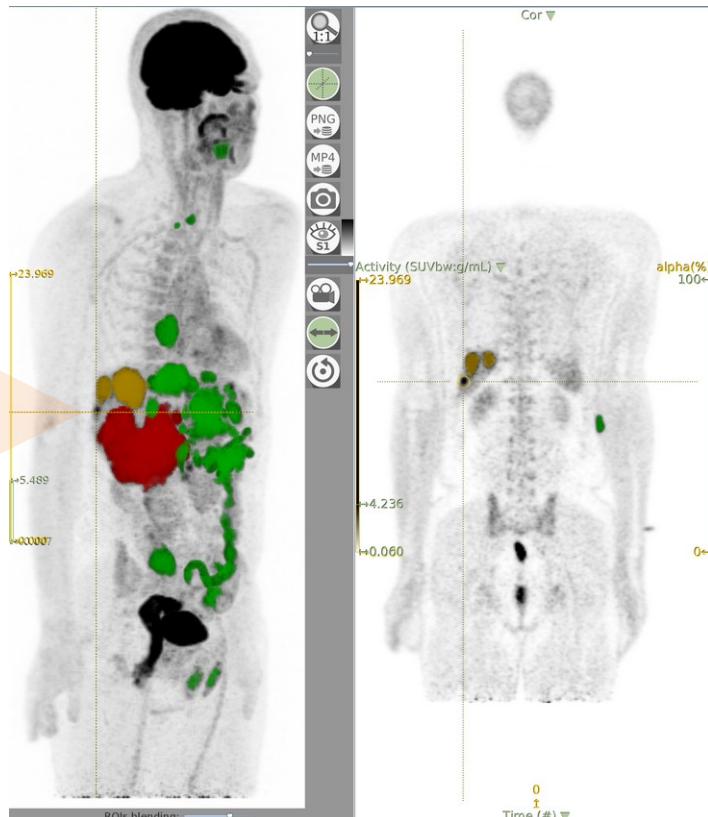
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MTV updates

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MIP updates





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To remember the algorithm:
Click&Draw



Click&Draw

Creates a VOI using the following approach:

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

(specially designed for PET images)



To remember the algorithm:
Click40&Draw



Click40&Draw

The "click40" method is a variant tool.

The step SegF is made :

with $I * 40/100$
instead of $I * 70/100$.

(specially designed for PET images)



MTV updates (summary)

Article definition	LIFEx <v7.3.1	LIFEx >= v7.3.4	LIFEx Legend
MTV	MTV(mL)	MTV(mL)	The tumor volume
TLG	TLG(SUV*mL)	TLG(SUV*mL)	MTV * SUVmean
SUVmean	SUVmean(SUV)	SUVmean(SUV)	The mean SUV value of the VOI
SUVmax	SUVmax(SUV)	SUVmax(SUV)	The SUV of the voxel with the highest SUV within the VOI
SUVpeak	no exist	MAX_peakmL(SUV)	The SUV of the 3mL with the highest SUV within the VOI (global peak)
Number of lesions	NumberOfROI	NumberOfROI	The number of separated lesion selections within the VOI
Dmax	Dmax	Dmax	The maximum distance between two lesions
DmaxBulk	MaxBindCOM(cm)	DmaxBulk(cm)	The maximum distance between the largest lesion and any other lesion
Spread	no exist	SUM_sumBindCOM(cm)	The sum of the distance between all lesions
SpreadBulk	sumBindCOM(cm)	BulkSumBindCOM(cm)	The sum of the distance between the largest lesion and all other lesions
Dvol	no exist	DiffVolBulkSmallest(mL)	The difference in volume between the largest and the smallest lesion
VolSpread	no exist	VolSpread	The sum of the differences in volume between all lesions
VolSpreadBulk	no exist	VolSpreadBulk	The sum of the differences in volume between the largest lesion and all other lesions
DSUVmax	no exist	DiffSUVmax	The difference in SUVmax between the lesion with the highest SUVmax and the lesion with the lowest SUVmax
DSUVmaxSum	no exist	DiffSUVmaxSum	The sum of the differences in SUVMax of all lesions
DSUVmaxBulk	no exist	DiffSUVmaxBulk	The difference in SUVmax between the largest lesion and the minimum of all SUVmax of other lesions
DSUVmaxSumBulk	no exist	DiffSUVmaxSumBulk	The sum of the differences in SUVmax between the largest lesion and all other lesions
DSUVmaxSumHot	no exist	DiffSUVmaxSumHot	The sum of the differences in SUVmax between the lesion with the highest SUVmax and all SUVmax of other lesions
DSUVpeak	no exist	DiffSUVpeak	The difference in SUVpeak between the lesion with the highest SUVpeak and the lesion with the lowest SUVpeak
DSUVpeakSum	no exist	DiffSUVpeakSum	The sum of the differences in SUVpeak of all lesions
DSUVpeakBulk	no exist	DiffSUVpeakBulk	The differences between the SUVpeak of the largest lesion and the SUVpeak of the lowest SUVpeak of all other lesions
DSUVpeakSumBulk	no exist	DiffSUVpeakSumBulk	The sum of the differences in SUVpeak between the largest lesion and all other lesions
DSUVpeakSumHot	no exist	DiffSUVpeakSumHot	The sum of the differences between the lesion with the highest SUVpeak and SUVpeak of all other lesions

Julia Driessen, Gerben JC Zwezerijnen, Heiko Schöder, Esther EE Drees, Marie José Kersten, Alison J Moskowitz, Craig H Moskowitz, Jakoba J Eertink, Henrica CW De Vet, Otto S Hoekstra, Joséé M Zijlstra, Ronald Boellaard. **The impact of semi-automatic segmentation methods on metabolic tumor volume, intensity and dissemination radiomics in 18F-FDG PET scans of patients with classical Hodgkin lymphoma.** Journal of Nuclear Medicine Jan 2022, jnmed.121.263067; DOI: 10.2967/jnmed.121.263067



LIFEx v7.4.0

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MTV updates

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MTV protocol:

- added: legend of feature names on result file
- added: SUM_sumBindCOM(cm) feature (Spread feature -> The sum of the distances between all lesions)
- added: SUM_sumBindWCOM(cm) feature (sum of all bind WCOM of all ROI)
- added: SUVpeak0.5mL(SUV) feature
- added: SUVpeak1mL(SUV) feature
- added: NumberOfROI feature
- added: DiffVolBulkSmallest(mL) feature -> The difference in volume between the largest and the smallest lesions
- added: VolSpread feature -> The sum of the differences in volume between all lesions
- added: VolSpreadBulk feature -> The sum of the differences in volume between the largest lesion and all other lesions
- added: DiffSUVmax feature -> The difference in SUVmax between the lesion with the highest SUVmax and the lesion with the lowest SUVmax
- added: DiffSUVmaxSum feature -> The sum of the differences in SUVMax of all lesions
- added: DiffSUVmaxBulk feature -> The difference in SUVmax between the largest lesion and the minimum of all SUVmax of other lesions
- added: DSUVmaxSumBulk feature -> The sum of the differences in SUVmax between the largest lesion and all other lesions
- added: DiffSUVmaxSumHot feature -> The sum of the differences in SUVmax between the lesion with the highest SUVmax and all SUVmax of other lesions
- added: DiffSUVpeak feature -> The difference in SUVpeak between the lesion with the highest SUVpeak and the lesion with the lowest SUVpeak
- added: DiffSUVpeakSum feature -> The sum of the differences in SUVpeak of all lesions
- added: DiffSUVpeakBulk feature -> The differences between the SUVpeak of the largest lesion and the SUVpeak of the lowest SUVpeak of all other lesions
- added: DiffSUVpeakSumBulk feature -> The sum of the differences in SUVpeak between the largest lesion and all other lesions
- added: DiffSUVpeakSumHot feature -> The sum of the differences between the lesion with the highest SUVpeak and SUVpeak of all other lesions
- fixed: the minimum values are no longer zero.
- fixed: sum of all bind of COM is corrected
- changed: the MTV result has become independent of the automatic generation of ROIs: the MTV results can therefore now be saved with already existing ROIs
- changed: an extra digit after the decimal point of MTV (mL) feature
- changed: MTV script gives the same features as the "Save results" button of the protocol
- changed: COMofROI feature is renamed into COM
- changed: WeightedCOMofROI feature is renamed into WCOM
- changed: sumBindCOM(cm) feature is renamed into BulkSumBindCOM (sum of the distance between the largest lesion and all other lesions=SpreadBulk feature)
- changed: avBindCOM(cm) feature is renamed into BulkMeanBindCOM(cm)
- changed: stdBindCOM(cm) feature is renamed into BulkStdBindCOM(cm)
- changed: minBindCOM(cm) feature is renamed into BulkMinBindCOM(cm)
- changed: maxBindCOM(cm) feature is renamed into BulkMaxBindCOM(cm)
- changed: avTotBindCOM(cm) feature is renamed into BulkMeanBindCOM(cm)
- changed: COM(vx) feature is renamed into BulkCOM(vx)
- changed: wCOM(vx) feature is renamed into BulkWCOM(vx)
- changed: sumBindWeightedCOM(cm) feature is renamed into BulkSumBindWCOM(cm)
- changed: avBindWeightedCOM feature is renamed into BulkMeanBindWCOM(cm)
- changed: stdBindWeightedCOM feature is renamed into BulkStdBindWCOM(cm)
- changed: minBindWeightedCOM feature is renamed into BulkMinBindWCOM(cm)
- changed: avTotBindWeightedCOM feature is renamed into BulkMeanBindWCOM(cm)



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Texture updates

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Texture protocol:

- added: areaUnderCurveCsh feature is now calculated on CT with negative intensities
- changed: AreaUnderCurveCsh renamed into AreaUnderCurveCIVH (Cumulative Intensity Volume Histogram)
- changed: in AreaUnderCurveCsh, binsize is (maximumGreyLevel - minimumGreyLevel) / 1000
 - IBSI, Intensity-volume histogram features / Arbitrary intensity units
- changed: Range feature is renamed into IntensityRange
- changed: Mean feature is renamed into MeanIntensity
- changed: Variance feature is renamed into IntensityVariance
- changed: Skewness feature is renamed into IntensitySkewness
- changed: Kurtosis feature is renamed into IntensityKurtosis
- changed: Median feature is renamed into MedianIntensity
- changed: MinimumGreyLevel feature is renamed into MinimumIntensity
- changed: MaximumGreyLevel feature is renamed into MaximumIntensity
- changed: 10thPercentile feature is renamed into 10thIntensityPercentile
- changed: 25thPercentile feature is renamed into 25thIntensityPercentile
- changed: 50thPercentile feature is renamed into 50thIntensityPercentile
- changed: 75thPercentile feature is renamed into 75thIntensityPercentile
- changed: 90thPercentile feature is renamed into 90thIntensityPercentile
- changed: InterquartileRange feature is renamed into IntensityInterquartileRange
- changed: MeanAbsoluteDeviation feature is renamed into IntensityBasedMeanAbsoluteDeviation
- changed: RobustMeanAbsoluteDeviation feature is renamed into IntensityBasedRobustMeanAbsoluteDeviation
- changed: MedianAbsoluteDeviation feature is renamed into IntensityBasedMedianAbsoluteDeviation
- changed: CoefficientOfVariation feature is renamed into IntensityBasedCoefficientOfVariation
- changed: QuartileCoefficientOfDispersion feature is renamed into IntensityBasedQuartileCoefficientOfDispersion
- changed: Energy feature is renamed into IntensityBasedEnergy
- changed: RootMeanSquare is renamed into RootMeanSquareIntensity

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ROI updates



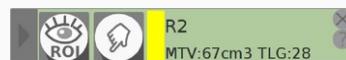
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ROI updates

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ROI:
Old display options (v7.3.0)



ROI:
New display options (v7.4.0)

- one-click: Localize max value
- double-clicks: On/Off display



Quick editing
with predefined organ names

Recent items	Predefined Organ	Predefined Lymph Node
Mediastinum X	Adrenal-glands	Abdomen-LN
Pancreas X	Aorta	Axillary-LN
Skin X	Bone	Cervical-LN
Spine X	Bone-marrow	Common-iliac-LN
	Brain	Internal-iliac-LN
	Breast	External-iliac-LN
	Bronchi	Deep-cervical-LN
	Esophagus	Deep-inguinal-LN
	Ear	Chest-LN
	Eye	Head-LN
	Gallbladder	Hilaire-liver-LN
	Heart	Liver-hilus-LN
	Kidneys	Inguinal-LN
	Interstitium	Inferior-deep-cervical-LN
	Large bowel	Mediastinal-LN
	Larynx	Mastoid-LN
	Liver	Neck-LN
	Lungs	Occipital-LN
	Mediastinum	Pelvic-LN
	Muscular	Parotid-LN
	Nasal-cavity	Periaortic-LN
	Oesophageal	Popliteal-LN
	Osteo-medullary	Praeauric-LN
	Pancreas	Retro-aortic-LN
	Paramedullary	Retro-peritoneal-LN
	Parathyroid-glands	Retro-clavicular-LN
	Pelvis	Retro-crural-LN
	Peritoneum	Sacral-LN
	Pineal-gland	Superficial-inguinal-LN
	Pituitary-gland	Supraclavicular-LN
	Pharynx	
	Pleural	
	Prostate	
	Rectum	
	Retroperitoneum	
	Skin	
	Small-bowel	
	Soft-tissue	
	Spine	
	Spleen	
	Sternum	
	Stomach	
	Subcutaneous	
	Trachea	
	Thyroid-gland	
	Thymus	
	Urinary-Bladder	
	Urethra	
	Ureter	
	Uterus	



LIFEx v7.4.0

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ROI multi-selection

C. Nioche



new display
tool bar

2 new buttons
for un/select all

5 selected ROI, all: select unselect		
undo the last ROI deletion		
▶	R105	T R8_Rel_thres40.0 SUVmax:10.5
▶	R110	T R60_Rel_thres40.0 SUVmax:10.1
▶	R119	T R54_Rel_thres40.0 SUVmax:9.6
▶	R106	T R41_Rel_thres40.0 SUVmax:8.9
▶	R107	T R44_Rel_thres40.0 SUVmax:8.7
▶	R108	T R59_Rel_thres40.0 SUVmax:8.6
▶	R109	T R70_Rel_thres40.0 SUVmax:8.6
▶	R111	T R18_Rel_thres40.0 SUVmax:8.5
▶	R112	T R82_Rel_thres40.0 SUVmax:8.4
▶	R132	T R64_Rel_thres40.0 SUVmax:8.3
▶	R133	T R94_Rel_thres40.0 SUVmax:7.1
▶	R117	T R92_Rel_thres40.0 SUVmax:7.0

73 selected ROI, all: select unselect		
undo the last ROI deletion		
▶	R105	T R8_Rel_thres40.0 SUVmax:10.5
▶	R110	T R60_Rel_thres40.0 SUVmax:10.1
▶	R119	T R54_Rel_thres40.0 SUVmax:9.6
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▶	R107	T R44_Rel_thres40.0 SUVmax:8.7
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▶	R133	T R94_Rel_thres40.0 SUVmax:7.1
▶	R117	T R92_Rel_thres40.0 SUVmax:7.0

quick shortcut
Ctrl+A: un/selection all



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ROI updates

C. Nioche

ROI:

- deleted: all uint8 of nifti format (keep only uint16 to have more than 16 ROI with Save-M menu)
- added: quick labelling with predefined organ names
- added: remove ROI with click on ROI on image with combined right button mouse and shift (=Shift+RMB)
- changed: All delete actions delete the file (as before) but also unload it from the application.
- improved: creating a new ROI no longer disables the Nii save button
- improved: the volume of SUVpeak1mL is closer to the real desired volume 1mL (the result is not much changed)
- improved: the volume of SUVpeak0.5mL is closer to the real desired volume 0.5mL (the result is not much changed)
- improved: ROIpeak is integrated by default in the basic ROI statistics calculations
- fixed: issue when drawing segmentation with absolute filter threshold activated
- fixed: issue on translate ROI
- fixed: issue on dispose all ROI
- fixed: freeze of union ROI when number of ROI to be merged is greater than 10
- fixed: series not found in ROI comparison tool
- fixed: new alert message if the 3D crosshairs are not in the area to be filled, or the filling is in an open structure.



End of the
announcement

don't forget



LIFEx v7.4.0

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LIFEx is still evolving

C. Nioche

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 Pellet-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