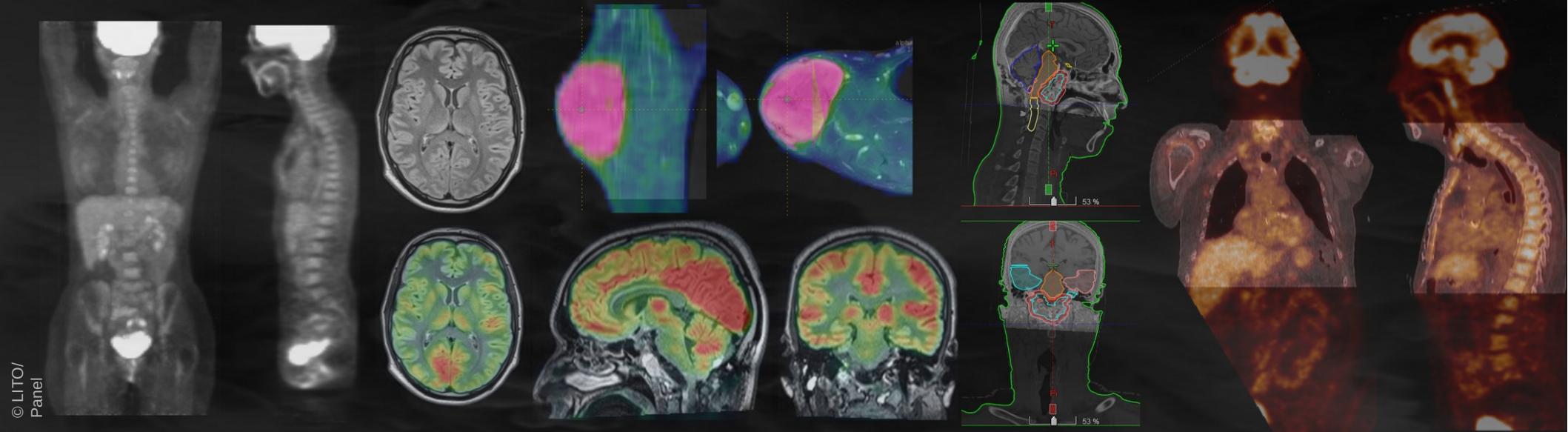




## Developpements logiciels





Dépôt à faire sur le gitlab du LITO

- Python :
  - Méthodes de correction du biais du champ magnétique pour images IRM (cerveau & sein)
  - Méthodes de normalisation (normalisation White-Stripe, RAVEL, Histogram-matching)
  - Méthodes de resampling
  - Script pour extraction d'indices radiomiques à l'aide de Pyradiomics
- R :
  - Méthodes de correction de l'effet scanner pour de petites cohortes multicentriques
  - Markdown de traitement complet des indices radiomiques :
    - prétraitement
    - correction de l'effet scanner par l'approche ComBat
    - normalisation
    - vérification de la robustesse des indices
    - sélection univariée complétée par une sélection par l'algorithme de Boruta
    - construction de modèles prédictifs et évaluation des modèles



- Statistiques :
  - scripts R



- Python :
  - Segmentation automatique des tumeurs du sein (réalisée par Masoomeh) = Visual Ensemble Segmentation (VES)
  - Installation faite sous litofs1 (quid du litoa1)



Personal / private repository such as my PhD thesis BIOMEDE and PREBIOMDED MR processing pipelines.

Projects shared with colleagues eg (the recent HECKTOR challenge)

Mostly python codes, a few of basic C++.

-  AntoineMerlet/VessLement
-  FahadKhalid1/awesome-semantic-segmentation
-  FahadKhalid1/MRI-Brain-Segmentation-and-3D-Reconstruction-of-Brain
-  FahadKhalid1/starter-academic
-  Lrebaud/HECKTOR\_LITO
-  Lrebaud/ICARE
-  FahadKhalid1/Fahad\_thesis

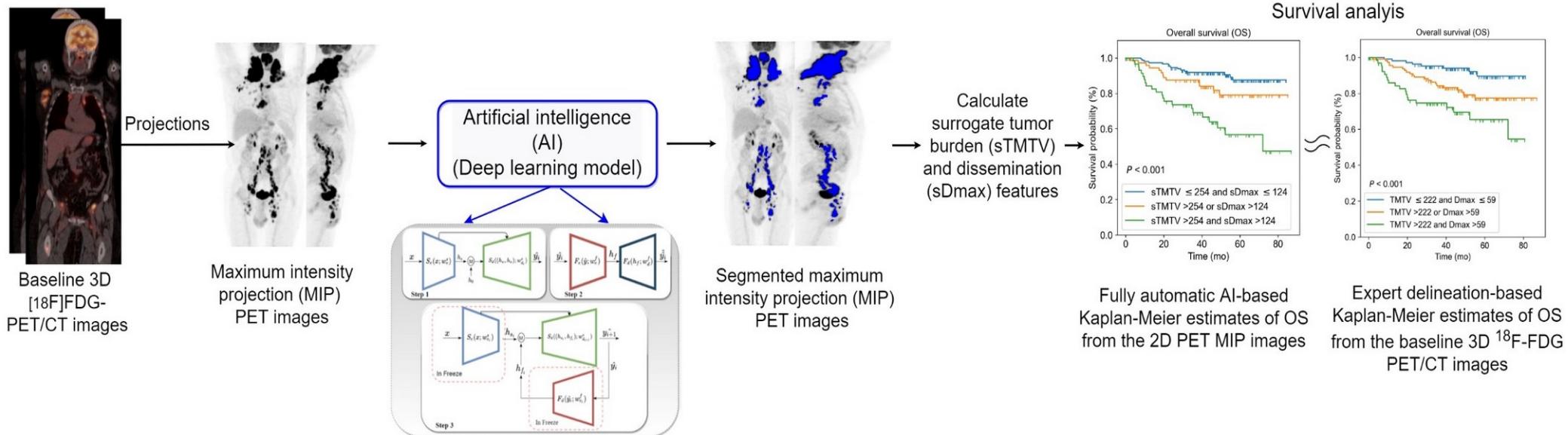
Sneak peak of repository list



[<sup>18</sup>F]FDG-PET maximum intensity projections and artificial intelligence:  
a win-win combination to easily measure prognostic biomarkers in DLBCL patients

Aim of the study:

To investigate whether TMTV and Dmax features could be replaced by surrogate features automatically calculated using an artificial intelligence algorithm from only two maximum intensity projections (MIP) of the whole-body <sup>18</sup>F-FDG PET images.





KibromBerihu / ai4elife Public

<> Code Issues Pull requests Discussions Actions Projects Security Insights

main · branches · 1 tag

Go to file Code

KibromBerihu Update readme.md 81a38fd 10 hours ago 119 commits

📄 documentation	Delete jupyter_notebook_step_by_step_illustration.html	27 days ago
📄 images	setup.py	3 months ago
📄 src	update	3 months ago
📄 Dockerfile	Update Dockerfile	4 months ago
📄 LICENSE	Initial commit	14 months ago
📄 environment.yml	environment	4 months ago
📄 readme.md	Update readme.md	10 hours ago
📄 requirements.txt	requirements add	4 months ago
📄 run_docker_image.bat	setup.py	3 months ago
📄 setup.py	Update setup.py	2 months ago
📄 test_docker.py	test-decker.py	3 months ago
📄 test_env.py	.test_env.py	3 months ago

readme.md

License MIT docker build passing

[2022\_06\_24] Update: AI4eLIFE: Easing local image feature extraction using AI.

readme.md

## Table of contents

- Summary
- Table of Contents
- Required folder structure
- Installation
- Usage
  - Easy use: testing mode
  - Transfer learning mode: development
- Results
- FAQ
- Citations
- Adapting LFBNet for other configurations or segmentation tasks
- Useful resources
- Acknowledgements

## 📁 Required folder structure

Please provide all data in a single directory. The method automatically analyses all given data batch-wise.

To run the program, you only need PET scans (CT is not required) of patients in nifty format, where the PET images are coded in SUV units. If your images have already been segmented, you can also provide the mask (ground truth (gt)) as a binary image in nifty format. Suppose you provided ground truth (gt) data; it will print the dice, sensitivity, and specificity metrics between the reference segmentation by the expert (i.e., gt) and the predicted segmentation by the model. If the ground truth is NOT AVAILABLE, the model will only predict the segmentation.

A typical data directory might look like:

```

-- main_folder                                     <-- The main folder or all patient folder

|   |-- parent folder (patient_folder_1)          <-- Individual patient folder name with uniq
|       |-- pet                                      <-- The pet folder for the .nii suv file
|           | -- name.nii or name.nii.gz          <-- The pet image in nifti format (Name can
|       |-- gt                                       <-- The corresponding ground truth folder fo
|           | -- name.nii or name.nii.gz          <-- The ground truth (gt) image in nifti fo
|   |-- parent folder (patient_folder_2)          <-- Individual patient folder name with uniq
|       |-- gt                                      <-- The pet folder for the .nii suv file
|           | -- name.nii or name.nii.gz          <-- The pet image in nifti format (Name can
|       |-- pet                                      <-- The corresponding ground truth folder for
|           | -- name.nii or name.nii.gz          <-- The ground truth (gt) image in nifti for
|
|   .
|
|   .
|
|   |-- parent folder (patient_folder_N)          <-- Individual patient folder name with uniq
|       |-- pet                                      <-- The pet folder for the .nii suv file
|           | -- name.nii or name.nii.gz          <-- The pet image in nifti format (Name can

```

LITO-Curie / [lito\\_image](#) Private

<> Code Issues Pull requests Actions Projects Security Insights

master 2 branches 0 tags Go to file Code

 Lrebaud initial commit	9701d79 13 days ago	1 commit
 lito_image	initial commit	13 days ago
 README.md	initial commit	13 days ago

README.md

## Lito\_image

This repository proposes a Python toolbox to process medical images and facilitate the analysis workflow of LITO members. It proposes a large variety of tools, going from a tool to anonymize DICOM files to a tool to convert DICOM PET images to nifti format.

### Install

### Authors and acknowledgment

- Nicolas Captier
- Thibault Escobar
- Louis Rebaud



LITO-Curie / [lito\\_ml](#) Private

<> Code Issues Pull requests Actions Projects Security Insights

master 2 branches 0 tags Go to file Code

 Lrebaud initial commit	97f4187 13 days ago	1 commit
 lito_ml	initial commit	13 days ago
 README.md	initial commit	13 days ago

README.md

## Lito\_ml

This repository proposes a Python toolbox for machine learning and aims to gather all the useful and re-usable pieces of code developed by LITO members.

### Install

### Authors and acknowledgment

- Nicolas Captier
- Thibault Escobar
- Louis Rebaud

LITO-Curie / **lito\_radiomics** Private

Code Issues Pull requests Actions Projects Security Insights

master 2 branches 0 tags Go to file Code ▾

Lrebaud initial commit	aa947e6 13 days ago	1 commit
lito_radiomics	initial commit	13 days ago
README.md	initial commit	13 days ago
pyradiomics_params_CTyaml	initial commit	13 days ago
pyradiomics_params_PETyaml	initial commit	13 days ago
radiomics_extraction.ipynb	initial commit	13 days ago

## README.md

### Lito\_radiomics

This repository proposes a customizable Python radiomics extractor based on [Pyradiomics](#). It inherits from all the functionalities of Pyradiomics extractor and will allow the integration of new features developed by LITO. It will also allow each user to test and develop their own features before definitively integrating them to this custom extractor.

### Install

#### Apply the extractor to a directory of images and masks

lito-radiomics package contains a function `lito_radiomics.extraction.directory_extraction` which will allow the users to apply the custom radiomics extractor to a whole dataset of images and associated masks (it will return the values of the specified radiomic features for each pair of image and mask).

The user is offered three options for specifying the couples of image and mask he wants to extract features from:

1. The user can provide the path to the directory which contains the images and the masks with the



LITO-Curie / **lito\_segmentation** Private

Code Issues Pull requests Actions Projects Security Insights

This repository is empty.

Care to check out the [GitHub Channel on YouTube](#) while you wait?

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## Développements radiomique :

caractérisation du gliome infiltrant du tronc cérébral  
à partir d'imagerie par résonance magnétique

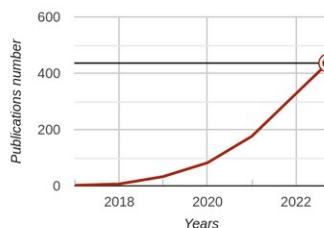
The screenshot shows the GitLab interface for a project named 'jessica'. The top navigation bar includes a search bar, a user profile icon, and various project management icons. The main header displays the project name 'jessica' and its identifier 'christophe.nioche > jessica'. Below the header, it shows '1 commit', '1 branche', '0 étiquette', and '473,5 Mo Project Storage'. A prominent modal window titled 'Auto DevOps' explains the feature and provides a link to documentation. The main content area lists a commit by 'Frederique Frouin' from 3 years ago, adding files related to a thesis. Below the commit are several dashed buttons for adding README, LICENSE, CHANGELOG, CONTRIBUTING, and Kubernetes configurations. The bottom section is a table of commits, each with a file icon, the commit message, the author, and the date.

Nom	Dernier commit	Dernière mise à jour
AvecJUPYTER	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans
Chap5_These_Mutation	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans
Chap6_These_Survie	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans
Features	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans
Gliomes_FANNY	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans
Methodologie_NE_PAS_GARDER	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans
Pour_LC_FANNY	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans
Standardization_Pipeline	ajout fichiers fin de these Jessica Goya Outi	il y a 3 ans



## Valorisation et collaborations (2022-10)

436 publications:



Evolution of the publications:

(from PubMed)

2016: 2 publications

2017: 5 publications

2018: 26 publications

2019: 49 publications

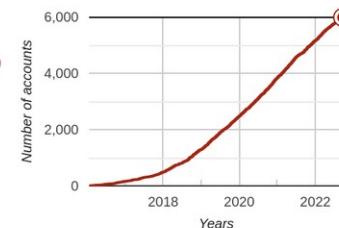
2020: 94 publications

2021: 151 publications

2022: 109 publications

(2022 in progress)

5984 user accounts:



Evolution of the accounts:

(from our site web)

2016: #161 (0.4 account/day)

2017: #323 (0.9 account/day)

2018: #802 (2.2 accounts/day)

2019: #1182 (3.2 accounts/day)

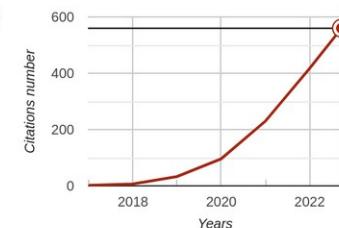
2020: #1358 (3.7 accounts/day)

2021: #1328 (3.6 accounts/day)

2022: #830 (3.1 accounts/day)

(2022 in progress)

560 citations:



Evolution of citations:

(from google scholar)

2016: 2 citations

2017: 5 citations

2018: 26 citations

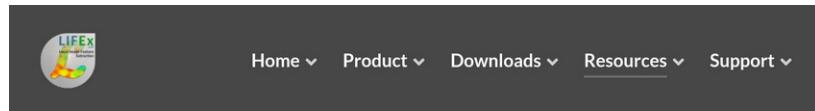
2019: 63 citations

2020: 134 citations

2021: 187 citations

2022: 143 citations

(2022 in progress)



## Open sources (registered account)

The source code of the protocols is open and can be downloaded below:

- lifex-7.3.0
  - [lifex-7.3.0-protocolCalciumQuantitation.zip](#)
  - [lifex-7.3.0-protocolLabelling.zip](#)
  - [lifex-7.3.0-protocolLabelling.zip](#)
  - [lifex-7.3.0-protocolLateMeasure.zip](#)
  - [lifex-7.3.0-protocolMrPerf.zip](#)
  - [lifex-7.3.0-protocolMtv.zip](#)
  - [lifex-7.3.0-protocolMtvNotation.zip](#)
  - [lifex-7.3.0-protocolPtComp.zip](#)
  - [lifex-7.3.0-protocolPtPerf.zip](#)
  - [lifex-7.3.0-protocolPve.zip](#)
  - [lifex-7.3.0-protocolQualityControl.zip](#)
  - [lifex-7.3.0-protocolTexture.zip](#)

# Le bazar ? Un peu, mais contrôlé

The screenshot shows a GitLab interface for the 'lito-team' group. The left sidebar displays various project categories. The main area shows the 'lito-team' group page with three projects listed under 'Sous-groupes et projets':

- lito\_image**: Python toolbox for medical image processing. Last updated 1 week ago.
- lito\_radiomics**: Customizable Python radiomics extractor based on Pyradiomics. Last updated 1 week ago.
- lito\_ml**: Python toolbox for the development of machine learning pipelines in LITO. Last updated 2 weeks ago.

Web (blog), github, gitlab, intro ?

# Valorisation et collaborations : où les placer ?

→ vitrine de tous ces outils mis à disposition de la communauté  
- au niveau Curie CDR / Vision ?

The screenshot shows the Curie intranet homepage. At the top, there's a navigation bar with links like News, Agenda, Focus on, In the media, Did you know?, Journals, Documents, FAQ, and Tools. The main header features the Institut Curie logo and the text "Clic C'est l'intranet Curie". Below the header, there's a search bar and a "Managers area" section with a gold ribbon icon. The main content area is divided into several sections:

- STRATEGIC PLAN**: A sidebar with links to CID iManage, KineFold, Recherche Clinique, Catalogue CRB, BioSource, Bioinformatics, Electronic lab notebook elabFTW, and Data tools.
- ABOUT CURIE**: Includes profiles of Prof. Alain Puisieux and Tatiana Malherbe.
- JOB TOOLS**: Includes links to Immunothérapie, Chemical Library, How to sign publications?, and Online scientists reviews.
- IN PRACTICE**: Includes sections for Identification (with a login form), Managers area, and Social life and Leisure time.
- SOCIAL LIFE AND LEISURE TIME**: Includes a RECHERCHER search bar and options for On the intranet and On SEQUIDON.
- Risk**: Includes a dropdown menu for Sécurité des personnes et des locaux.
- Professional software**: A large yellow-highlighted section containing links to various software tools.
- Courier**: Address: Centre de Recherche, 26 rue d'Ulm, 75248 Paris Cedex 05.
- Bureaux**: Address: Centre de Recherche et Fonctions support, 187 rue Saint-Jacques, 75005 Paris.
- Organization chart**: Includes a "LIST Units/Teams Contacts" link and an "Organisational chart Research Center 2022" link.

The screenshot shows a Microsoft Teams channel named "6.Software" with a blue background. The channel has tabs for Posts, Files, and +. There are several messages from users:

- Chervon Alexander** (6/26/2021, 4:59 PM): DeepCycle reconstructs a cyclic cell cycle trajectory from unsegmented cell images using Luca Rappe1,2 , Alexander Rakhlin3 , Angelos Rigopoulos1 , Sergey Nikolenko4,5 & The
- Kapoor Varun** (10/20/2021, 12:25 PM): For coloring of tracks coming out of 3D trackmate tracking and obtaining track statistics have been updated. It allows to re-label the 3D + t segmentation image with any spot or track provide distribution plots for all the track attributes, to do so we have the xml, tracks and the notebooks provided here: <https://github.com/kapoorlab/NapaTrackMater/blob/main/ex> See more
- NapaTrackMater/ColorTracks.ipynb at main · kapoorlab/NapaTrackMater** (10/20/2021, 12:25 PM): Napa Visualization tool for Trackmate & 6.0 and bTrackmate XML files for 2D package napatrackmater - NapaTrackMater/ColorTracks.ipynb at main · kapoorlab/naptarckmater
- Dos Santos Groeneweld Clarice** (12/8/2021, 10:10 AM): Open-source python-based alternative to ImageJ, to avoid having to go back-and-forth be interacting with images. Looks promising, but still in alpha.
- napari** (<https://napari.org/>): napari is a fast, interactive, multi-dimensional image viewer for Python. It's designed for analyzing large multi-dimensional images. It's built on top of Qt (for the GUI)... napari.org

At the bottom right, there's a "New conversation" button.