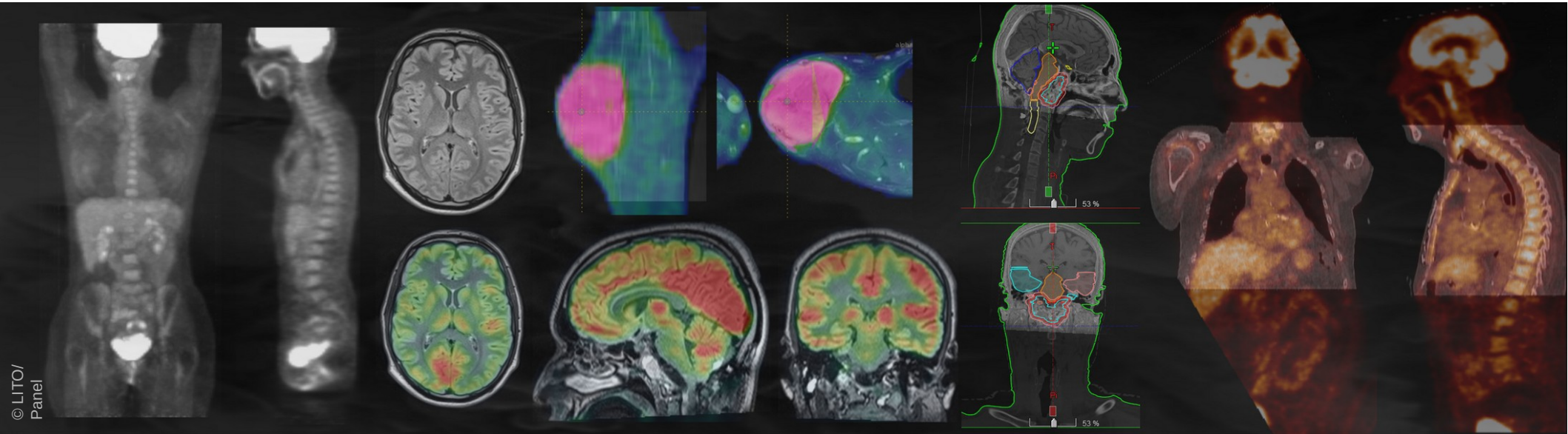
LITO

Developpements logiciels

institut Curie

Inserm
La science pour la santé
From science to health



© LITO/
Panel

Emplacement à venir

Marie-judith

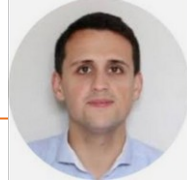
Dépôt à faire sur le gitlab du LITO

- 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

Emplacement à venir

Romain



- Statistiques :
  - scripts R

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

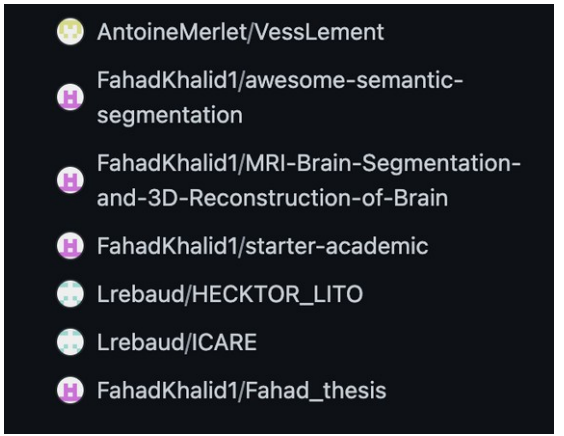
https://github.com/FahadKhalid1

Fahad

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

Projects shared with collegeues eg (the recent HECKTOR challenge)

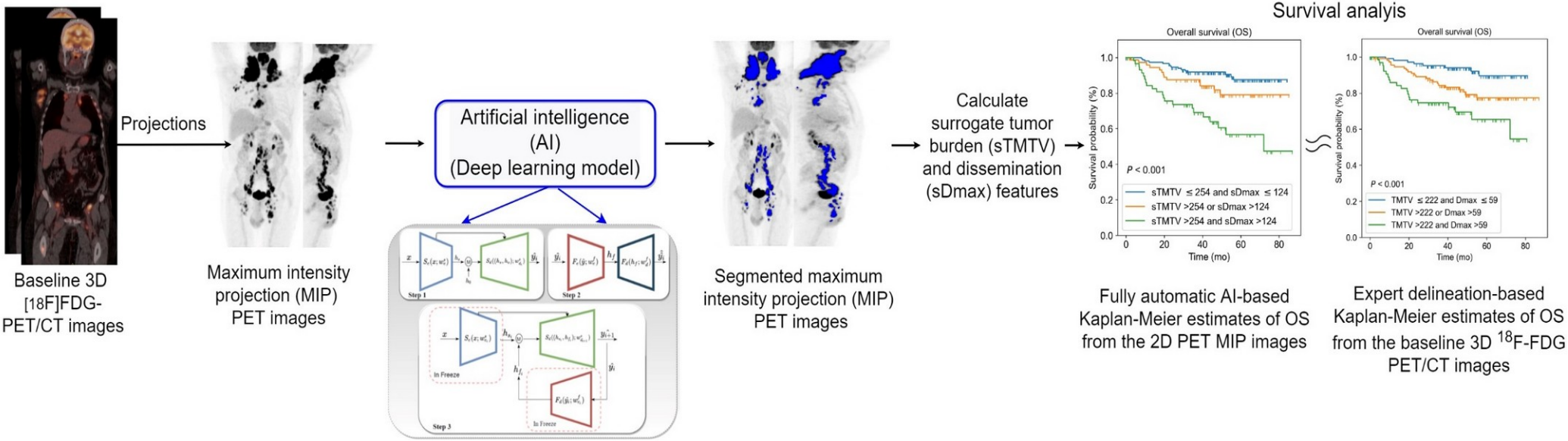
Mostly python codes, a few of basic C++.



Sneak peak of repository list

[18F]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 18F-FDG PET images.



KibromBerihu / **ai4elife** Public

Code | Issues | Pull requests | Discussions | Actions | Projects | Security | Insights

main | 2 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.

18F-FDG PET maximum intensity projections and artificial intelligence: a win-win combination to easily measure prognostic biomarkers in DLBCL patients. Journal of Nuclear Medicine Jun 2022, jnumed.121.263501. DOI: https://doi.org/10.2967/jnumed.121.263501

Introduction: Baseline 18F-FDG PET/CT image-driven features have shown predictive values in Diffuse Large B-cell lymphoma (DLBCL) patients. Notably, total metabolic active tumor volume (TMTV) and tumor dissemination (Dmax) have shown predictive values to characterize tumor burden and dissemination. However, TMTV and Dmax calculation require tumor volume delineation over the whole-body 3D 18F-FDG PET/CT images, which is prone to observer-variability and complicates using these quantitative features in clinical routine. In this regard, we hypothesized that tumor burden and spread could be automatically evaluated from only two PET Maximum Intensity Projections (MIPs) images corresponding to coronal and sagittal views, thereby easy the calculation and validation of these features.

Here, we developed data-driven AI to calculate surrogate biomarkers for DLBCL patients automatically. Briefly, first, the (3D) 18F-FDG PET images were projected in the coronal and sagittal directions. The projected PET MIP images are then fed to an AI algorithm to segment lymphoma regions automatically. From the segmented images, the surrogate TMTV (sTMTV) and surrogate Dmax (sDmax) are calculated and evaluated in terms of predictions for overall survival (OS) and progression-free survival (PFS).

readme.md

Table of contents

📁 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 folde

|      |-- 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
```

https://github.com/LITO-Curie

Nicolas, Thibault, Louis



LITO-Curie / **lito_image** Private

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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

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LITO-Curie / **lito_ml** Private

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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

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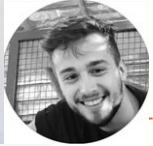
https://github.com/LITO-Curie

Nicolas, Thibault, Louis





LITO-Curie / **lito_radiomics** Private

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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_CT.yaml	initial commit	13 days ago
pyradiomics_params_PET.yaml	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 developped 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

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This repository is empty.

Care to check out the GitHub Channel on YouTube while you wait?

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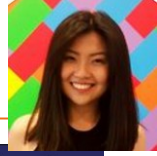
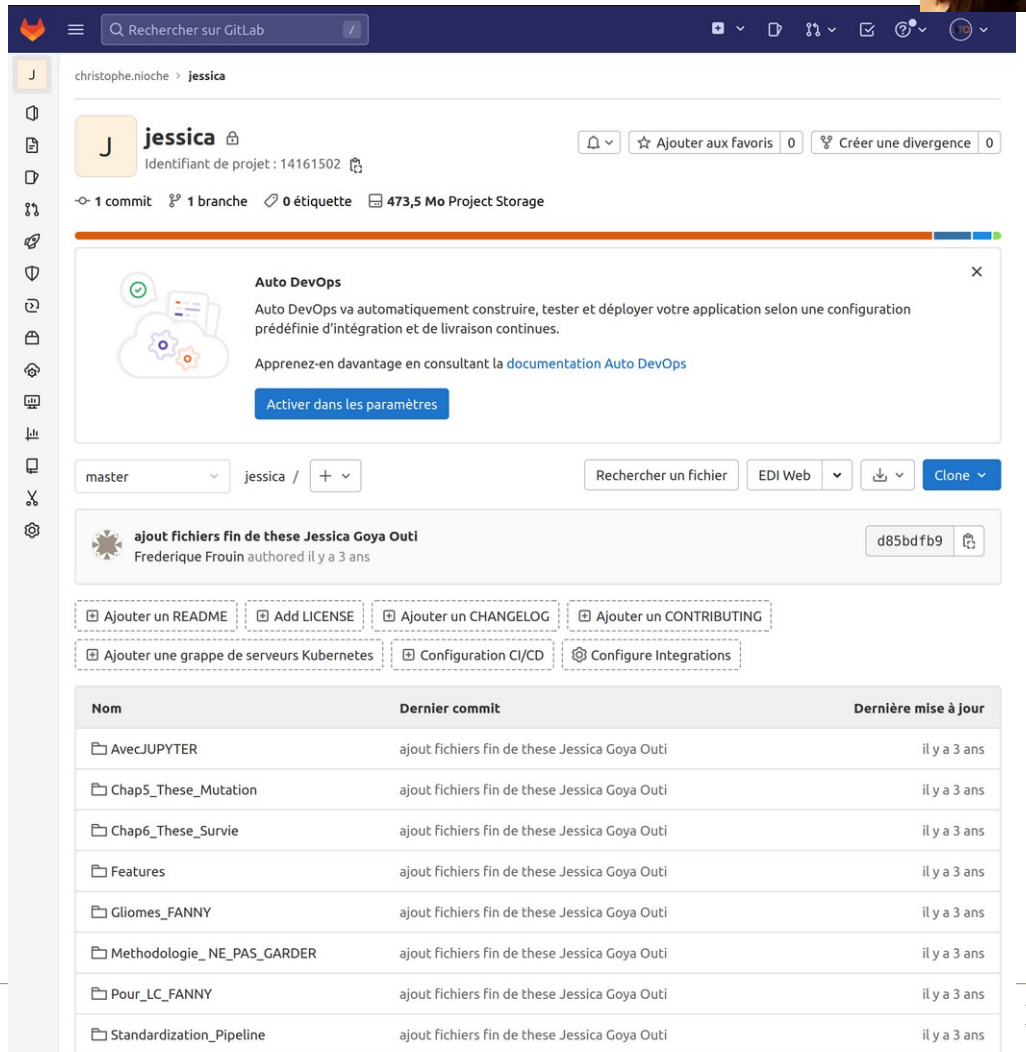
Jessica



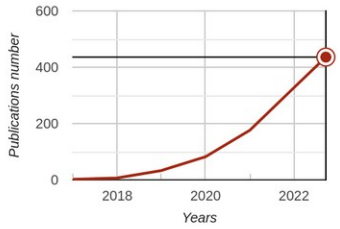
Développements radiomique :

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



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

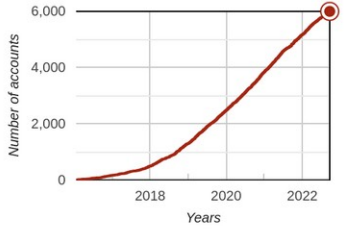
2020: 94 publications

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)

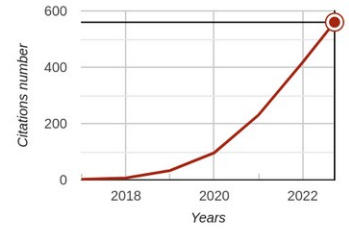
2020: #1358 (3.7 accounts/day)

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

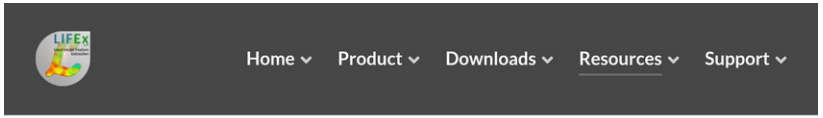
2019: 63 citations

2020: 134 citations

2021: 187 citations

2022: 143 citations

(2022 in progress)

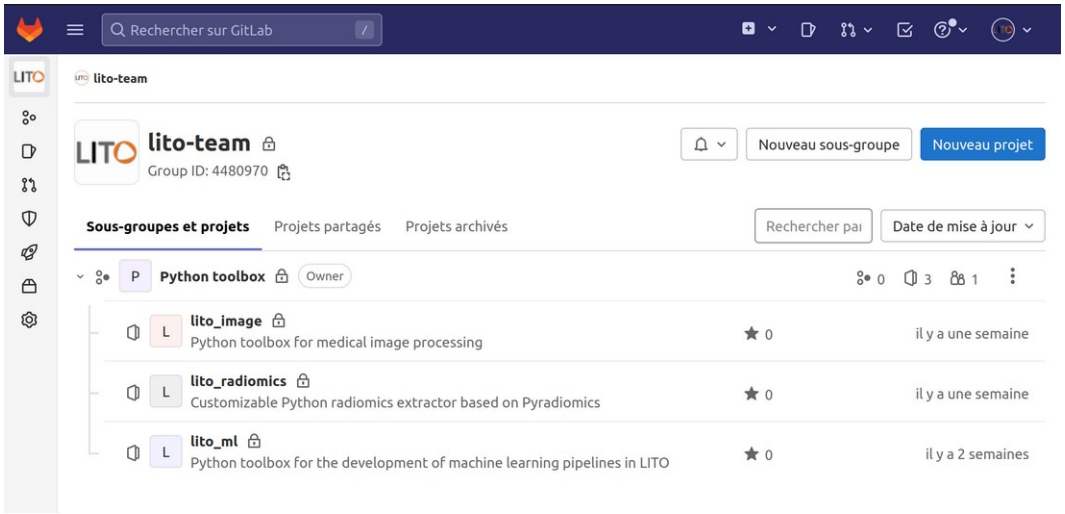


Open sources (registered account)

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



Web (blog), github, gitlab, intra ?

Valorisation et collaborations : ou les placer ?

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