**ReadMe GUI MENINGIOMA (Graphical User Interface)**

<https://github.com/theMIDAgroup/GUI-Meningioma>

A package providing Matlab and Python tools for image visualization, segmentation, and radiomics analysis. Tested with Matlab versions 2021b and 2022a, Python version 3.11.0. Usage of the package FLIRT, a tool of FSL version 6.0.5.1 (FMRIB Library version 6.0).

**REFERENCES**

[1] I. Cama, V. Candiani, M. Piana and C. Campi, "*A comprehensive tool for image segmentation and radiomics analysis of MR images*", submitted (2022).

[2] I. Cama, V. Candiani, L. Roccatagliata, P. Fiaschi, G. Rebella, M. Resaz, M. Piana and C. Campi, "*Segmentation accuracy and the reliability of radiomics features*", submitted (2022), preprint available at

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<https://github.com/theMIDAgroup/GUI-Meningioma>: MATLAB/Python programming tools for

image segmentation and radiomics analysis

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USAGE:

With this implemented package one can:

1. browse the MR T1 images of a patient with a first GUI,
2. insert the necessary ROIs around the tumor region(s) one aims to extract,
3. produce an automatic segmentation of such images via a level set method algorithm,
4. check (and possibly modify) the segmentation results for the T1 images in a second GUI,
5. co-registrate the masks produced by the segmentation algorithm with the ADC images,
6. check (and possibly modify) the co-registration results for the ADC images in a third GUI,
7. compute radiomics features for both T1 and ADC images (where present) with different quantization algorithms.

In the following, we will present some guidelines for the use of such GUIs and the associated functions. Note that it is assumed that Matlab and Python are correctly installed, and that the FSL package is included in the Python documentation.

Disclaimer: the GUIs are implemented for the application to MR images, but they work, to a certain extent, also with different types of images (CT, PET). The variables and functions’ names, however, remain specific for the MR case.

## PIPELINE:

* Open Matlab.
* Open main\_gui\_brain.m and click "run", a GUI will appear (GUI 1), GUI panels’ positions may slitghly differ depending on the computer used.
* Click on LOAD and load the whole folder containing the T1 images of the considered patient (not the single slices/DICOM images).
* Adjust the contrast if needed (usually, a value of around 1000 will do).
* Insert the ROIs around the tumor by choosing “District 1” from the pop-up menu and then clicking on the rectangular (circular, polygonal) shape on the right-hand side, browse the slices to put the ROI in all the slices involved. When finished, press “END”. To add the ROIs around a second tumor, change to “District 2” and redo the process.   
  If more than one tumor is present in the same slice, initially put different ROIs, then use “MERGE” to produce only one volume mask (see the “MERGE” command in the following).
* After checking all the slices, tick “ENABLE ROI”.
* The default quantization algorithm for radiomics feature computation is “Equal”, select a different one from the pop-up menu in the bottom right corner of GUI 1 depending on the application in mind.
* Click on “START ANALYSIS”, the segmentation algorithm will start.

A new GUI will appear (GUI 2). There, one can check the outcome of the automatic segmentation algorithm. At this point:

* Browse all the slices and check whether the automatic segmentation is reasonable. If not, one can always adjust the vertices of the polygon (the red/green dots) depending on the desired result. The vertices can also be removed or added with a right click of the mouse.
* The automatic segmentation algorithm might generate two different segmentation proposals for those slices that differ consistently from the previous/next slice. In order to facilitate the manual intervention, one can choose which of the two segmentations to select (with the buttons above the images) and possibly still adjust the polygon that surrounds the tumor. In addition, one can also choose to replace the current slice segmentation with the previous or the next one (in the latter case, only after checking the segmentation in the next slice): the replaced segmentation will depend on the choice made in the related slice (automatic level set/continuity criteria).
* Once all the slices have been checked, click on “DONE”, the computation of the radiomics features for the T1 images will start with the quantization algorithm selected in GUI 1.

If ADC images are not included in the patient’s folder, then an Excel file will be produced with the radiomics features extracted only from the T1 segmented images (2D and 3D), and the analysis is terminated. If ADC images are included, then another step is needed.

----------------------------------------- If using Windows --------------------------------------------------

Co-registrate first the two series with FSL.

* Open Python.
* Open file coregistrationT1\_ADC.py, this will generate the NIFTI format for the T1 mask.
* Insert the patient’s number and press "run" to co-registrate.
* Open file maskT1\_2\_maskADC.py, this will generate the transformation matrix from the T1 mask to ADC mask in NIIFTI format.
* Insert the patient’s number and the considered tumor’s number, then press "run".
* Click on "run" for each tumor of the patient under examination (change the tumor’s number only).

T1 and ADC images of the considered patient have been correctly co-registered, and the considered T1 binary masks have been transferred on the ADC images. Then:

* Go back to Matlab.
* Open file mask\_adc\_nii2mat.m and press “run".

----------------------------------------- If using Mac---------------------------------------------------------

All the previously described steps are integrated in the function mask2dcm.m.

A third GUI (GUI 3) showing the result of the T1 masks on the ADC images will open. Then:

* Browse all the ADC slices and modify the segmentation if needed, once again by clicking on the dots and moving them around the tumor’s edges. If not satisfactory, one can also replace the current segmentation with the one from the previous/next slice (hence possibly adding or removing the segmentation).
* Once all the ADC slices have been checked, click on “DONE”, the computation of the radiomics features for the ADC images will start.

An excel file with radiomics features on ADC images will be produced and the analysis will end.

## Buttons of the ROIs and functionalities for modifying the initial ROI definitions without necessarily starting from scratch.

## START SEGMENTATION:

This function starts the segmentation analysis for all the slices in all the created ROIs. If it is the first time one launches the analysis, the segmentation will automatically proceed, and the second GUI will then open. If a segmentation result is already present from previous computations, then there can be different cases when clicking on “START ANALYSIS”: “YES”, “NO”, “CANCEL”.

* “CANCEL”: leaves everything unvaried.
* “YES”: the segmentation analysis starts from scratch for each ROI, meaning that the function overwrites the field ROI.SegmentationPixelIdList with the newly computed (automatic) segmentation. Moreover, the function calls “Initialize\_ROI\_brain.m”, that removes all the fields associated to ADC (if present) and removes the field ROI{it}.aux\_pos\_fwd (needed for the check in merge\_masks.m).
* “NO”: the second GUI will open and will show the (already present) segmentation. No changes in the ROI positions and in the segmented images will be done at this stage. However, in the second GUI one can modify the masks.

**Panel “SAVE”**

## RESET ROI

This button resets the settings for the currently selected ROI{val}. The function calls Initialize\_ROI\_brain.m that: 1) empties all the fields associated to T1 in the related cell (val) of the global ROI, 2) removes ADC related fields in the related cell (val) of the global ROI and 3) removes ROI.aux\_pos\_fwd in the related cell (val) of the global ROI.

## RESET ALL

This function performs the same initialization as in RESET ROI, but for all the existing cells in ROI (val = 1,…,5).

## SAVE ALL

This function saves the existing global ROI to a file.mat.

**Panel “Delete slices from ROI”**

## DELETE

This function allows one to remove some slices from the selected ROI, provided that the slices are at the beginning or at the end of the ROI, and not in the middle. In order to do that:

* In the field “ROI”, select the district to remove slices from.
* Insert the number of the new first slice of the ROI in the field “NEW START” (it can coincide with the old first slice of the ROI).
* Insert the number of the new last slice of the ROI in the field “NEW END” (it can coincide with the old last slice of the ROI).
* Click on “DELETE” to delete the slices not included in the range NEW START - NEW END.

This function can be used:

* Right after the ROI initialization/creation in the main GUI, before the segmentation analysis is performed.
* When the segmentation analysis on the ROI is already finished but one wishes to modify the ROI (after modifying the ROI, click on “START ANALYSIS” and check again all the slices). The files in the corresponding folders will be updated with the new analysis (?).

The function also removes the ADC related fields and ROI.aux\_pos\_fwd from the current cell (val) of the global ROI.

**Panel “Append ROI”**

## APPEND

This function allows one to add slices to the selected ROI. In order to do that, one needs to have two separate ROIs, with one containing the to-be-added slices.

* Insert the number of the first ROI in the field “ROI head”, this is the ROI to which one aims to add slices (always at the end of ROI head).
* Insert the number of the ROI containing the slices to add at the end of ROI head in the field “ROI tail”.
* Click on “APPEND” to merge the two masks.

This function can be used

* Right after the ROI initialisation/creation in the main GUI, before the segmentation analysis is performed.
* When the analysis on the ROI is already finished but one wishes to modify the ROI (after modifying the ROI, click on “START ANALYSIS” and check again all the slices).

The district corresponding to “ROI tail” will be deleted from the GUI, but not from the created folders: if the analysis had already been performed before using this functionality, the folders containing mat files, xlsx and dcm related to the tumor “ROI tail” will keep existing on your PC.

**Panel “Merge components of the same ROI”**

## MERGE

The function “MERGE” can be used when the same tumor has two connected components on one or more slices. Firstly, detect the two connected components and put two different ROIs around them, then click on “START ANALYSIS”.

When the analysis on T1 and ADC is complete, one needs to go back to the main GUI and merge the two connected components.

* Insert the number of the ROI corresponding to the first connected component in the field “ROI part 1".
* Insert the number of the ROI corresponding to the second connected component in the field “ROI part 2”.
* Click on “MERGE” to merge the masks of the two connected components and compute the radiomics features of the union. This function creates a new mat file with the mask of the union from the two components of T1. The same happens with ADC masks.

Note that, when (re)opening the GUIs with Run\_GUI\_CheckSlices.m, both in GUI\_Check\_T1 and in GUI\_Check\_ADC the two connected components will anyway be shown separately and will have to be modified separately.

## MERGE

The button “MERGE 3” is used for merging three different connected components, and it must be used after the button “MERGE”.

**Panel “Other GUIs”**

## Check T1 segmentation

If a segmentation result is present, this button directly opens the second GUI for checking the segmentation outcome on T1 images. If it is the first opening, a warning message will appear.

## Check ADC segmentation

If a segmentation result is present, this button directly opens the third GUI for checking the segmentation outcome on ADC images. If it is the first opening, a warning message will appear.

**Panel “Quantization algorithms”**

This pop-up menu allows one to choose the desired quantization algorithm, in order to compute the radiomics features with a specific setting for the computation of grey levels (options are: Equal, Uniform, Lloyd and no quantization).

## Content of the folders.

The structure of the folders is the following.

* **DATA**. This folder contains two examples of patient data that can be used with our GUIs. T1 and ADC folders contain the DICOM files of T1 and ADC images, respectively. T1\_MAT contains the .mat files with information about the created ROIs and the patient metadata. T1\_OUTPUT\_MASK has all the necessary files regarding the segmentation results on T1 images and the co-registration masks for ADC images. RADIOMICS\_OUTPUT has all the radiomics-related files, as an example there are 2D and 3D radiomics feature values for T1 and ADC volumes, all computed with quantization “Equal”.
* **GUI**. All the implemented codes for the GUIs are in this folder.
* **packages**. This folder contains all the radiomics packages taken from Vallières et al (see the Acknowledgments section).

ACKNOWLEDGEMENTS: other software code

LEVEL SET METHOD

* Level set algorithm from T.F. Chan and L.A. Vese, “Active contours without edges”, IEEE Transactions on Image Processing, 2001, 10(2), 266-277.

RADIOMICS ANALYSIS PACKAGES (taken from Vallieres’ GitHub ReadMe)

* Martin Vallières <https://github.com/mvallieres/radiomics/>
* Wei's GLRLM toolbox: Xunkai Wei, Gray Level Run Length Matrix Toolbox v1.0, Software,Beijing Aeronautical Technology Research Center, 2007.  
   <http://www.mathworks.com/matlabcentral/fileexchange/17482-gray-level-run-length-matrix-toolbox>
* Q. Li: <http://www.mathworks.com/matlabcentral/fileexchange/23377-ellipsoid-fitting>
* CERR development team:   
  <http://www.cerr.info/>
* Dirk-Jan Kroon (imresize3D.m):   
  <http://www.mathworks.com/matlabcentral/fileexchange/21451-multimodality-non-rigid-demon-algorithm-image-registration/content//functions/imresize3d.m>
* David Reshef and Yakir Reshef: MINE version 1.0.1d   
  <http://www.exploredata.net/>
* DREES development team:   
  <http://www.cerr.info/drees>
* Enric Junqué de Fortuny (fastAUC.cpp):   
  <http://www.mathworks.com/matlabcentral/fileexchange/41258-faster-roc-auc>
* François Beauducel (roundsd.m):   
  <http://www.mathworks.com/matlabcentral/fileexchange/26212-round-with-significant-digits>
* Jos van der Geest (herrorbar.m):   
  <http://www.mathworks.com/matlabcentral/fileexchange/3963-herrorbar>