

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.

REFERENCES:

[1] I. Cama, V. Candiani, M. Piana and C. Campi, "Impact of segmentation accuracy on features quality and robustness in radiomics", to be submitted (2022).

AUTHORS:

Isabella Cama*, Valentina Candiani*, Michele Piana^{*a}, Cristina Campi^{*a}

* Department of Mathematics (DIMA), University of Genova, Italy
The Life Science Computational Laboratory (LiscompLab): <https://liscomp.dima.unige.it>
MIDA group: <https://mida.unige.it>

^a IRCCS Ospedale Policlinico San Martino, Largo Rosanna Benzi 10, Genova, Italy, 16132

NOTES:

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).

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;
- Click on LOAD and load the whole folder containing the T1 images of the considered patient (not the single slices);
- Adjust the contrast if needed (usually, a value of around 1000 will do);
- Insert the ROIs around the tumor by choosing "district 1" 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 "district" and redo the process.
If more than one tumors are 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" and "DICOM";
- Click on "START ANALYSIS", the segmentation algorithm will run;

A new GUI will appear. 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;
- 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 this case, after checking it): the replaced segmentation will depend on the choice made in the related slice;
- Once all the slices have been checked, click on "DONE", the computation of the radiomics features for the T1 images will start.

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, and the analysis is terminated. If ADC images are included, then another step is needed. 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-register;
- Open file maskT1_2_maskADC.py, this will generate the transformation matrix from the T1 mask to ADC mask in NIFTI 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";

A third GUI 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.

FUNCTIONALITIES FOR MODIFYING THE INITIAL ROIs WITHOUT NECESSARILY STARTING FROM SCRATCH

START ANALYSIS:

This function starts the segmentation analysis for all the slices in all the ROIs. If it is the first time one launches the analysis, the segmentation will automatically proceed and the second GUI will then open. On the other hand, if a ROI is already present, 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.

RESET ROI

This button resets the setting 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.

DELETE SLICES

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 remove the ADC related fields and ROI.aux_pos_fwd from the current cell (val) of the global ROI.

APPEND SLICES

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.

MERGE ROI COMPONENTS

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.

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

ACKNOWLEDGEMENTS: other software code

LEVEL SET METHOD

- Level set algorithm? 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 Vallières' 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>>