GlioMap Manual

Requirement

- MATLAB (R2020b or newer recommended)
- Image Processing Toolbox

Installation

1. Clone the repository:

```
git clone https://github.com/GlioMap-GUI/GlioMap.git
```

2. Open MATLAB and add the cloned folder to the MATLAB path:

```
addpath(genpath('GlioMap'))
```

3. Launch GlioMap:

```
"GlioMap.m"
```

or

1. Download all the files in the repository as a zipfile

   For download instructions https://gliomap-gui.github.io/how%20to%20download.html

2. Extract the zipfile

3. Run the "Gliomap.m" file

GlioMap consists of four main windows. Figure 1

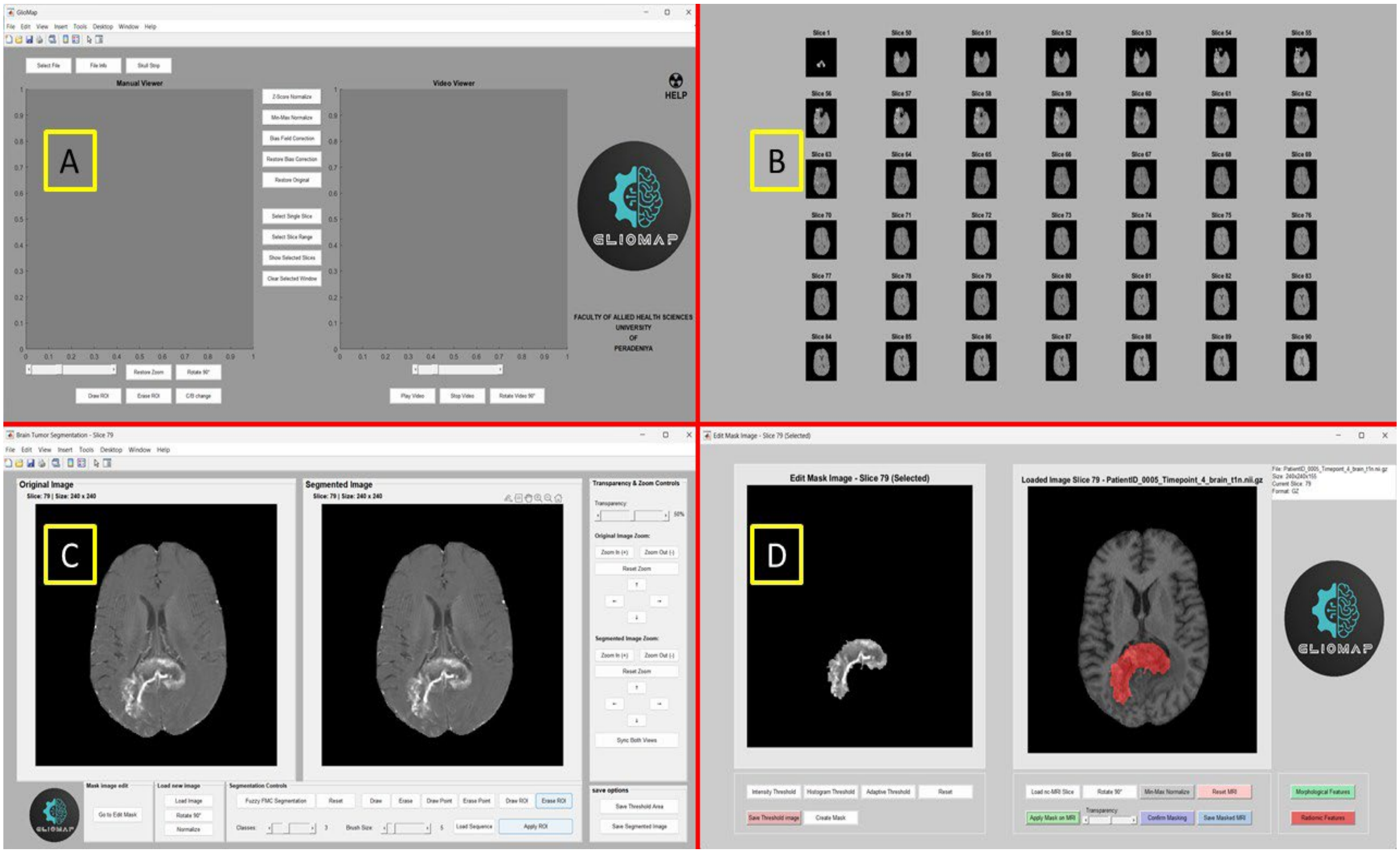


Figure 1: Four main windows of GlioMap: (A) Main window; (B) Selected slice window; (C) Segmentation window; (D) Edit mask window. Sample images are obtained from The Cancer Imaging Archive (TCIA).

The main window

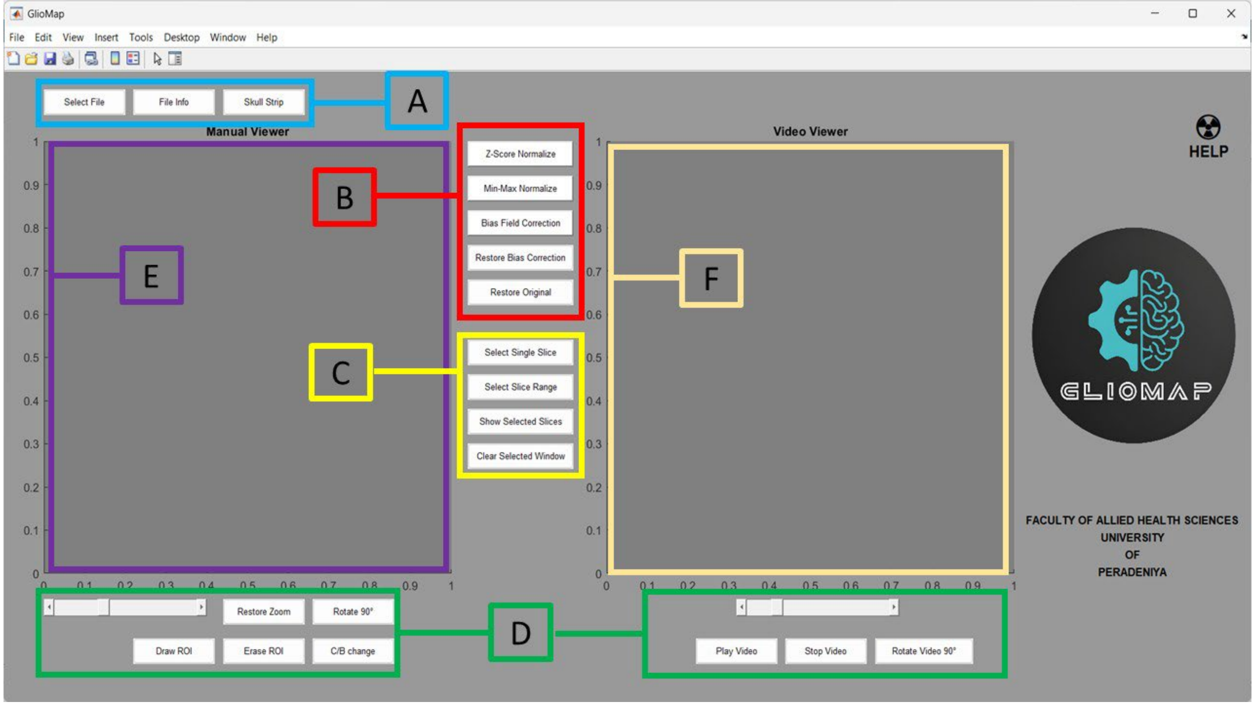


Figure 1: The main window of GlioMap. (A) File selection, file information and skull striping function; (B) Normalization and bias field correction functions; (C) Slice selection function; (D) Manual and viewer controls; (E) Manual viewing area; (F) Video viewing area.

This is the first window of GlioMap GUI, and the Other three windows can be accessed through this window.

Figure 3

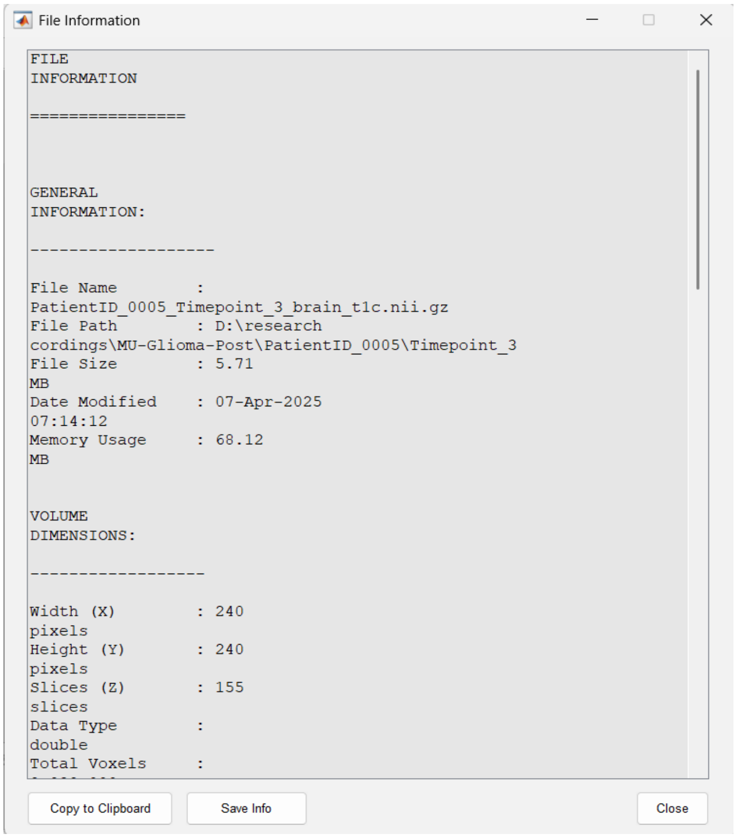
❖ Click on the **select file** push button (Figure 3), and the user can load the 2D MRI sequence. (GlioMap v1.0 only supports 2D images.).

The loaded image appears in the manual viewer area.

Support file formats:

NIfTI (.nii, .nii.gz), MetaImage (.mhd, .mha), NRRD (.nrrd, .nhdr), DICOM (.dcm, .dicom), Analyze (.hdr, .img), FreeSurfer (.mgz, .mgh), GIPL (.gipl, .gipl.gz), VTK (.vtk, .vti, .vtp, .vtu), MINC (.mnc, .minc), PIC, LSM, and standard image formats (.tif, .png, .jpg), etc.

- Click on the **File Info** push button (Figure 3), and view the loaded sequence file information. (Figure 4)



```
FILE
INFORMATION

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GENERAL
INFORMATION:

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File Name        :
PatientID_0005_Timepoint_3_brain_t1c.nii.gz
File Path        : D:\research
cordings\MU-Glioma-Post\PatientID_0005\Timepoint_3
File Size        : 5.71
MB
Date Modified    : 07-Apr-2025
07:14:12
Memory Usage     : 68.12
MB


VOLUME
DIMENSIONS:

------------------


Width (X)        : 240
pixels
Height (Y)       : 240
pixels
Slices (Z)       : 155
slices
Data Type        :
double
Total Voxels     :
```

Figure 4

Visualize all the file information of the loaded sequence.

If the user applies normalization, bias field correction, and rotation automatically updated in the file information section.

Copy to clipboard option and save the loaded file information as a text file option are also there.

- Using the **Skull Strip** push button (Figure 3), the user can load the skull stripping window in GlioMap (Figure 5).

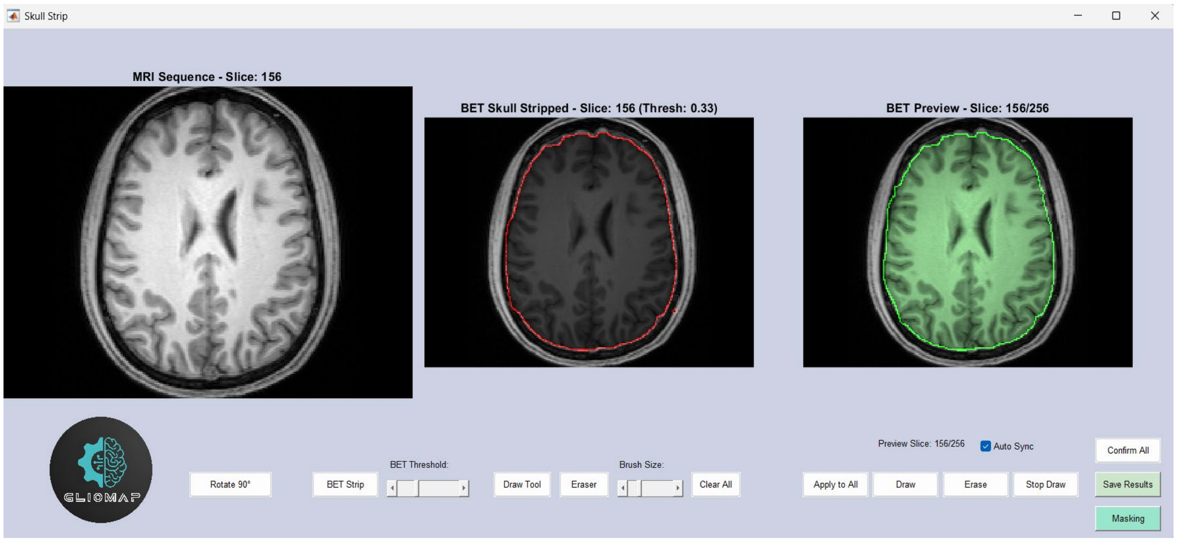


Figure 5: Skull stripping window

When accessing the skull stripping window, automatically load the currently loaded sequence in the Main window. Using the mouse scroll wheel can go through the slice sequence in the left side panel. Dabble, click one selected slice among the sequence, and the selected slice is loaded into the middle panel.

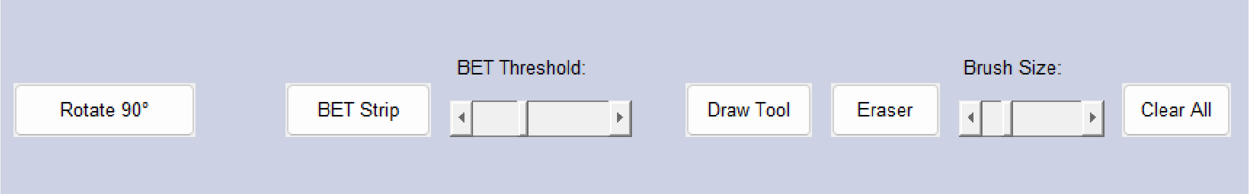


Figure 6

Using the **90^0 rotate** button can rotate the loaded sequence. The user can apply BET on the selected slice (to the middle panel image) using the **BET strip** push button and use the **BET threshold** slider to adjust applying threshold value. The **Draw tool** and the **Erase tool** can be used to make the final adjustments to the BET applied middle panel image. The **Brush size** slider adjusts the draw and eraser tool brush size, and using the **Clear all** button can reset all the edits. This function (Figure 6) only works on the middle panel.

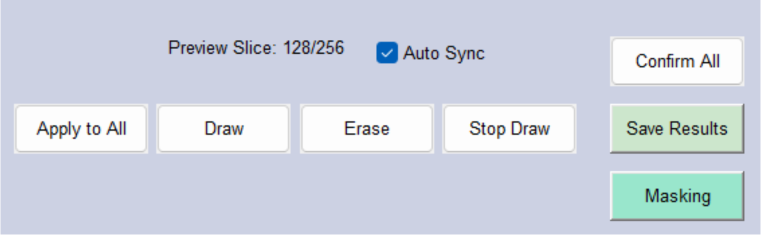


Figure 7

The **Apply to all** button can be used to apply the BET settings, which are applied to the middle panel image, to the whole sequence. New sequence with BET settings loaded to the right-side panel. The user can go through the slice sequence using the mouse scroll wheel and through the enable of the **Auto Sync** setting left side panel sequence will scroll in parallel with the right-side panel. The **Draw** and **Erase** button enables fine adjustment.

Using the **Confirm all** button can confirm that all settings apply to the sequence, and confirmation is essential to the saved result. The **Save Result** button can be used to save the skull-removal sequence. In the saving option, support for various file formats, and before saving user has to select the file format (Figure 8).

The **Masking** button can access the masking window (Figure 9) to remove the skull via masking

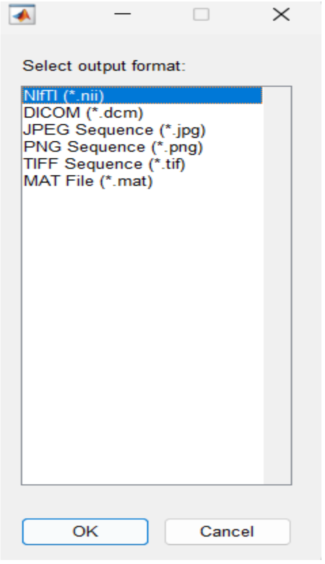


Figure 8

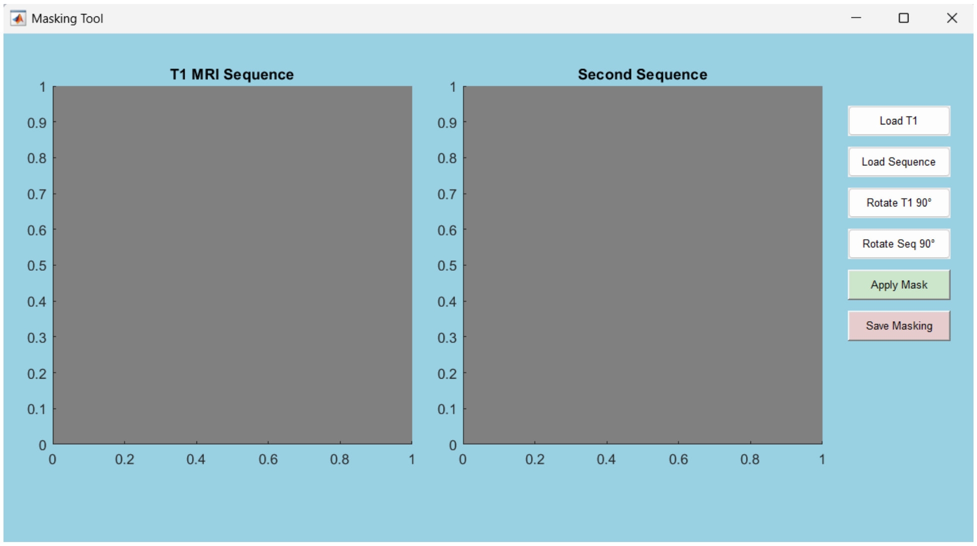


Figure 9

Using the **Load T1** button, load the T1w skull stripped sequence to the left side panel, and using the **Rotate T1 90^0** button, rotate the sequence. The **Load Sequence** button loads the second sequence that you want to remove the skull to the right panel, and using the **Rotate Seq 90^0** button can rotate second sequence. Both sequences must be from the same patient and free of rotation. Using the **Apply Mask** button can apply the mask from the T1w sequence to the loaded second sequence (left panel to right panel). The **Save Mask** button saves the result.

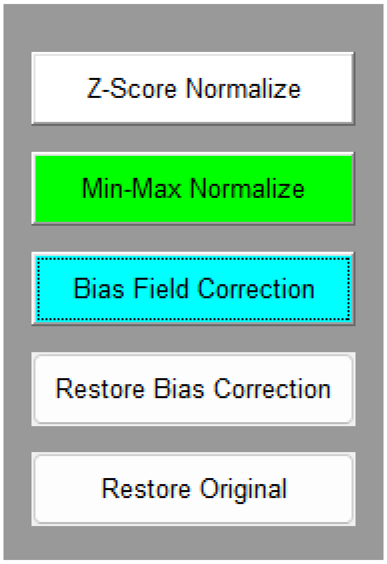
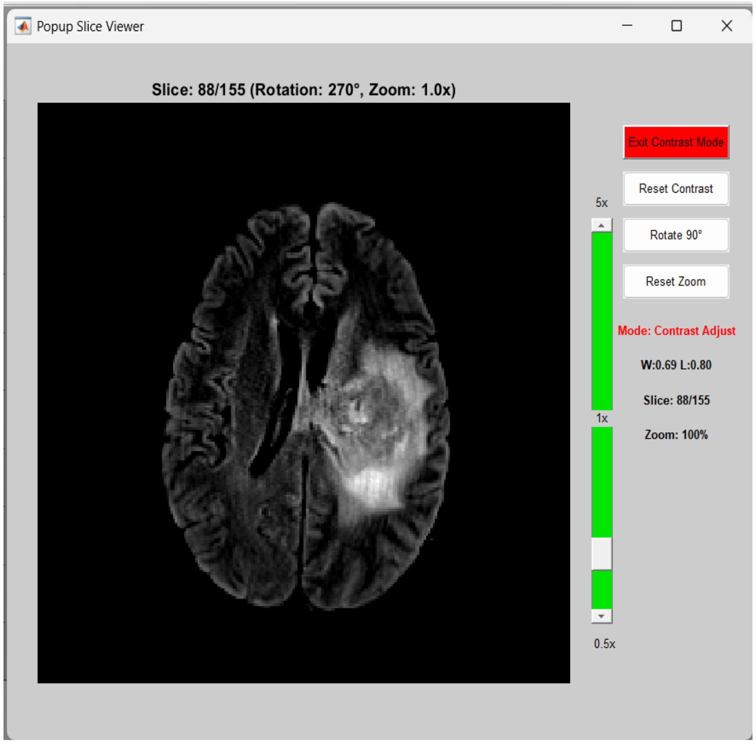


Figure 10

- Z-Score normalization, Min-Max normalization, and Bias field correction can be applied to the loaded sequence in the manual viewer through the **Z-Score Normalize**, **Min-Max Normalize**, and **Bias Field Correction** buttons (Figure 10).
The **Restore Bias Correction** button restores the applied bias correction to the sequence, and the **Restore Original** button restores all applied bias and normalization settings.

- Using the keyboard up and down keys can go through the slice sequence in the manual viewer panel. Using the zoom slider in the main window can zoom sequence in the manual viewer, and the **Restore Zoom** button restores it to the original. **Rotate 90^0** rotates the loaded sequence. The **Draw ROI** and **Erase ROI** buttons are used to draw and erase the ROI on the loaded sequence. The **C/B change** button (Figure 11) can handle contrast and brightness of the loaded sequence (Figure 12).

Figure 11



Slice: 88/155 (Rotation: 270°, Zoom: 1.0x)

Mode: Contrast Adjust
W:0.69 L:0.80
Slice: 88/155
Zoom: 100%

Figure 12: Contrast and Brightness changing panel

❖ In contrast, and brightness changing panel (Figure 12) user can change the contrast and brightness of the loaded sequence.
The **Contrast Change** button enables contrast and brightness changes with the mouse up and down and left–right movement.
Using mouse scrolling can go through the slice sequence.
Using the zooming slider can zoom the image, and the **Reset Zoom** button resets it to the original.
Using the **Rotate 90^0** button can rotate the sequence.

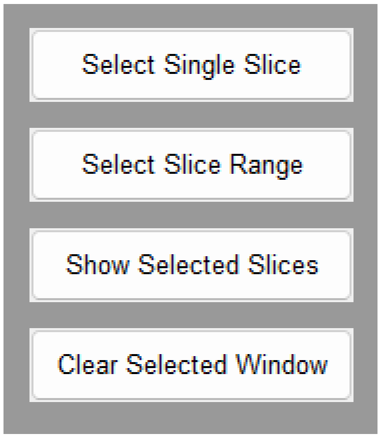
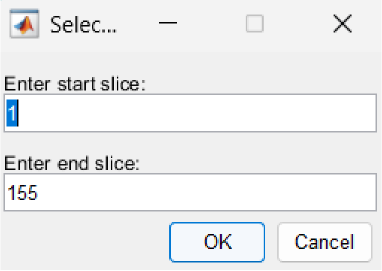


Figure 13

❖ The user can select a single slice through the **Select Single Slice** button, and can select a slice range using the **Select Slice Range** button (Figure 14). Using the **Show Selected Slices** button can access the selected slice window (Figure 16). The **Clear Selected Window** button clears the selected slice window.



Enter start slice:
1
Enter end slice:
155

Figure 14

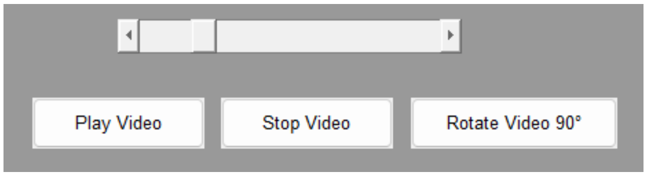


Figure 15

- The **Play Video** button plays the loaded sequence as the video in the video viewer panel, and the **Stop Video** button and **Rotate Video 90^0** allow to stop the video and rotate the video. Using the speed control slider user can change the playback speed of the video.

The selected slice window

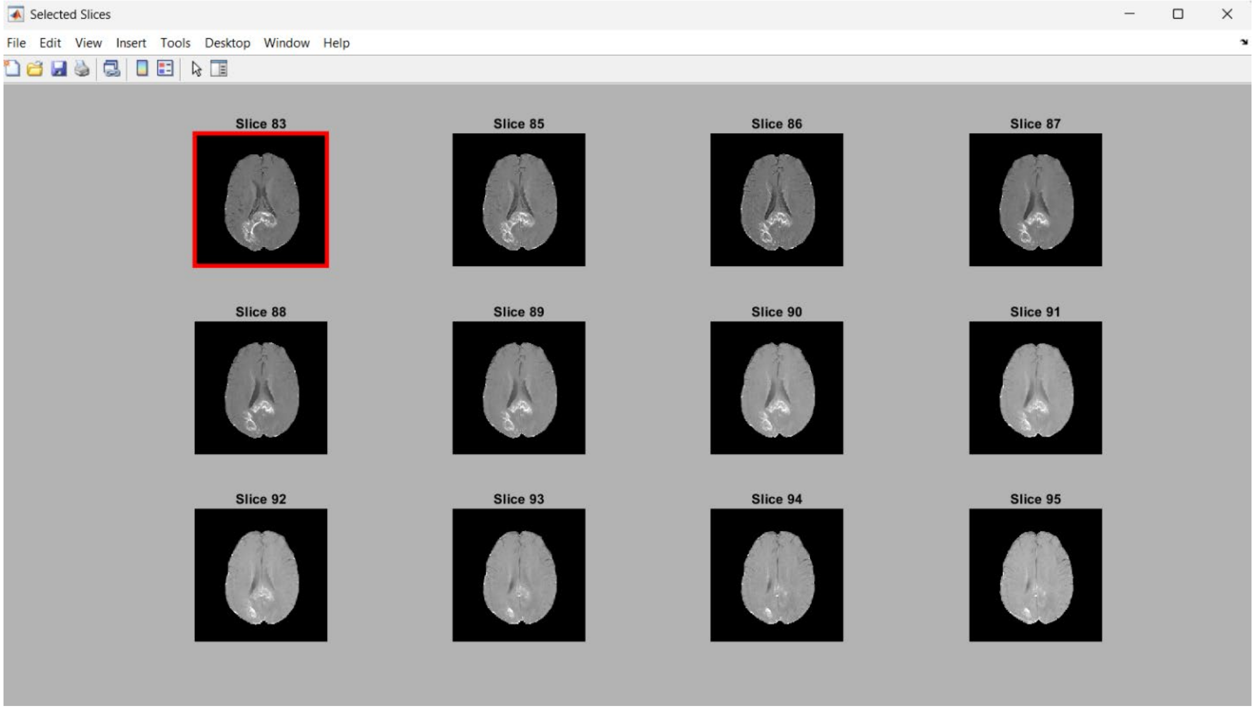


Figure 16: Selected slice window

- The selected slice window can be accessed through the Show **Selected Slices** button (Figure 13). By dabbling, clicking on the selected slice, and then opening it in the segmentation window (Figure 17), and selected slice is marked with the red border.

Segmentation window

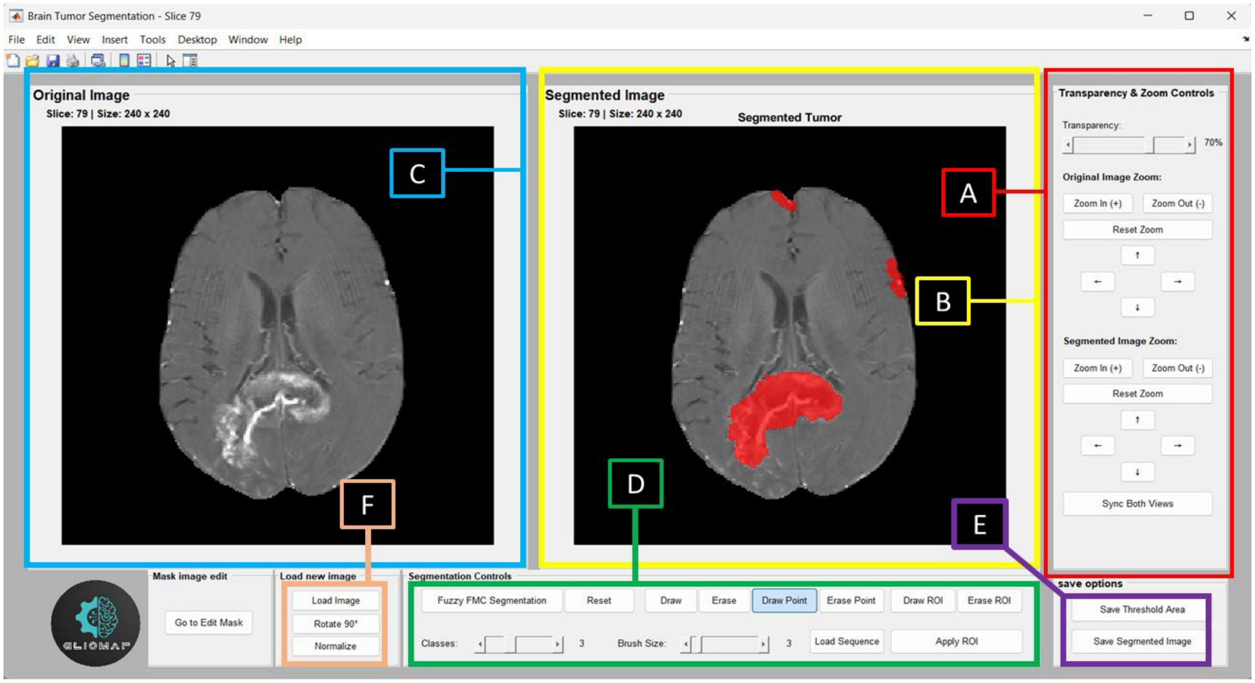


Figure 17: Segmentation window in GlioMap. (A) Transparency slider and zoom controls; (B) Segmented image panel; (C) Original image panel; (D) Segmentation options; (E) Save options; (F) New file selection options.

In this window, all segmentation settings apply to the right side panel (segmented image).

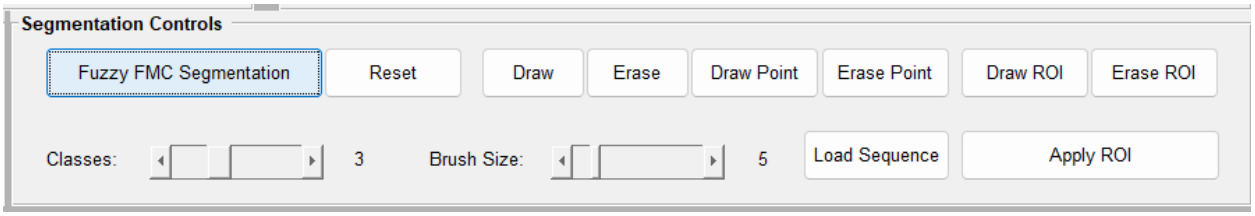


Figure 18: Segmentation options

- Figure 18 shows the segmentation options. using the **Fuzzy FMC Segmentation** button user can apply the FMC thresholding technique to the image, and the **Classes** slider allows to change the FMC class. using **Draw** (continuous drawing), **Draw point** (pixel-wise drawing), **Erase** (continuous erasing), and **Erase Point** (pixel-wise erasing) buttons, users can do fine adjustments of the thresholding area. The **Bush Size** slider allows to change brush size.

The ROI tools (**Draw ROI** and **Erase ROI** buttons) allow for segmentation using ROI, and **Apply ROI** confirms the applied ROI area (Figure 18).

The **Reset** button reset the all-applied settings, and **Load Sequence** button (Figure 18) load the whole sequence related to loaded image and can go through the sequence using mouse scrolling (Figure 19).

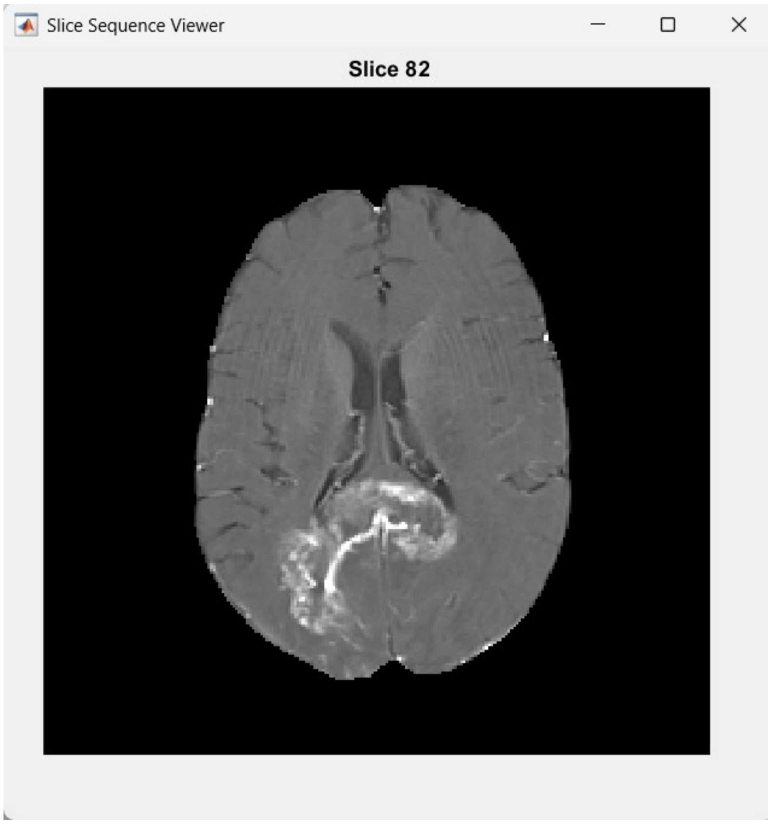
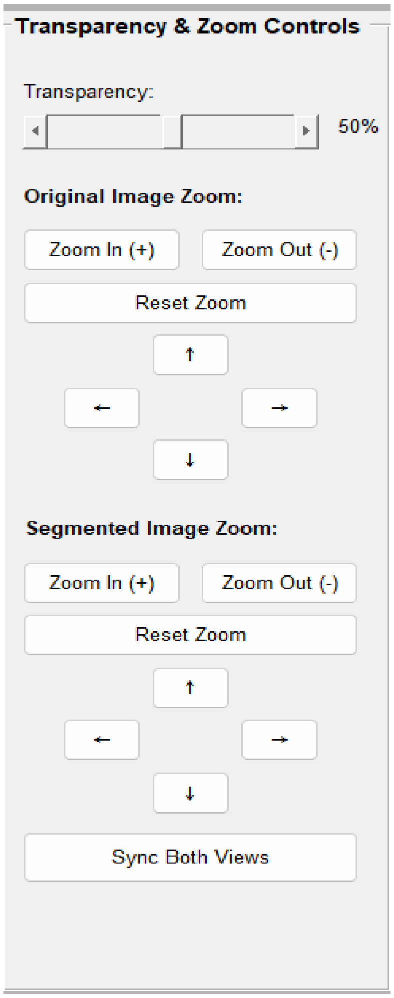


Figure 19: The loaded sequence



Transparency: 50%

Figure 20: Transparency and Zooming controls

❖ The **Transparency Slider** (Figure 20) allows the user to change the transparency of the applied thresholding area. Using the zooming controls (Figure 20) user can zoom both images separately and use the **Sync Both Views** button can zoom both images simultaneously. The arrow keys allow the user to move images.

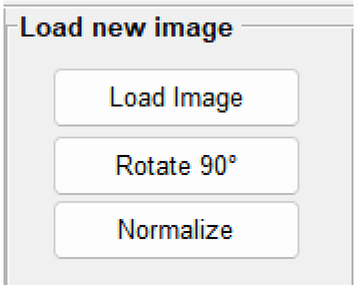


Figure 21

❖ The **Load Image** button (Figure 21) allows the user to load a new image with the same slice number from another sequence, and the **Rotate 90^0** and **Normalize** buttons rotate and normalize the newly loaded image.

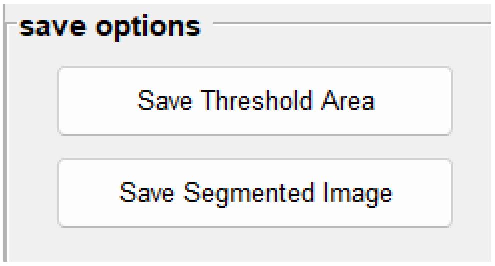
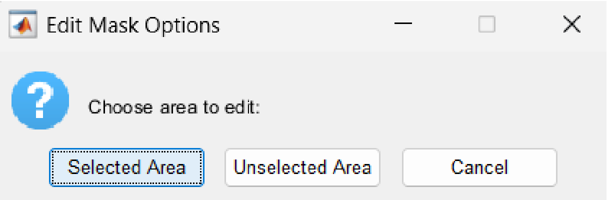


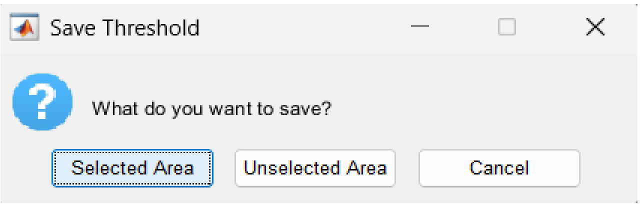
Figure 22

❖ The **Save Threshold Area** button (Figure 22) allows to user to save only the threshold applied or the outer area as a JPG file with the same matrix of the loaded image (Figure 24). Using the **Save Segmentation Image** button can save the whole image with segmentation as a JPG file with the same matrix as the loaded image.


Edit Mask Options

Choose area to edit:

Figure 23


Save Threshold

What do you want to save?

Figure 24

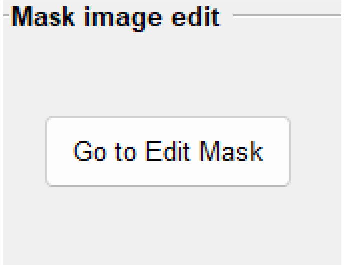


Figure 25

❖ Using the **Go To Edit Mask** button (Figure 25) can access the edit mask window (Figure 26) to create a mask image, tumor masking, and feature calculation. The user can select the threshold area or the outer area to create a mask image (Figure 23).

Edit mask window

ile: PatientID_0005_Timepoint_4_brain_t1n.nii.gz
ize: 240x240x155
urrent Slice: 79
ormat: GZ

Figure 26: Edit mask window in GlioMap. (A) Generate mask image options and mask image thresholding options; (B) Apply mask options; (C) Radiomic and morphological feature calculation options; (D) Preview mask image panel; (E) Preview masking panel

Figure 27

- The buttons shown in Figure 27 allow editing the mask image in the edit mask image panel. Using thresholding buttons, the user can threshold a mask image via various thresholding methods. Figure 28 shows histogram thresholding, using the user can change the thresholding level. The **Reset** button resets the applied settings to the masked image, and the **Save Threshold image** button saves the threshold image as a JPG file with the same matrix as the loaded image.

The **Create Mask** button saves the mask image with the threshold value of 1 and saves it as a JPG file with the same matrix as the loaded image (Figure 29).

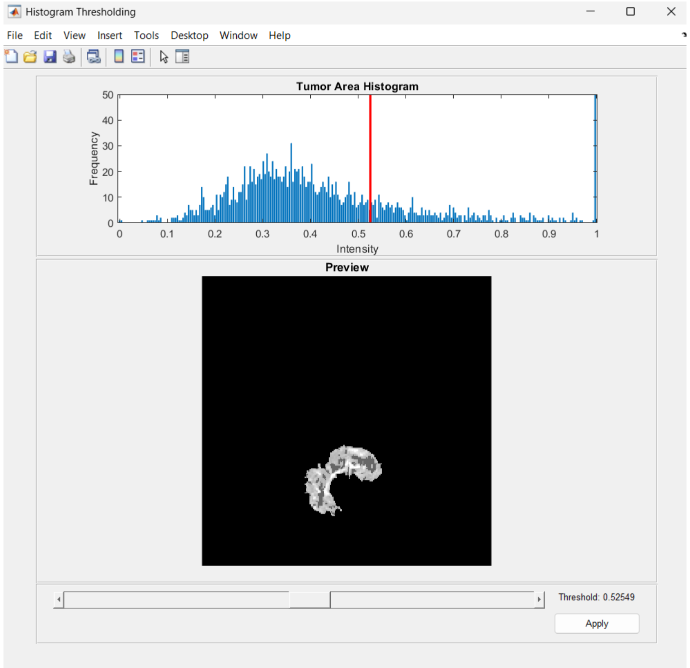


Figure 28

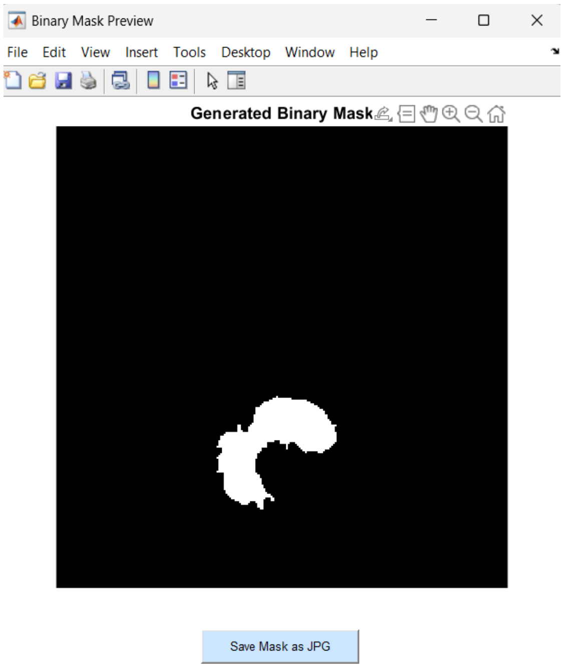


Figure 29

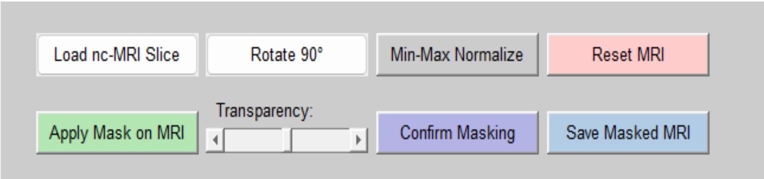


Figure 30

- Figure 30 shows the masking options. The **Load nc-MRI Slice** button loads the MRI image with the same slice number that is loaded in the edit mask panel. The **Rotate 90^0** and **Min-Max Normalize** buttons allow for rotation and normalization. The **Reset MRI** button resets all applied settings to the loaded image. The **Apply Mask on MRI** button applies the masking to the loaded image (not essential to create a mask image, and saves it using mask editing options (Figure 27)). The **Transparency** slider changes the transparency of masking. The **Confirm Masking** confirms the applied masking, and the **Save Masked MRI** button saves the masked image as a JPG file with the same matrix as the loaded image (confirm masking is essential for this).

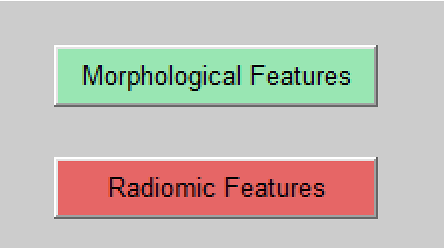
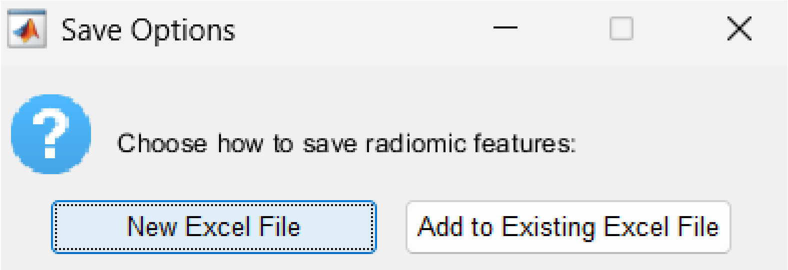


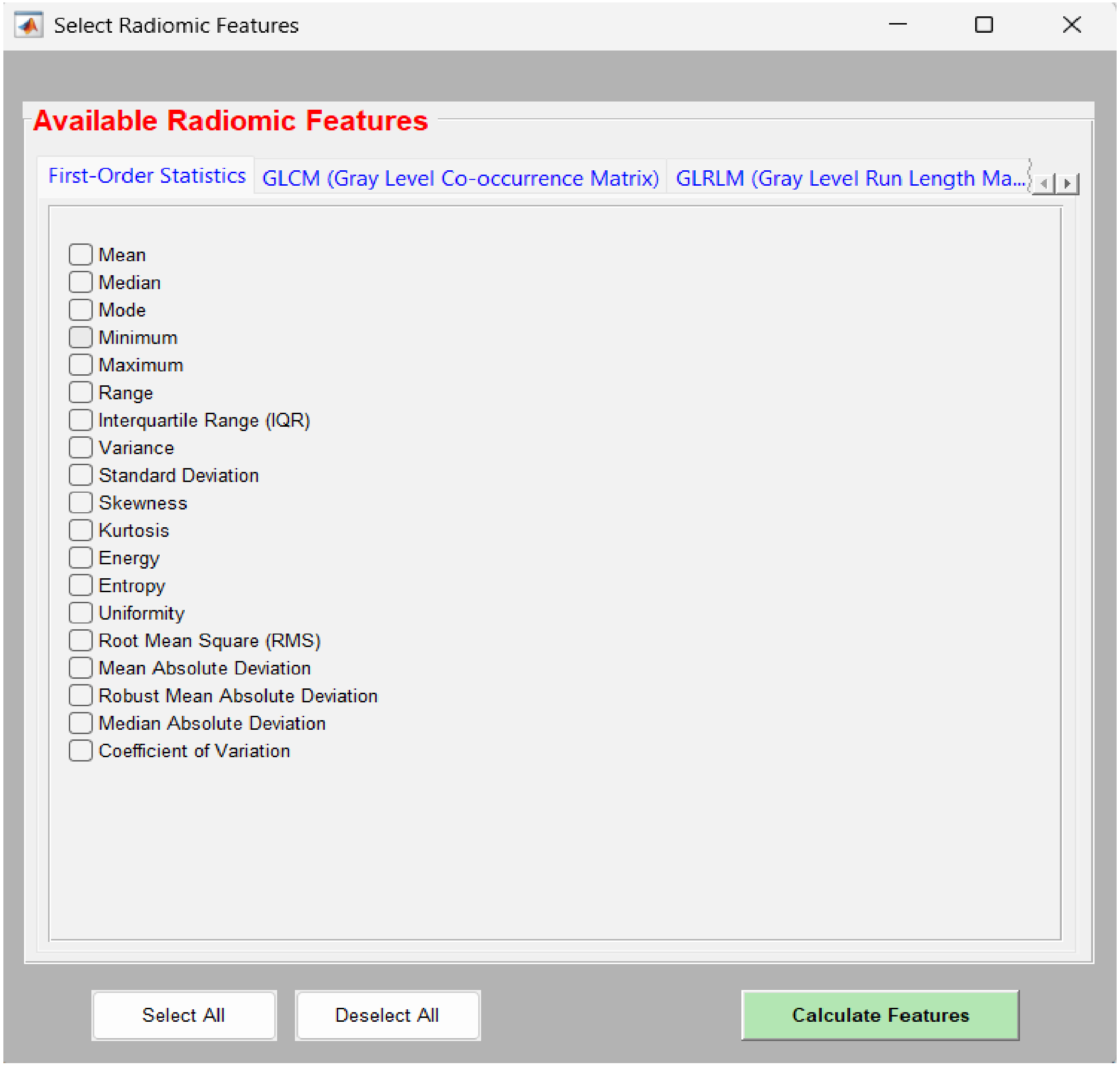
Figure 31

- The **Radiomic Features** and **Morphological Features** buttons (Figure 31) allow to calculation of 100 radiomic features (Figure 33) and 33 morphological features (Figure 34) of the confirmed masked image, and give a save option to save data in a CSV file (Figure 32).



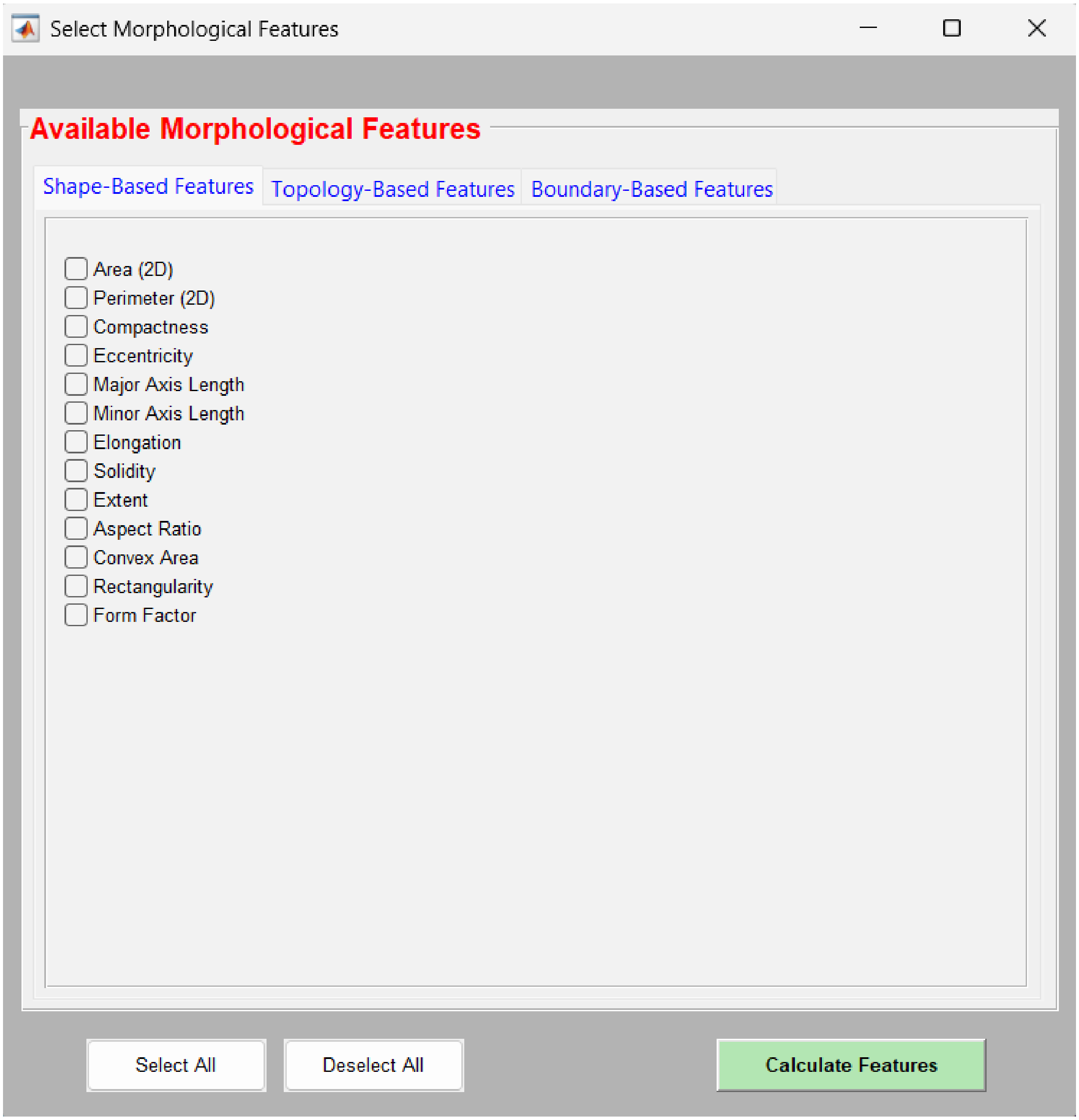
Choose how to save radiomic features:

Figure 32



☐ Mean
☐ Median
☐ Mode
☐ Minimum
☐ Maximum
☐ Range
☐ Interquartile Range (IQR)
☐ Variance
☐ Standard Deviation
☐ Skewness
☐ Kurtosis
☐ Energy
☐ Entropy
☐ Uniformity
☐ Root Mean Square (RMS)
☐ Mean Absolute Deviation
☐ Robust Mean Absolute Deviation
☐ Median Absolute Deviation
☐ Coefficient of Variation

Figure 33: Radiomic features selection panel



☐ Area (2D)
☐ Perimeter (2D)
☐ Compactness
☐ Eccentricity
☐ Major Axis Length
☐ Minor Axis Length
☐ Elongation
☐ Solidity
☐ Extent
☐ Aspect Ratio
☐ Convex Area
☐ Rectangularity
☐ Form Factor

Figure 34: Morphological features selection panel