



A Graphical User Interface for Automatic Segmentation of Brain Tumors

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Abstract

In recent years, automatic segmentation of brain tumors has become a popular research topic. Therefore, designing a graphical user interface that is easy to use and provides high-precision automatic segmentation functionality is particularly important. The design of this graphical user interface aims to simplify the entire automatic segmentation process, allowing the user to input relevant image data and then use the program to automatically perform image segmentation and tumor labeling. Compared to traditional manual segmentation methods, this graphical user interface can help medical professionals save time and effort while providing high-precision automatic segmentation functionality.

Problem description

There are four modalities of MRI images: T1, T1CE, T2, FLAIR, which can be 3-dimensional. However, these images contain many black voxels that do not provide useful information. We want to use machine learning to detect the tumor region in the images and present the results to doctors in an easily interpretable manner. Additionally, we want to differentiate between the different types of tumors within the region, including Whole Tumor (WT), Enhancing Tumor (ET), Tumor Core (TC). In our process, we first use image registration to ensure that all images are the same size, and then use Brain Extraction Tool (BET) to obtain skull-stripped brain images. Next, we apply Optimal Mass Transportation (OMT) to convert the raw image into the cube image with size $128 \times 128 \times 128$ in order to remove the useless information. After that, we feed the cube image into the machine learning model to obtain predicted labels corresponding to the types of tumor. To make our approach user-friendly, we have developed a GUI that integrates all the necessary steps and includes several relevant functions for users.

Results and discussion

On the predictor page, users can upload their T1ce and T2 NIFTI images at the bottom, and then click the "Run" button to start the tumor prediction process (Fig.1). During the prediction process, a progress bar is displayed to show users which step is currently being performed (Fig.2).

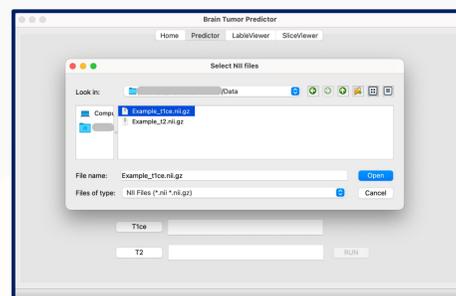
The process is divided into three parts:

1. image registration
2. skull stripping
3. the application of Optimal Mass Transportation (OMT) to convert the raw image into a cube image for segmentation. The resulting cube is then inverted back to its original brain shape

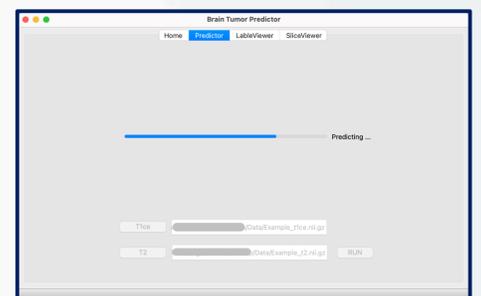
After the prediction is complete, the screen displays relevant information such as the volume of each tumor type for user understanding. Furthermore, users can select which type of tumor they would like to view in the brain and use a slider to select the desired slice of image layers to view (Fig.3-1, 3-2).

The predicted label is also saved for future use by the user.

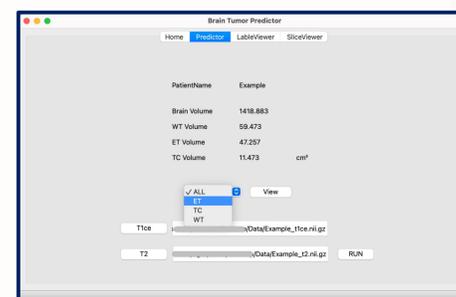
In addition to the main prediction page, we have also designed separate "SliceViewer" and "LabelViewer" pages. The former allows users to view multiple NIFTI images simultaneously, while the latter enables users to upload brain images and labels previously saved from the prediction page to view the location of different types of tumors in the brain. Similarly, users can select the desired slice using a slider.



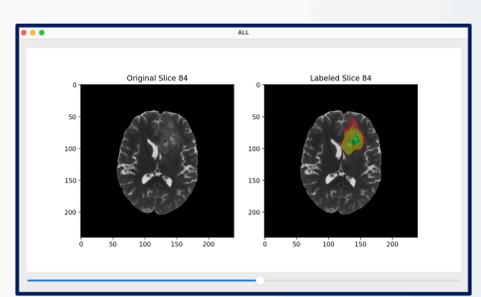
Upload data
(Fig.1)



Automatic processing
(Fig.2)



Select type
(Fig.3-1)



Use slider to view
(Fig.3-2)

Conclusions

Constructing a graphical user interface not only simplifies the entire automatic segmentation process but also enables users who are not familiar with the inner workings to quickly get started. Currently, we have completed the initial brain tumor prediction functionality and successfully visualized it. In the future, we will actively collaborate with hospitals and hope to add more functions to this program and make it more comprehensive. We envision packaging everything into a formal application and releasing it someday in the future.

References

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