

Problem statement

This topic is about classifying and predicting the genetic subtypes of glioblastoma through MRI (magnetic resonance imaging) scanning. Glioma, the most common primary brain tumors, occurs due to the carcinogenesis of glial cells in the spinal cord and brain. By training and testing the self-made model, the goal of the competitors is to detect the presence of MGMT promoter methylation.

The importance of the topic lies on the life-threatening damage caused by the malignant tumor. Being called glioblastoma, it is one of the most common central nervous system tumor, with an incidence of about 70% of all primary brain malignancies. Also, it belongs to one of the major brain diseases with high mortality and disability. Even worse, the median survival time of patients with glioblastoma is only 12 to 14 months. There is no satisfactory treatment for glioma so far, and the resistance of patients to chemotherapy drugs is one of the important reasons for the poor treatment effect.

In the current state of science and technology, in order to carry out an accurate analysis of cancer, most of the samples need to be extracted from the operation. It often takes a long time to confirm the genetic characteristics of a tumor in this way, up to several weeks. Therefore, if only the method of MRI (magnetic resonance imaging) can predict the genetic type of cell tumor, it will greatly reduce invasive diagnoses and treatments suffered by the patients, and will have a positive impact on the survival of patients.

Applications

The main application of this technology is mainly in medical areas, including hospital (mostly radiology and oncology departments) and other research departments in the medical field.

Once this technology is proven to be effective for detecting the genetic subtype in advance, it will provide hospitals and doctors with a simpler and faster treatment plan, giving them more chances to give out a new and more hopeful treatment strategies. For patients, this couldn't be better. The technological innovation may help them to

carry out targeted treatment earlier, thereby improving their survival possibilities and prospects.

For the researchers in the field of medical imaging behind the scenes, this provides them with an opportunity to benefit the majority of patients, and at the same time, they can have a lot of sample data to update and do further advance in this field.

Literature review

Given the information shown on the Kaggle, I found that most of the solutions are based on a certain paper. For the purpose of research different approaches, I studied two of them and try my best to understand the thinking.

The first solution I have found is on Github, and the main research ideas coming from an article called "Brain tumor segmentation based on deep learning and an attention mechanism using MRI multi-modalities brain images", which has the website of <https://www.nature.com/articles/s41598-021-90428-8>.

And the github webpage is:

<https://github.com/weka511/rsna>

The first article introduces some ways to obtain a flexible and effective brain tumor segmentation system. First, it proposes a preprocessing way on part of the image and reduce the computing time; Second, it proposed a simple network called Cascade Convolutional Neural Network (C-CNN) which mines local and global features in two routes. Lastly, it introduced a Distance-Wise Attention (DWA) mechanism to increase the segmentation accuracy. After making segment for the each, the codes then turn to visualize and do segment in 3D.

The second solution I have found is on Kaggle, and has the website of

<https://www.kaggle.com/furcifer/torch-effnet-for-mri-no-inference?scriptVersionId=68974998>

According to the solution given by the coder, the first step also grouped the MRI results into T1, T1c, T2, and FLAIR. So, the coder treats the problem as a binary classification.

For the 3D images, it considers 4 sequences and take 64 slides from the images each. In the next step, resize the slices and construct an efficient 3D in pytorch. Lastly, do the binary classification.

For the 2D images, firstly, construct a 4-channel image of the 4 sequences. Then, in pytorch, design a 4 channel model. After that, add augmentation, few heuristics to avoid black/empty scans, design modified efficient-net as model, and finally perform classification.

Open Source research

Both of the two resources are open source. The one shown on the github has the MIT license, which means that copyright notice and permission notice should be included in all copies or substantial portions of the software. And the solutions given by the Kaggle is open source too, means that anyone can use his codes and make some changes on his own. The only need is to show out the reference kernel.