Brain Tumors Classification for MR images based on Attention Guided Deep Learning Model

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Abstract—In the clinical diagnosis and treatment of brain tumors, manual image reading consumes a lot of energy and time. In recent years, the automatic tumor classification technology based on deep learning has entered people's field of vision. Brain tumors can be divided into primary and secondary intracranial tumors according to their source. However to our best knowledge, most existing research on brain tumors are limited to primary intracranial tumor images and cannot classify the source of the tumor. In order to solve the task of tumor source type classification, we analyze the existing technology and propose an attention guided deep convolution neural network (CNN) model. Meanwhile, the method proposed in this paper also effectively improves the accuracy of classifying the presence or absence of tumor. For the brain MR dataset, our method can achieve the average accuracy of 99.18% under ten-fold cross-validation for identifying the presence or absence of tumor, and 83.38% for classifying the source of tumor. Experimental results show that our method is consistent with the method of medical experts. It can assist doctors in achieving efficient clinical diagnosis of brain tumors.

I. INTRODUCTION

According to the World Cancer Report provided by the World Health Organization (WHO), there are approximately 297,000 new cases of brain tumor cases worldwide in 2018. Brain tumors can be divided into two categories according to the origin: primary and secondary intracranial tumors. Primary intracranial tumors are tumors of origin that grow in the brain. And the types that generally occur based on the affected area are meningioma, glioma, and pituitary. Secondary intracranial brain tumors are tumors growing within the brain that has arisen from the spread of a malignant tumors elsewhere in the body. And common metastatic sites are colorectal, lung, and breast. Usually, the doctor will make a preliminary assessment of the situation through medical imaging technology. In recent years, magnetic resonance imaging (MRI) technology has been widely used to generate high-resolution images of brain structures. It has the advantages of diverse imaging methods and rich information. However, for a large number of MR images, it takes a long time to read. For this problem, automatic brain tumor classification is a possible solution.

CNNs based on deep learning are currently the best way to classify data in the field of computer vision. In recent years, CNNs have been widely used for medical image diagnosis. Unlike traditional methods, CNNs preserve the input’s neighborhood relations and spatial locality in their latent higher-level feature representations. In 2015, He et al. adopted the residual block structure and proposed a deep residual network ResNet [2] for image recognition. In 2017, Hu et al. proposed SENet [5] based on channel attention module. In 2020, Zhang et al. proposed ResNeSt [7] based on the Split attention module. In addition, based on the existing CNNs [1]-[7]. The proposal of numerous excellent CNNs makes it possible to classify brain tumor MR images. In general, deep learning is a typical data-driven technology. Especially for medical tasks, not only the labeling data is expensive, but there is also the problem of scarcity of dataset. For this situation, a favorable substitute for training CNNs from scratch is to use a pre-trained model based on transfer learning [8]. It applies knowledge and skills learned in previous domains or tasks to novel domains or tasks.

Currently, there are plenty of literatures based on CNNs to achieve classification of brain tumor images [10]. Here we review the most recent and related research works on the paper topic. In 2018, Ge et al. proposed a novel multiscale CNN architecture to realize the grading of gliomas and got the accuracy of 89.47% [11]. In 2019, Swati et al. used a pre-trained CNN model and proposed a block-wise fine-tuning strategy to classify glioma, meningioma, and pituitary [12]. It achieved the accuracy of 94.82%. In 2020, Zhang et al. used the Pyramid Scene Analysis Network to realize the detection and grading evaluation of meningiomas [13]. The accuracy of meningioma detection and three grades classification are 100% and 81.36%. Although these methods can perform well in predicting the presence, type, or grade on primary intracranial tumor dataset, they rarely involve secondary intracranial tumor images. Moreover, to the best of our knowledge, there is still a technical gap in distinguishing the source type of tumor (primary or secondary intracranial tumor), which needs to be resolved urgently.

This paper proposes an experimental method for classifying the presence or absence of tumors and the source of tumors. Our scheme is to send tumor images into our proposed network ResNeSAt. Under the prior knowledge provided by transfer learning, the model is fine-tuned to achieve the best performance. Unlike traditional methods that only target a specific type of tumor, our task is more complex.
and challenging. For our brain MR image dataset, we achieve a higher accuracy than previous methods. In addition, we have also achieved certain results in the new application domain of distinguishing the types of tumor sources.

II. MATERIAL

In this paper, we used the new brain MR dataset provided by Ruijin Hospital, Shanghai Jiao Tong University School of Medicine. All experiments were performed in compliance with the Declaration of Helsinki. Written informed consent was acquired from each patient or next of kin. Patients underwent MR scans on a 3T scanner using a 16-channel head coil in a supine position. In order to facilitate the therapeutic planning and treatment of GKRS, a gamma knife rigid head frame (Elekta, Stockholm, Sweden), which was matched with the head coil, was fixed on patient’s head. The T1 MPRAGE sequence was performed on all of the patients 5 minutes after administration of 0.1 mmol/kg body weight of contrast agent (Gadoxetic Acid Disodium Injection, Primovist, Bayer Vital GmbH, Leverkusen, Germany). The dataset contains 3670 T1 MPRAGE sequence brain MRI’s images and includes 7 types of tumors: cavernous hemangioma, glioma, meningioma, acoustic neuroma, colorectal cancer brain metastasis, lung cancer brain metastasis, breast cancer brain metastasis. And it covers 70 cases, patients with brain tumors and patients without brain tumors. The physician provides complete manual annotation for each image. Table I lists the number of images of each class in the dataset. Figure 1 shows a sample of various tumors of the dataset used in this paper.

![Table I: Details of Used Image Dataset.](image)

III. METHODOLOGY

We propose an experimental method for classifying the presence or absence of tumor and the source of tumor (primary or secondary intracranial tumor) based on brain MR images. The model is trained and optimized through the existing artificially annotated dataset to realize the classification of new images. In this section, the following sub-sections will introduce proposed methodology in detail.

A. Proposed Method

![Figure 2: Flow chart of the proposed method.](image)

Figure 2 shows the flow chart of the proposed method. First, the images in the brain MR dataset are selected into the presence or absence of tumor dataset and the tumor source type dataset according to tumor presence and source type labels. In the preprocessing stage, we use the bilinear interpolation method to unify the image size to 256×256. And we randomly flip 50% of the pictures horizontally. In this way, although the position of the pixels in the image is changed, the features are kept unchanged, which can enhance the generalization ability of the model. In the following CNN model, the values of pixels in the image will be converted into features. Therefore, the classification effect is dependent on these pixel values. We use normalization to limit the data to a certain range we need. This can prevent the unbalanced image pixel intensity distribution from interfering with subsequent processing. After preprocessing, we send the image to the model for training. For large-scale network model with huge parameters, when performing medical tasks with relatively rare dataset, there is a certain gap in task performance between using pre-trained model and training from scratch [14]. We used the ImageNet pre-trained model based on pytorch. In each round of iterative training, the model parameters are automatically adjusted based on the prediction results of the previous round. The maximum number of training iterations is set to 100 epochs. We use SGD optimizer to update the weights of the network with a batch size of 16. And an initial learning rate of $\alpha_0$ at the very beginning and cosine decays are as following:

$$\alpha = \frac{1}{2} \times \left(1 + \cos\left(\frac{e \times \pi}{N_e}\right)\right) \times \alpha_0$$

where $e$ is the round number and $N_e$ is the maximum number of training epochs.
where \( e \) is an epoch counter, and \( N_e \) is a total number of epochs. The \( \alpha_0 \) for presence or absence of tumor model and source of tumor model are 1e-3 and 1e-4 respectively. After the two models are trained, the two optimized prediction models can be used to sequentially classify the presence or absence of tumors and the type of tumor source on the new image. The model is mounted on Huawei G5500 series servers and uses 1 NVIDIA V100 GPU card. The implementation of our network is based on PyTorch.

B. Existing Classification Networks Comparison

We compare the effects of commonly used CNNs in recent years in the classification of tumor presence and source. 80% of brain MR dataset were used to train the model, and the remaining images were used to test the model. Finally, the testing accuracy is as shown in Figure 3.

\[ \text{Recall} = \frac{TP}{TP + FN} \]  
\[ \text{Specificity} = \frac{TN}{TN + FP} \]  
\[ \text{Precision} = \frac{TP}{TP + FP} \]  
\[ F1 - \text{Score} = 2 \times \frac{Recall \times Precision}{Recall + Precision} \]  
\[ \text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \]

Recall and Specificity describe how good the classifier is at classifying the positive and negative condition. Precision is the positive predictive rate. F1-score measure the classification performance in term of recall and precision. Accuracy is the overall classification accuracy of the proposed method.

IV. EXPERIMENTAL RESULTS

The variability of a single model can be quite high. We evaluated the classification performance of the proposed model ResNeSAt and compared it with ResNeSt on ten-fold cross-validation and summarized our results in the form of tables. Table III and Table IV show the average recall, specificity, precision, F1-score, and accuracy. As shown in Table III, we can see that our proposed model ResNeSAt has improved recall, specificity, precision, F1-score and accuracy in classifying the presence or absence of tumor. This shows that ResNeSAt pays more attention to the tumor area, so it can better judge whether there is a tumor in the image. As shown in Table IV, in terms of judging the type of tumor source, we found that the improved model ResNeSAt has improved recall, F1-score, and accuracy. Specificity and precision can be almost ignored compared to the more comprehensive indicators F1-score and...
Accuracy. This shows that when judging the source type of the tumor, ResNeSAt better analyses the details of the tumor area and improves the classification performance to a certain extent. The parameter of the ResNeSt is 97.45 MB, and the parameter of the ResNeSAt is only 97.46 MB. In general, ResNeSAt effectively improves the accuracy of classification of tumor presence or absence and tumor source type, almost without increasing the model size.

### TABLE II
**DETAILS OF NETWORK RESNESA T.**

| ResNeSAt | Name | Details | Repeat |
|----------|------|---------|--------|
| Input    | InitConv | Conv3, BN, ReLU | 2 |
|          | InitConv 1 | Conv3, BN, ReLU, MaxPool | 1 |
|          | Bottleneck 1 | Conv1, BN, SplAtConv, Conv1, BN, ReLU, SA, AvgPool, Conv1, BN | 1 |
|          | Bottleneck 2 | Conv1, BN, SplAtConv, Conv1, BN, ReLU, SA | 2 |
| Layer 1  | Bottleneck 3 | Conv1, BN, AvgPool, SplAtConv, Conv1, BN, ReLU, SA, AvgPool, Conv1, BN | 1 |
|          | Bottleneck 4 | Conv1, BN, SplAtConv, Conv1, BN, ReLU, SA | 3 |
| Layer 2  | Bottleneck 5 | Conv1, BN, AvgPool, SplAtConv, Conv1, BN, ReLU, SA, AvgPool, Conv1, BN | 1 |
|          | Bottleneck 6 | Conv1, BN, SplAtConv, Conv1, BN, ReLU, SA | 5 |
| Layer 3  | Bottleneck 7 | Conv1, BN, AvgPool, SplAtConv, Conv1, BN, ReLU, SA, AvgPool, Conv1, BN | 1 |
|          | Bottleneck 8 | Conv1, BN, SplAtConv, Conv1, BN, ReLU, SA | 2 |
| Classifier | GlobalAvgPool, FC | 1 |

### TABLE III
**PRESENCE OR ABSENCE OF TUMOR MODEL.**

| Recall | Specificity | Precision | F1-score | Accuracy |
|--------|-------------|-----------|----------|----------|
| ResNeSt | 0.9733 | 0.9772 | 0.9803 | 0.9768 | 0.9751 |
| ResNeSAt | 0.9864 | 0.9981 | 0.9983 | 0.9923 | 0.9918 |

### TABLE IV
**SOURCE OF TUMOR MODEL (PRIMARY OR SECONDARY).**

| Recall | Specificity | Precision | F1-score | Accuracy |
|--------|-------------|-----------|----------|----------|
| ResNeSt | 0.7927 | 0.8684 | 0.8718 | 0.8304 | 0.8283 |
| ResNeSAt | 0.8212 | 0.8480 | 0.8591 | 0.8397 | 0.8338 |

### V. CONCLUSIONS & FUTURE WORK

In this paper, we use an attention guided deep learning method to solve the problem of tumor source classification, and further improve the effect of classifying the presence or absence of tumor. Using clinical case data generated by Shanghai Ruijin Hospital, we propose the ResNeSAt network for training and optimization, and classify the presence or absence of tumor and the type of tumor source on the tumor image within the error tolerance. This method produces a fast and accurate differential diagnosis with less subjective bias. It can reduce the dependence on experts in the clinical tumor image prediction process, and improve the efficiency and accuracy of diagnosis. Meanwhile, there is still room for improvement in the classification task of tumor source type. In future work, we can try segmentation of key areas to capture small differences between different images, which may aid to differentiate tumors classification further.

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