Brain Tumor Classification Using Medial Residual Encoder Layers

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Abstract. According to the World Health Organization, cancer is the second leading cause of death worldwide, responsible for over 9.5 million deaths in 2018 alone. Brain tumors count for one out of every four cancer deaths. Accurate and timely diagnosis of brain tumors will lead to more effective treatments. To date, several image classification approaches have been proposed to aid diagnosis and treatment. We propose an encoder layer that uses post-max-pooling features for residual learning. Our approach shows promising results by improving the tumor classification accuracy in MR images using a limited medical image dataset. Experimental evaluations of this model on a dataset consisting of 3064 MR images show 95-98% accuracy, which is better than previous studies on this database.

Keywords: deep learning; brain tumor classification; image classification.

1 Introduction

In recent years the importance of detection of brain tumors has led to the proposal of various automated and semi-automatic methods for type classification and segmentation of them [4] [5] [6] [7].

Various methods are proposed for image classification, extracting features from the input data, and applying classification algorithms on the extracted features. For instance, for brain tumor classification, Cheng et al. [6] extracted the region of interest (ROI) by using morphological operation. Then, for better feature extraction, they used a space pyramid matching (SPM) method. Extracted features were given to some classifiers such as SVM, SRC, and KNN to perform the classification operation [8]. In another approach, Asodekar et al. [9], after shape-based features extraction, applied SVM, and random forest classifiers for the classification task.

Convolutional neural network (CNN) is a machine-learning algorithm that has had a significant effect on image segmentation and classification without handcraft feature extraction. As an example, Abiwinanda et al. [10] applied CNN for tumor classification. Ismael et al. used a CNN network on MR images and statistical image features as input data for tumor classification [11]. Afshar et al. [12] studied a different architecture
of CapsNet networks [13] for tumor type classification. Also, Pashaei et al. [5] and Gumaei et al. [4] presented a method based on deep ELM networks.

In this paper, we propose an approach based on a deep neural network called ResBlock classifier for the classification of tumor types in MRI images. The database that was studied in this research is more extensive than other available databases on brain tumors. However, it is not an ideal database for deep learning approaches in terms of the number of images. Besides providing a high-precision deep learning approach, we intend to present the network’s architecture as simple as possible to cope with a limited database. Our research has used a database consisting of 3064 T1-contrast MR images, and we did not perform data augmentation. The experimental results show that the proposed model is competitive with state-of-the-art methods.

The structure of the paper is as follows. In section 2, we will discuss the background of the research. The proposed method is presented in section 3, and experimental results are discussed in section 4 of the paper. Section 5 is dedicated to concluding remarks.

2 Background and Problem Formulation

The brain is one of the most important and complex human organs protected inside the skull. This mass of nervous tissue can suffer tumors due to abnormal and uncontrolled cell growth. In general, tumors can be divided into three categories: benign, pre-carcinoma, or malignant. The difference between benign and malignant is that benign tumors do not invade other tissues and organs of the body and can surgically be removed [1]. More specifically, primary tumors that can be mentioned are gliomas, meningioma, and pituitary tumors. One of the differences between these tumors is that generally, gliomas are malignant, while meningiomas are typically benign. Slow-growing tumors are benign and malignant, but even benign tumors can damage other organs [2].

An essential step in the effective treating of tumors is early diagnosis and accurate identification of their types.

Magnetic resonance imaging (MRI) is a non-ionizing medical imaging modality that provides better contrast in the body’s soft tissues. Furthermore, MRI distinguishes between muscle, fat, water, and other soft tissues. MRI is the most prevalent human brain tumor technique that allows experts to diagnose tumor presence and type. Correct diagnosis depends on the experience and expertise of specialists investigating the characteristics of the images. Also, these analyses are time-consuming and prone to error. In this regard, computer-aided diagnostic methods (CAD) can be used to help tumor diagnostics without surgery or invasive methods. Up to now, all CAD approaches can be divided into two groups. The first group of CAD methods can classify images into two categories of images with brain tumors and those with no tumors. Algorithms of the second category of CAD methods classify brain images depending on brain tumor pathological types. The distinction between normal and abnormal images is relatively easy and can be performed by extracting handcrafted features. In contrast, identifying the tumor type is challenging because of the variety of shapes, sizes, and brain tumors’ textures. Some samples of MR images that contain brain tumors are shown in Fig. 1. Accurate classification of tumor types is not possible by handcrafted features, and deep
neural networks should be used for this purpose. Another difficulty in the classification of tumor types is the presence of different MR images captured from different views. In Fig. 1, we can see (a) axial, (b) sagittal, and (c) coronal images are taken from three directions. Our proposed network overcomes the mentioned challenges.

![Fig. 1. Samples of brain MR images contain three common tumors (a) glioma, (b) meningioma, and (c) pituitary tumor. Tumors specified with red boundary lines](image)  

### 3 Proposed Method

Generally, primitive CNNs used for classification tasks have similar structures and are only different in the number of convolution layers, stride, and kernel dimensions [14]. The proposed CNN is inspired by LeNet [15] and is used to classify images according to the tumor type. We first adapted LeNet to improve the accuracy by some modifications to the arrangement and number of layers. As shown in Fig. 2, this network consists of 18 convolution and pooling layers. After features are extracted from these layers, there are two fully connected layers with 4096 nodes. Extracted features are sent to these fully connected layers, and tumor type classification is performed in the last layer. The last fully connected layer has three neurons representing glioma, meningioma, and pituitary tumors.

![Fig. 2. The proposed model inspired by LeNet [15].](image)
After evaluating this CNN network performance and observing satisfactory brain tumor classification results, another CNN network is proposed that is inspired by LeNet architecture and residual learning [16]. Instead of considering sequential convolutional and pooling layers, we propose encoding using medial residual blocks (MidResBlock). The structure of the proposed encoding block is shown in Fig. 3.

![Fig. 3. Proposed MidResBlock encoder layer.](image)

In the encoder block of Fig. 3, the output feature map is smaller than the input of the block because of the max-pooling layer. Hence, we use residual learning by adding medial features and the encoder’s output features, which have the same size. These blocks provide a network architecture model in which we can better monitor its behavior. Applying many convolution and pooling layers in the network and passage of information through these layers lead to the loss of some desirable features. This loss of features reduces the performance and accuracy of the network. For this reason, the residual link is considered in the structure of each encoder block.

Adding information about middle convolution layers to each encoder layer’s output helps preserve information during the training process. The addition of information in the proposed MidResBlock classifier network is shown in Fig. 4. This network consists of 4 encoder units that extract features. Then the network performs the classification operation with two fully connected layers, which determines dimensions. We applied categorical cross-entropy for the proposed network training as the loss function that is most commonly used for multi-label classifications.

![Fig. 4. Proposed classifier using MidResBlocks](image)
4 Experimental Results

Presented models were trained and evaluated on a benchmark brain tumor MRI images dataset [3], which contains 3064 T1-weighted MR images gathered from 2005 to 2010. Three experienced radiologists have manually bordered tumor areas. These images include 1426 gliomas, 930 pituitary, and 708 meningiomas tumors. The resolution of images is 512×512, with 0.49×0.49 mm² pixel size. Our model is implemented on Python 3.7 and Tensorflow. Proposed models trained over 150 epochs using stochastic gradient descent (SGD algorithm) with momentum (learning rate = 0.001). Training time on NVIDIA GeForce GTX 1080 Ti was about 12 hours.

Accuracy, a typical criterion used to evaluate classification models, is defined as the ratio of the number of correct predictions by the total number of predictions. This criterion works poorly for an imbalanced dataset, as it may report high accuracy while biased toward the class with the largest number of samples. Data is divided to demonstrate the uniform distribution of tumor types based on the cross-validation method to address the imbalanced dataset.

In this paper, mean accuracy is used to report the final result. We used k-fold learning; hence the average of all folds is reported. The accuracy of the proposed model for brain tumor classification is investigated. Table 1 shows the results of the two proposed networks of LeNet-based and the MidResBlock classifier. Also, results of references [4] and [5], using the same benchmark data set, are shown in Table 1. Pashaei et al. [5] report that they achieved an accuracy of 93.68% by presenting a deep ELM network method. Gumaei et al. [4] also reported 94.23% accuracy using a feature extraction method and a deep ELM network. The reported evaluation based on the accuracy indicates that considering the residual links in the network classification architecture positively affects the classification accuracy.

| Proposed Method                  | Accuracy     |
|----------------------------------|--------------|
| Proposed LeNet based network     | 90.06%       |
| Pashaei et al. [5]               | 93.68%       |
| Gumaei et al. [4]                | 94.23%       |
| Proposed MidResBlock classifier network | 95.98%       |

5 Conclusion

Providing accurate diagnostic tools for detecting brain tumors can significantly impact early cancer detection, treatment, and outcome. This paper presented a classification architecture with high accuracy for detecting brain tumors from MRI images. Our results show that adapting network architecture by modifying the number of layers and
adding residual links as skip connection has an impressive impact on classification accuracy. Given the limitation of medical image datasets, CNN’s appropriate depth and simplicity significantly improve accuracy. Our results show that the proposed classifier using MidResBlock encoder layers is highly accurate compared to state of the art. Furthermore, due to model simplicity, it can preserve important image features and information. Our future work involves applying the proposed model to other medical images. We intend to use the proposed method for ultrasound [17], histopathological [18], and non-dermoscopic images [19].

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