MULTI-VIEW CNN FOR AUTOMATED GRADING OF GLIOMA USING MULTI-MODAL MRI SCANS

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ABSTRACT

Glioma has been one of the most life-threatening brain cancer diseases for adults. An accurate and fast glioma grade classification can help to appropriate treatment strategy and effective diagnosis to tumor patients. Recently, convolutional neural networks (CNNs) has been studied in medical image analysis. However, CNNs demands large annotated training datasets and a high computational cost. Yet in medical imaging analysis, especially for a brain tumor, collecting and curating large annotated volume of images is typically difficult, and resource-intensive. To address these issues, this paper presents a fully automatic CNN-based pre-trained model on natural images with high performances for noninvasively classifying glioma into two groups using MRI data obtained from BraTS'17 dataset.

1 INTRODUCTION

Originating from glial cells, gliomas are the most common primary brain neoplasms. Depending on the underlying histology and molecular characteristics of the tumor, gliomas can be categorized as high-grade glioma (HGG) or low-grade glioma (LGG) (Louis et al., 2016). Patients with LGG and HGG follow different treatment options and are significantly different in prognosis. The survival rate is lower in HGGs than that in the LGGs tumors (Ostrom et al., 2018). Therefore, accurate pre-operative stratification of glioma grades is critical in predicting disease prognosis and in considering treatment options.

Conventional prediction of glioma grading is based on microscopic examination of tissue or the visual inspection of morphological features of the segmented tumor region in the whole brain MRI images. However, these approaches are often inaccurate, subjective task, and even time-consuming for experienced specialists due to the complex mechanical properties of the tissues, which vary from person to person. Therefore, the development of artificial intelligence (AI)- based systems to aid the radiologists for more accurate and fast glioma grading based on the multimodal brain MRI data acquired prior to any invasive examination is of great current interest (Kong et al., 2013).

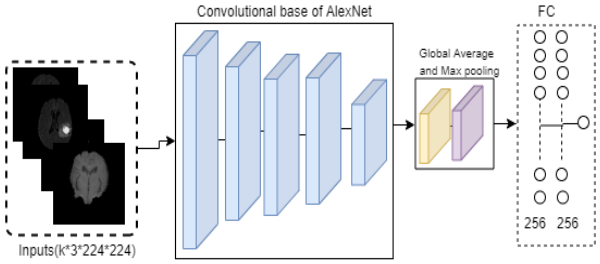
2 MATERIALS AND METHODS

The dataset we used to train and evaluate our proposed models are obtained from BRATS'17 (Menze et al., 2014; Bakas et al., 2017) training dataset, which consists of multi-modal MRI images of 285 patients (75 LGG and 210 HGG). For each patient, four MR imaging modalities are provided: FLAIR, T1CE, T1, and T2. This training data of 285 patients is split into five-folds for cross-validation using stratified random sampling to ensure that each fold contains an approximately equal proportion of patients of both the classes.

In this paper, we present an AI-based framework to discriminate between LGG and HGG using pre-operative multi-modal MRI images. Specifically, first we reconstructed all the multi-modal 3D MRI scans as a set of 2D projections in the axial plane, resulting four different 2D projected stacked slices for a single patient. Then, we implemented Multi-View CNN (Mv-CNN) architectures that perform end-to-end binary classification on each one of the four 2D projected images. Finally, the probability predictions of the four Mv-CNN models were averaged to obtain the final more accurate classification result. To the best of our knowledge, this method is the first work that attempts to differentiate between LGG and HGG by using an ensemble of multiple Mv-CNN models.

The Mv-CNN architecture that we used (fig 1) consists of four core parts: (i) the convolutional base of pre-trained AlexNet for extracting features. It takes k×3×224×224 stacked png images as inputs, and out-puts k×256×6×6 features sizes where 3 indicates the number color channels, and k is the number of axial slices of the 3D MRI scan. (ii) Global average pooling on top of the convolutional base of AlexNet applied across the spatial dimensions to reduce features to k×256. (iii) Max pooling layer on top of global average pooling applied across slices to reduce features to 256 dimensional vector, and (iv) Final dense layers with sigmoid activation function to map from the computed hidden representation to the output probability prediction. Similar architecture has been used in some papers for TB report generation (Mossa et al., 2019).

Figure 1: The Multi-View CNN architecture



3 Results and Discussions

The prediction performance of each of the four Mv-CNN models is shown in table 1. It is observed that all the models obtained an AUC value greater than 0.9, demonstrating that finetuned Mv-CNN models are able to extract discriminative features from MRI images for distinguishing between LGG and HGG. In addition, Mv-CNN model trained solely with T1CE has a better classification performance than the other modalities.The results indicates that T1CE modalities have more discriminative features for glioma grading compared to the other modalities implemented in this paper. Moreover, ensemble of the four models resulted an improved performance over the individual models.

Table 1: Performances using stratified five-fold cross validation

MODELS	AUC	Accuracy	Specificity	Precision	Sensitivity	F1-score
FLAIR	0.90	80.6	0.78	0.92	0.80	0.86
T1	0.92	87.6	0.94	0.96	0.85	0.92
T1CE	0.95	93.6	0.91	0.98	0.94	0.94
T2	0.92	87.3	**0.99**	**0.99**	0.83	0.85
Fused	**0.96**	**94.9**	**0.99**	**0.99**	**0.95**	**0.96**

A comparison of our results with some of recently published works for glioma grading is presented in Table 2.

Table 2: Results of our proposed approach and state-of-the-art results for glioma grading

Authors	Years	Dataset Size	Methods	AUC	Accuracy
(Hsieh et al., 2017)	2017	107	Handcrafted features	0.89	88
(Cho & Park, 2017)	2017	274	Handcrafted features	0.89	89.8
(Chen et al., 2018)	2018	274	Handcrafted features	0.96	91.3
(Zhu et al., 2019)	2019	181	DL and Handcrafted features	0.82	-
Prposed	2020	285	Deep learning	**0.96**	**94.9**

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