An Attention based Network for Improved Glioma Grading

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Abstract. Accurate prediction of glioma grade is significant for treatment planning and management. Prior studies require a segmentation network to extract the tumor region, which was then used by classification network for grade prediction. However, tumor segmentation was a challenging pre-processing task and inaccurate tumor extraction can lead to poor classification performance. In this work, we propose an attention based model for grade prediction. The model contains attention layers to estimate the regions of interest that are relevant for grade classification. The F1-score of the proposed model is 91.18%, which is at least 6% higher than the state-of-the-art deep learning models. In addition, the proposed model was able to generate a more interpretable output.

Keywords: glioma grading · attention · accuracy.

1 Introduction

Gliomas are the most prevalent primary brain tumor in adults [7]. These tumors originate from glial cells that are accountable for supporting the central nervous system. Depending on the aggressiveness, gliomas are categorized into four grades from I to IV. Grades I and II, termed as low-grade gliomas, are the least-aggressive and grades III and IV, termed as high-grade gliomas are the most-aggressive. Accurate diagnosis of grade is significant for treatment planning [4]. The current gold-standard way of determining tumor grade is through biopsy. However, biopsy is an invasive and an expensive process. In addition, patients with aggressive tumor require frequent determination of grade. The goal is to develop a non-invasive method for predicting grade.

Recently, several machine learning (ML) algorithms on magnetic resonance imaging (MRI) datasets were proposed for glioma grade prediction [5, 6, 3, 1, 10]. It is important to note that these ML algorithms require pre-processing, which include co-registering to the same anatomical template, interpolating to the same resolution, skull-stripping, and segmentation of tumors [5, 6, 3]. These tumors are either manually segmented by experienced neuro-radiologists or by using deep learning algorithms. Note that it is challenging to accurately segment the tumor and inaccurate segmentation may lead to poor grade prediction. Additionally, so far limited efforts have been made to interpret which part of the image the deep learning model focuses on for grade prediction. In this paper, we propose

an attention based network that automatically identifies the tumor region as part of the grading process and doesn't require segmentation. We compared the proposed network with several other state-of-the-art deep learning models.

2 Imaging Data Description

The dataset was collected from Multimodal Brain Tumor Segmentation Challenge 2018 hosted by the University of Pennsylvania [8, 2]. The dataset has multimodal 3D brain MRI scans of 285 patients. Out of 285 patients, 210 belong to the glioblastoma (GBM/HGG) category and the rest 75 belong to LGG category. Each patient has four sequences, fluid attenuated inversion recovery (FLAIR), T1, T1 contrast-enhanced (T1CE), and T2. The dimension of each sequence is 240x240x155. Representative scans of a LGG and a HGG patient are shown in Fig. 1.

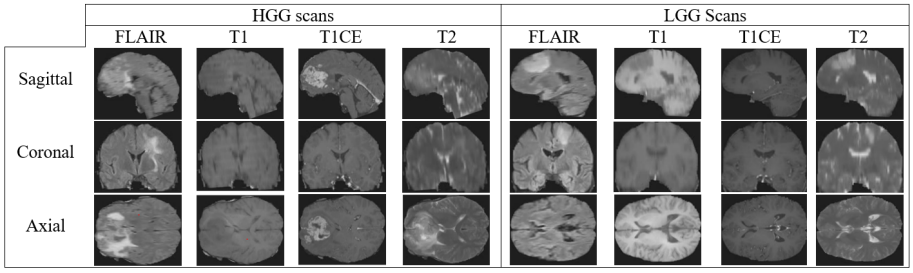

Fig. 1. Representative LGG and HGG scans. Each column corresponds to a sequence: FLAIR, T1, T1CE, and T2. Each row corresponds to a plane: sagittal, coronal, and axial.

The following three pre-processing steps were implemented before publishing the data online. Firstly, all the four sequences were registered to the same anatomical template. Secondly, the sequences were interpolated to the same 1 mm^3 resolution. Lastly, skull-stripping was performed to remove the skull. Along with the four sequences, manual segmentation provided by expert neuro-radiologists were also provided.

3 Proposed Attention Model

Inspired by the visual attention model built for melanoma recognition [9], we propose a network to focus on the tumor region, rather than irrelevant areas in the background. This network eliminates the need of segmentation of tumors, reducing the burden of a complex pre-processing step. The proposed network architecture is shown in Fig. 2.

The VGG-16 model was used as backbone network after removing all the dense layers. It was followed by a series of five convolutional layers with rectified linear unit (ReLU) activation function and max-pooling layers. The convolution layers have a filter size 3x3 and stride of 1 and max-pooling layer have a filter size 2x2 and stride of 2. The outputs from third, fourth, and fifth convolutional blocks are pool-3, pool-4, and global features respectively. Pool-3 and global features are passed through an attention block to extract first set of features, Features 1. In the attention block, global features are upsampled via bilinear interpolation and an element-wise sum is performed to obtain feature map. Similarly, pool-4 and global features are passed through an attention block to extract second set of features, Features 2. The final feature vector is obtained by concatenating features 1, 2, and 3. Finally, the concatenated feature vector is passed through a softmax classification layer for prediction of glioma grade.

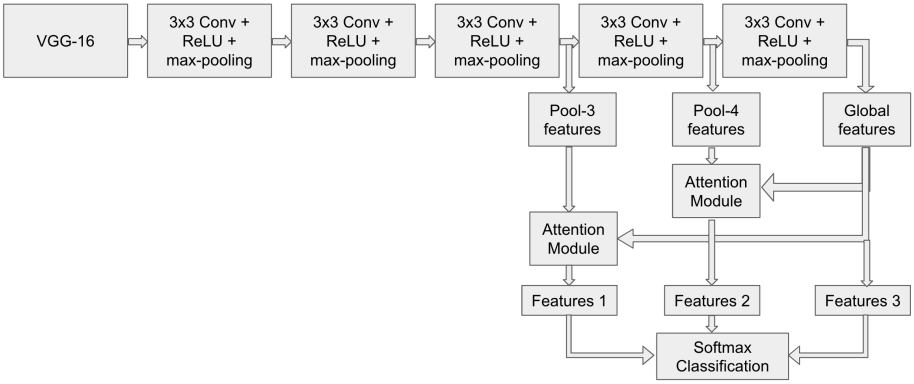

Fig. 2. Illustration of the proposed network architecture. It consists of a pre-trained VGG-16, followed by five convolutional and max-pooling layers. The pool-3 and pool-4 features, extracted from third and fourth convolutional layers, are passed through an attention block to obtain two sets of attention maps. These maps along with global features (extracted from the last convolutional layer) are concatenated and passed through softmax classification layer to predict glioma grade.

Before training the model, the dataset is first split into training and testing sets in the ratio of 75% and 25%. Training set is further divided into training and validation sets. Since the dataset is imbalanced, oversampling was performed on the training set to balance the dataset and avoid bias. Note that we fine-tuned hyperparameters dropout rate, learning rate, and weight decay based on the performance on validation dataset. The learning rate, which is a key parameter influencing the convergence of our model, was altered across four values: 0.01, 0.001, 0.0005, and 0.0001. As for the dropout rate, we explored a range of values from 0.2 to 0.5. Lastly, we adjusted the weight decay across the following range: 0.01, 0.001, and 1e-05. Note that focal loss was used as loss function, that can

automatically give less weight to easy samples in the training set. After selecting the optimal hyperparameters, the model was evaluated on the test dataset.

4 Results and Discussion

The performance of the proposed attention model was compared with other state-of-the-art DL models, MobileNet, DenseNet, and EfficientNet. The confusion matrix, accuracy, precision, recall, and F1-score were reported in Table 1. We focused on F1-score since it is a harmonic mean between precision and recall and we want to correctly identify low-grade and high-grade tumors. The F1-score for MobileNet, EfficientNet, and DenseNet models are 80.85%, 81.48%, and 84.70% respectively. For the proposed model, the F1-score is 91.18%, which is at least 6% higher than the other DL models.

Table 1. Performance of proposed attention model and other state-of-the-art DL models. The proposed model has an F1-score of 91.18%, which is at least 6% higher than the other models.

Model Names	**Accuracy(%)**	**Precision(%)**	**Recall(%)**	**F1-score(%)**
MobileNetV2	70.18	76.59	85.71	80.85
DenseNet201	77.19	83.72	85.71	84.70
EfficientNet-B2	71.93	79.55	83.33	81.48
Proposed Model	85.96	85.42	97.62	91.18

The visualizations produced by the pool-3 and pool-4 attention layer for both low-grade and high-grade glioma are shown in Fig. 3. It can be seen that the proposed attention model was able to detect the tumor from the input images.

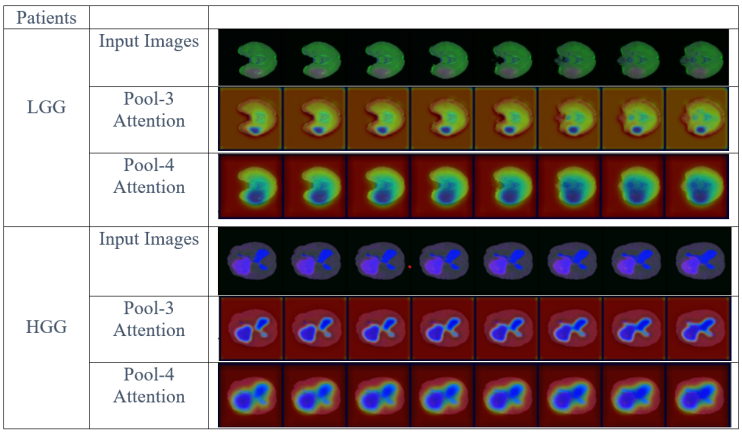

Fig. 3. Visualization of attention maps for the proposed model.

5 Conclusion

This work introduces an attention network for predicting glioma grades. Unlike traditional methods requiring tumor segmentation, this network autonomously identifies the tumor region. Achieving an F1-score of 91.18%, our proposed model surpasses the performance of current state-of-the-art deep learning models by at least 6%. Moreover, our model provides insights into the specific areas of the input image it prioritizes for grade prediction. Such interpretable models hold significant value for accurate glioma grade classification.

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