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# A CNN-Model to Classify Low-Grade and High-Grade Glioma from MRI Images

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**ABSTRACT:** we explore better ways to segment the LGG based on the CNN in the binary framework. We firstly studied the effect of different depths and the number of neurons in the fully connected layers on the tumor segmentation. It was found that the deepening of the network can optimize the segmentation results without increasing the amount of computation. Increasing the number of neurons in the fully connected layers under the same conditions can also improve the segmentation results. Next, we found that the use of the fully connected CRF as the CNN postprocessing can improve the segmentation results of the contour and edge and greatly enhances the segmentation results. At last, we proposed two kinds of network structures combined with 3D information. Experiments showed that the combination of these two structures and CRF can get better results. Early fusion can improve the segmentation results globally, and late fusion can make the segmentation results more sensitive.

**KEYWORDS**: Computer science, Cancer imaging, Cancer screening, Statistics

## I. INTRODUCTION

Low-grade gliomas (LLG) [1] are brain tumors that arise from astrocytes and oligodendrocytes, which are two separate types of brain cells [1]. Low-grade gliomas can cause a variety of symptoms depending on where they are in the brain. The tumor in the area of the brain that governs language may prevent the patient from speaking or understanding. A brain tumor diagnosis can be devastating for patients. The majority of tumors are discovered as a result of a symptom that prompts doctors to perform a brain MRI or CT scan.

MRI is the most effective method for detecting brain malignancies. The scans provide a massive amount of image data. The radiologist examines these images. Tumors of the brain are difficult to diagnose and treat. The sizes and locations of brain tumors vary dramatically. As a result, fully comprehending the nature of the tumor is quite challenging. For MRI analysis, a qualified neurosurgeon is required. The absence of skilled doctors and a lack of information regarding tumors can make generating reports from MRIs extremely difficult and time-consuming. A manual inspection may be susceptible to errors due to the complexities involved in brain tumors and their characteristics. Machine learning-based automated classification systems have consistently outperformed manual classification.

The study of the relationship between cancer imaging features and gene expression is known as radiogenomics. Biomarkers that determine the genetics of a disease without the use of an intrusive biopsy can be created using radiogenomics. A biomarker is a biological indicator of some state or condition. The presence or lack of biomarkers is important in avoiding intrusive biopsies because certain treatments for brain tumors are more successful in the presence or absence of a biomarker. The detection of biomarkers can ensure that patients receive the most effective treatment for their specific situation [2].

Low-grade gliomas (LLG) [2–4] are tumors that are considered formed from glial cells, have infiltrative development, and lack malignant histopathological characteristics. One of the biomarkers that appear to be essential in low-grade

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gliomas is 1p/19q chromosomal codeletion. When 1p/19q codeletion is discovered in low-grade gliomas, studies demonstrate that they respond better to chemotherapy and radiotherapy. The novelty and promising results of combining deep learning with radiogenomics are what make this study noteworthy. The detection of 1p/19q codeletion using deep learning works better with T2 images than with T1 postcontrast images [2].

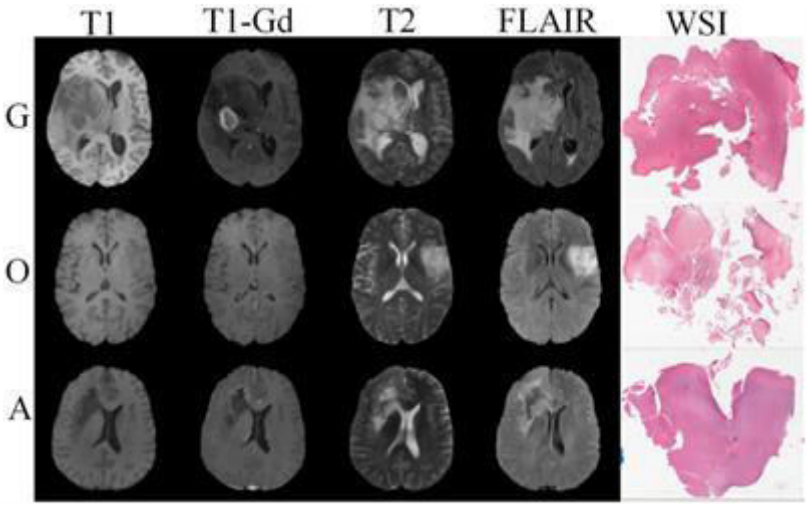


Fig 1: Combining Radiology and Pathology

In 2017, deep learning was firstly used by Akkus et al. [2] to predict 1p19q from LGG MRI; tumor segmentation, image registration, and CNN-based 1p/19q status classification are the three primary steps of their method. When data augmentation is not performed, their multiscale CNNs overfit the original training data. Lombardi et al. [4] used popular public networks, including AlexNet, VGG19, and GoogleNet, for 1p19q categorization through transfer learning [5–7]. According to their description, even with limited datasets, the results offered by transfer learning are robust. Abiwinanda et al. [8] used five different CNN designs, with the second design with two convolutional layers, one maxpool layer, and one ReLU layer, then come 64 hidden neurons, achieving the highest accuracy.

Why are there just thousands of training examples? Maithra Raghu et al. [9] wondered. They looked upon transfer learning in small data settings. They discovered that there was a significant performance difference between transfer learning and training from scratch for a big model (ResNet), but not for a smaller model. For a little amount of data, the large model built by ImageNet can have too many parameters. They discovered that transfer learning provides limited performance increases for the evaluated medical imaging tasks after a rigorous performance evaluation and examination of hidden representations of neural networks. Transfer learning had little effect on the performance of medical imaging tasks, and the model trained from the ground up was near as well as the ImageNet transfer model.

## II. BACKGROUND ANALYSIS

A large number of algorithms have been developed to complete the task of tumor segmentation. Many traditional segmentation methods were based on gray scale values, such as fuzzy clustering and region growing [5]. These methods would be likely to fail when processing nonenhanced tumor images. Another kind of popular methods was multiatlas segmentation, which was based on the correlation of the priori brain atlas and the medical images to be processed [6]. However, these methods are often problematic when the atlases and target images are obtained via different imaging protocols and the deformable registration is also considered as a difficult process.

Recently, several methods related with machine learning have been applied in brain tumor segmentation. Parisot et al. used the prior knowledge to classify the tumor first and then used another graph to determine the class of each voxel [7]. Huang et al. utilized the sparseness of samples to build up a particular dictionary and used a softmax model to optimize the error reconstruction coefficients for different classes [8]. Random forests have been considered to be good

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at dealing with a great number of features to accomplish brain tumor segmentation. Meier et al. applied a set of dedicated features to get decision forests to discriminate pathological regions from brain MRI volumes [9]. In addition, Markov random field (MRF) and conditional random field (CRF) are also often mentioned to obtain smooth edges. Zhao et al. proposed a semisegmentation method based on the MRF [10], in which one slice was labeled and other slices were sequentially labeled based on a MRF label. Meier et al. estimated the CRF to improve the voxel-wise classification performance on the top of the decision forest classifier [11]. These conventional machine learning methods are often based on a large number of features extracted from the image, reflecting the shape, gray value, and texture of the tumor area. But an important problem with these approaches is that the computation of too many features is too time-consuming and particular feature can cause difficulties in tuning.

## III. METHODS

Another kind of approach to segment gliomas is based on the well-known convolutional neural network (CNN). Primarily due to its abilities to obtain image global and local information directly from the convolution kernels, CNNs have made breakthrough progress in image processing and object recognition and been wildly used thereafter [12]. CNNs have shown good performances in the field of medical image processing in recent years, not only in terms of accuracy, but also in terms of efficiency [13]. Pereira et al. developed two CNN structures with different depths to deal with the HGG and the LGG [14]. Dvorak et al. evaluated the effectiveness of different patch selection strategies based on the segmentation results of CNNs [15]. Havaei et al. proposed a multiscale CNN structures in order to make better use of local and global information [16]. Rao et al. combined random forests with the final output of CNNs to achieve better classification results [17]. Several CNN methods mentioned previously are based on a two-dimensional convolution kernels and do not make good use of the natural three-dimensional (3D) information of medical images. Typically, 3D filters can take fully advantage of 3D connection characteristics of images. Kamnitsas et al. [18] evaluated the use of 3D filters. However, the 3D convolution algorithm limits the size of convolution kernels and causes a great increase of the computation load. Furthermore, 3D filters require high resolution on the vertical plane, while actual MRI images usually need interpolation and do not have such high resolution. The process of interpolation and down sampling in 3D filters often brings additional errors in segmentation. Therefore, how to make good use of 3D information with CNN in gliomas segmentation still remains an important problem.

On the other hand, segmentation methods mentioned above mainly focused on the segmentation of the HGG. Although the internal structure of the LGG is simpler than that of the HGG, the segmentation of the LGG is considered more difficult because of its lower contrast and smaller size [14]. Thus, these segmentation methods mentioned above often do not produce good results when dealing with the LGG.

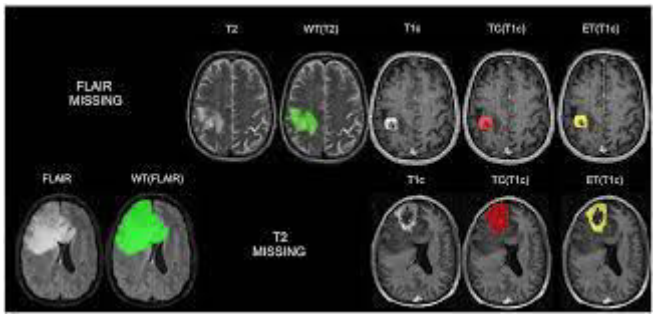


Fig 2: Multi-class glioma segmentation

As it is known, the lesion area of the LGG is more distinguishable from T2flair MRI than from other MRI modalities [19]. So in this study, we chose T2flair modal MRI images as the original data for image processing. LGG has high signal in the T2flair images. Compared with HGG, the signal intensity distribution of LGG is more uniform and the boundaries of tumors and surrounding brain tissues tend to be clearer. In addition, LGG usually shows no necrosis, perifocal edema, or hemorrhagic foci. Oligodendroglioma and astrocytoma were two major types of LGG. The two

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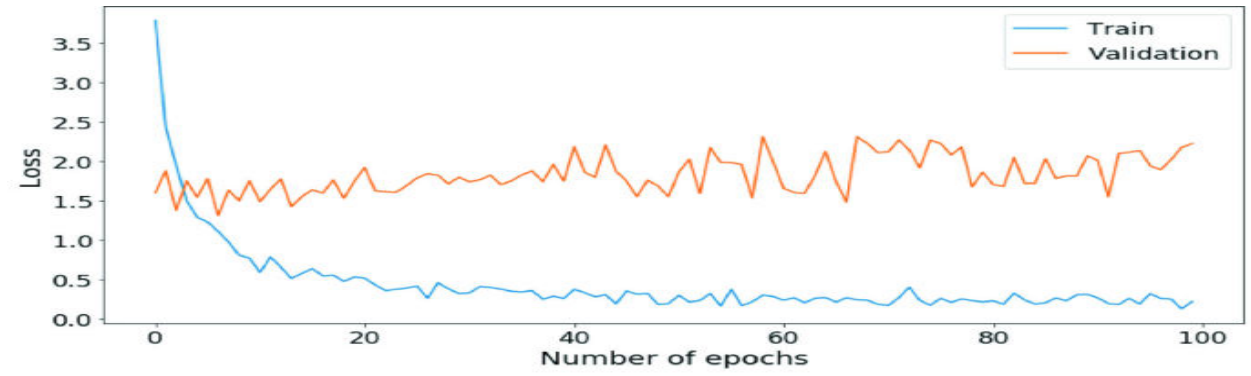
subtypes could be distinguished radiologically by the presence of calcification. Generally, calcification inside oligo tumor turns out hypointensity on T2-weighted and isointensity on T1-weighted precontrast MRI.

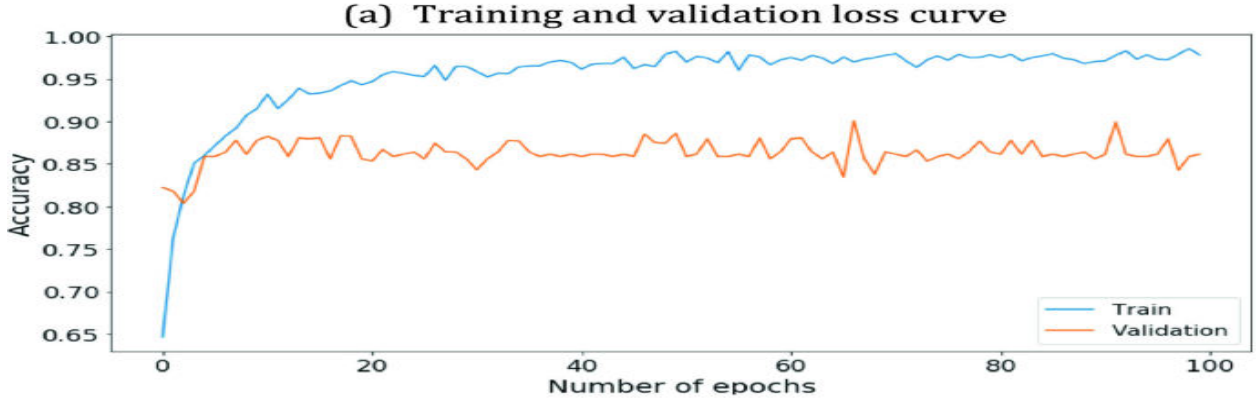
In this paper, a new method is presented aiming at automatic segmentation of LGG MRI images. Main contributions of the paper are as follows. Firstly, the effect of different CNN depths and the number of neurons in the fully connected layers on the segmentation result were thoroughly evaluated. Secondly, in order to use the 3D information, nearby slices were set into the network and connected with a fully connected CRF. Lastly, the results on the LGG T2flair dataset showed that the method is better than the state-of-the-art CNN method.

## IV. RESULT ANALYSIS

We provide a reliable and noninvasive approach for predicting 1p/19q chromosomal arm deletion in this work. Having a sufficient amount of datasets is a significant difficulty when applying deep learning approaches to medical imaging. Despite the fact that the initial data amount was limited, our data volume expanded as a result of data augmentation approaches. With larger patient populations and more varied data, it is possible that additional performance gains will be gained.




(a) Training and validation loss curve




(b) Training and validation accuracy curve

Fig 3: result analysis

As large convolution kernels are inefficient in terms of cost. We are reducing the number of irrelevant features conceivable by restricting the number of parameters. This drives the deep learning algorithm to learn traits that are common to a variety of scenarios, allowing it to generalize more effectively. Smaller odd-sized kernel filters would be preferable. However, is removed from the list of possible ideal filter sizes since the features recovered would be fine-grained and local, with no information from nearby pixels. Furthermore, it does not extract any useful features. Through experiments, we found that although VGG16 also uses a convolution kernel, it is prone to overfitting due to

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the complexity of the network, and the dataset is small. As a result, VGG16 categorization precision and recall of 1p/19q chromosomal arm deletion are not very good.

Because of the deep architecture of current networks like GoogleNet and ResNet, feature maps from these networks frequently have a very large receptive field. However, studies [20] reveal that the network gathers information from a considerably narrower portion of the receptive field, which is referred to as the valid receptive field in this research. In this experiment, we found that the recall rate was not high by using InceptionResNetV2 and VGG16. As a result, a large receptive field does not increase the performance of medical images on small datasets considerably.

## V. CONCLUSION

The results of our CNN approach for 1p/19q codeletion status classification noninvasively are promising. We create a brain tumor detection model that does not rely on transfer learning. Our network structure employs a deep convolution stack strategy when training with Gaussian noise, reducing overfitting and improving performance. Compared to transfer learning models, our model gives more accurate findings. With basic, lightweight models equivalent to ImageNet topology, we discovered that transfer learning offered no performance benefit in small datasets. By properly designing the network and optimizing the hyperparameters during training, CNNs without transfer learning can reach and surpass transfer learning.

## REFERENCES

1. J. Amin, M. Sharif, A. Haldorai, M. Yasmin, and R. S. Nayak, "Brain tumor detection and classification using machine learning: a comprehensive survey," *Complex & Intelligent Systems*, 2021.
2. View at: Publisher Site | Google Scholar
3. Z. Akkus, I. Ali, J. Sedlář et al., "Predicting deletion of chromosomal arms 1p/19q in low-grade gliomas from MR images using machine intelligence," *Journal of Digital Imaging*, vol. 30, no. 4, pp. 469–476, 2017.
4. View at: Publisher Site | Google Scholar
5. D. Bhattacharya, N. Sinha, and J. Saini, "Determining chromosomal arms 1p/19q co-deletion status in low graded glioma by cross correlation-periodogram pattern analysis," *Scientific Reports*, vol. 11, no. 1, p. 23866, 2021.
6. View at: Publisher Site | Google Scholar
7. G. Lombardi, V. Barresi, A. Castellano et al., "Clinical management of diffuse low-grade gliomas," *Cancers*, vol. 12, no. 10, article 3008, 2020.
8. View at: Publisher Site | Google Scholar
9. R. Chelghoum, A. Ikhlef, A. Hameurlaine, and S. Jacquir, "Transfer learning using convolutional neural network architectures for brain tumor classification from MRI images," *IFIP Advances in Information and Communication Technology*, Springer, 2020.
10. View at: Publisher Site | Google Scholar
11. M. F. Alanazi, M. U. Ali, S. J. Hussain et al., "Brain tumor/mass classification framework using magnetic-resonance-imaging-based isolated and developed transfer deep-learning model," *Sensors*, vol. 22, no. 1, p. 372, 2022.
12. View at: Publisher Site | Google Scholar
13. Z. N. K. Swati, Q. Zhao, M. Kabir et al., "Brain tumor classification for MR images using transfer learning and fine- tuning," *Computerized Medical Imaging and Graphics*, vol. 75, pp. 34–46, 2019.
14. View at: Publisher Site | Google Scholar
15. N. Abiwinanda, M. Hanif, S. T. Hesaputra, A. Handayani, and T. R. Mengko, *Brain Tumor Classification Using Convolutional Neural Network World Congress on Medical Physics and Biomedical Engineering 2018*, Springer, Singapore, 2019.
16. View at: Publisher Site
17. M. Raghu, C. Zhang, J. Kleinberg, and S. Bengio, "Transfusion: understanding transfer learning for medical imaging," *Advances in neural information processing systems*, vol. 32, 2019.
18. View at: Publisher Site | Google Scholar
19. J. Kang, Z. Ullah, and J. Gwak, "MRI-based brain tumor classification using ensemble of deep features and machine learning classifiers," *Sensors*, vol. 21, no. 6, article 2222, 2021.
20. View at: Publisher Site | Google Scholar

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