Innovative Convolutional Neural Network Hybrid for Brain Tumor Segmentation

ISSELMOU ABD EL KADER^{1,*}, JINGFEI HE², GUIZHI XU³, DANIL VODOLAZSKII⁴, SHIVANSH SINGH⁴, RUJUN LI⁴, YUNGE DUAN⁴ ¹School of International Education, Hebei University of Technology, CHINA

> ²School of Electronics and Information Engineering, Hebei University of Technology, Tianjin city, CHINA

> > ³School of Electrical Engineering, Hebei University of Technology, Tianjin city, CHINA

⁴HEBUT-LUT Double Degree Programs, Lappeenranta city, FINLAND

*Corresponding Author

Abstract: - Brain tumor segmentation and classification play vital roles in the treatment, diagnosis, therapy planning, and evaluation of responses to cancer treatment. Magnetic resonance imaging (MRI) is a prevalent method for analyzing brain tumors, utilizing various acquisition protocols, including both conventional and advanced techniques. This study introduces a fully automated model designed to segment abnormal tissues related to brain tumors from multimodal MRI images, thereby assisting radiologists in diagnosis and treatment planning. The proposed model, termed "CNN-FCM," combines a hybrid convolutional neural network with fuzzy c-means clustering to tackle the challenges posed by inaccurate segmentation and diverse input image dimensions. The architecture of the model consists of three layers: a convolutional layer, a ReLU activation layer, and a clustering layer. Comprehensive experiments conducted on the BRATS 2017 dataset reveal that the model delivers competitive outcomes, achieving performance metrics such as accuracy, sensitivity, specificity, overall Dice coefficient, and recall of 96.5%, 95.21%, 94.8%, 93.7%, and 94.1%, respectively. These findings suggest that the hybrid CNN-FCM model effectively resolves issues related to segmentation accuracy and variability in input images within the context of brain tumor analysis is.

Key-Words: - Brain tumor, Convolutional neural network, MRI dataset, segmentation, FCM algorithm, and accuracy value.

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1 Introduction

Abnormal proliferation of cells is the main factor contributing to the formation of brain tumors, with gliomas representing a prominent category that is divided into four distinct grades, [1]. Grades I and II are deemed low-grade tumors, whereas grades III and IV, which include glioblastoma (grade IV), are classified as high-grade. Glioblastoma can result in ischemic strokes within the brain, which develop through three phases: acute, subacute, and chronic. Throughout these phases, cellular damage modifies the molecular composition of brain tissue, as observed in MRI scans [2], complicating the automated detection of tumors and the planning of treatment. Deep learning has emerged as a popular method for segmenting brain tumors due to its capability to learn features specific to medical imaging tasks. Nevertheless, numerous current deep learning techniques face challenges in preserving spatial consistency and accuracy in their segmentation outcomes, [3], [4]. One key limitation is the difficulty in delineating visual objects effectively, [5]. Despite these challenges, deep learning techniques, which learn hierarchical feature representations directly from data, often outperform traditional handcrafted feature designs, [6]. In brain tumor segmentation, deep learning-based methods aggregate information across MRI modalities to improve segmentation accuracy, [7]. Various brain tumor segmentation techniques have been proposed in the literature, typically classified as automatic or approaches. semi-automatic [8]. Other categorizations include generative versus discriminative methods. Segmentation techniques are generally grouped into three categories based on the degree of human interaction: manual, semiautomatic, and fully automatic, [9], [10].

Authors [9] proposed a two-pathway deep network in 2014, featuring parallel convolutional and fully connected pipelines. Convolutional pipelines process larger patches to capture wider regions of the image, whereas fully connected pipelines focus on smaller patches to capture local details. Authors [3] later extended this approach using two-stage architectures with different kernel sizes for global and local segmentation. Authors [4] A segmentation technique based on convolutional neural networks (CNN) using small 3 x 3 kernels. This design facilitates deeper network architectures while reducing the risk of overfitting due to the smaller number of weights in the network. Their method was validated using the BRATS 2013 and BRATS 2015 datasets, showing high Dice similarity coefficients. In [11] a CNN model known as Deep Medic, features three parallel paths designed to process different input resolutions. This model achieved an average Dice coefficient of 0.87 for full tumor segmentation on the BRATS 2017 dataset. Other important

contributions include [12], who developed label distribution techniques to improve the performance of patch-based CNNs, and [13], who developed a two-path CNN (2PGCNN) model to integrate global and local information. [14] further improved segmentation by building multi-cascade CNNs supporting multi-scale features, while [15] applied Radionics-informed CNNs (RadCNN) to combine texture features with MRI scans for glioma segmentation. Although their approach yielded excellent results on the BRATS16 dataset, it failed to achieve top rankings on the BRATS17 dataset.

This study proposes a hybrid model combining convolutional neural networks with fuzzy c-means pooling (CNN-FCM) for the analysis and segmentation of brain tumors in MRI scans. The model is designed to identify abnormal brain cells and identify tumor regions by utilizing a rich set of features. Experimental results indicate that the CNN-FCM model achieves high levels of accuracy, sensitivity, specificity, Dice score, and recall, thus effectively distinguishing between normal and abnormal brain cells in MRI images. The combination of CNN and fuzzy c-means greatly improves the model's ability to accurately diagnose and segment brain tumors.

2 Dataset

In this research, the BRATS 2017 dataset was used, which includes a total of 3000 MRI scans. The dataset was split into training and testing subsets, with 75% of the images (1250 high-grade gliomas (HGG) and 1000 low-grade gliomas (LGG)) reserved for model training, while the remaining 25% (400 high-grade gliomas and 350 low-grade gliomas) for testing purposes. Three MRI modalities (FLAIR, T1ce, and T2) were used as input for the CNN-FCM, which was specially structured to accommodate five input layers. The tumor data obtained from these three MRI techniques facilitated accurate tumor segmentation, as shown in Figure 1 and Figure 2.



Fig. 1: MRI BRATS2017 brain images with tumor



Fig. 2: MRI BRATS2017 brain images without tumor

3 Methodology

This paper presents a convolutional neural networkintegrated with CNN-FCM for brain tumor segmentation in MRI scans. The model architecture is shown in Figure 3 (Appendix), which includes five basic elements: input data, image preprocessing, feature extraction, CNN and FCM fusion, and tumor segmentation. The process is carried out through the following stages:

Stage 1: Input Data

The model utilizes MRI images sourced from the BRATS 2017 dataset, where each image is captured at a resolution of 256×256 pixels in the axial plane.

Stage 2: Preprocessing

Preprocessing is a crucial step in image processing that enhances image quality by reducing noise and highlighting important features, resulting in more accurate analysis. In this work, Gaussian filtering is used for image denoising due to its effectiveness in medical imaging, particularly for reducing highfrequency noise. The Gaussian filter is defined as shown in equation (1):

$$G(x, y) = \frac{1}{2\pi\sigma^2} \exp{-\frac{x^2 + y^2}{2^{\sigma^2}}}$$
(1)

where σ the standard deviation of the Gaussian distribution, π is For Skull stripping in BMRI images, many methods are proposed.

Stage 3: Image Extraction

Image features are extracted using a discrete preview approach, where the image is transformed into the frequency domain through filtering with both lowpass and high-pass filters. This process divides the image into different levels of approximation, such as lower and upper layers. For brain tumor detection, feature extraction focuses on identifying the specific location of the tumor and its exact position during diagnosis. The characteristic vectors are measured from the center of mass to the tumor edges, capturing the geometric features of the tumor, including (1) area, (2) perimeter, (3) centroid, and (4) diameter. In handling a large dataset, feature extraction involves transforming the input data into a set of features that distinctly represent the various characteristics of the input images.

Stage 4: Feature Selection

Selecting relevant features for extraction is essential to reduce computational cost and improve processing time. This is achieved by applying component analysis, which transforms the input data and helps to avoid the curse of dimensionality. The model uses feature selection to identify tumor concentration regions, selecting thirteen features from the graylevel co-occurrence matrix (GLCM): variance, correlation, energy, entropy, homogeneity, inverse difference moment (IDM), mean, variance, and rms. (RMS), standard deviation, smoothing, skewness, detection asymmetry for tumor and and segmentation.

Stage 5: Convolutional Neural Network and Fuzzy C-Means Integration (CNN-FCM)

After feature selection from the BRATS 2017 dataset, a convolutional neural network is combined with fuzzy c-means. The CNN-FCM framework consists of several basic components: a knowledge base, convolutional layers, an extraction library, and inference and annotation utilities. The knowledge base acts as a central repository containing information about the dataset, which is essential to ensure that the data is accurately aligned during the training phase.

The convolution process starts with the prepared input data and includes multiple layers, including convolutional layers, ReLU layers, and pooling layers. The convolutional layers are responsible for mapping the features of the brain tumor images as they pass through consecutive layers. The pooling layers are used to reduce the dimensionality of the input images, fine-tuning the features for subsequent analysis, while the ReLU layers classify these features for image recognition.

The extraction rules apply conditions to the input data using "IF-THEN" logic to remove irrelevant information and implement appropriate rules. Afterward, the inference engine evaluates all the extracted data and uses the rule base for final processing. The hybrid CNN-FCM model integrates advanced machine learning methods to provide a powerful strategy for brain tumor segmentation and analysis.

3.1 Convolutional Neural Network with Fuzzy C-Mean Model

In this paper, based on a model implemented using a hybrid convolutional neural network with fuzzy cmeans, the advantage of the CNN-FCM model integrity between deep convolutional neural networks with traditional fuzzy c-means algorithm.

A. Fuzzy C-Means

The Fuzzy C-Means (FCM) algorithm is a collection of systems created by Dunn and Bezdek. It is categorized by the additional titration of Mathieu Patitucci's voxel groups (data) with magnetic resonance (MR) brain images, [16]. In addition, the clustering is specified by the PSO algorithm $(\hat{X} \rightarrow)(t+1)$, the updated position vector of the

particle (voxel or pixel) derived by the PSO algorithm serves as the centroid value, and based on this value, the number of clusters is used in the FCM algorithm, [17]. The algorithm also uses PSO allocation to determine the center of the member row and cluster duplication to limit the proposal and voxel grouping function in equation (2):

$$J_{k} = \sum_{i=j}^{N} \sum_{j=0}^{C} \partial_{i,j} || X_{i} - C_{j} ||^{2}$$
(2)

N Describes the number of incoming data points as input to the algorithm, and K shows the number of iterations to be performed.

B. Convolution Neural Network

Pattern recognition is a key feature of convolutional neural networks (CNNs), which have demonstrated exceptional performance in identifying patterns in a wide range of images. A typical CNN consists of several layers: input, convolutional, max pooling, fully connected (FC), and output layers, all arranged hierarchically. At the core of CNNs are filters of varying sizes, such as 3x3, 7x7, and 13x13, which are applied over the input data in a sliding window fashion to generate a feature map. The feature map is a structured collection of extracted features, with each point connected to the output of the previous layer via weights. As the size of the filter (or kernel) increases, the receptive field expands, incorporating more contextual information from the surrounding area of the image, [18]. To the function map in the form of neuronal activation. F_{aj} Feature map is calculated as in the equation (3):

$$F_{aj} = b_a + \sum_j K_{aj} * I_j \tag{3}$$

where b_a , $K_{a,j}$ and I_j are the bias term, convolution kernel, and input plane, respectively, whereas * it represents the convolution operation.

3.2 Implementation

The proposed CNN-FCM model was implemented using MATLAB 2020a on a PC equipped with an Intel Core i7 CPU and 16 GB of RAM, running the Windows 10 operating system. The implementation utilized the specialized MATLAB Deep Learning Toolbox and the Segmentation Learner Toolbox for training the CNN classifier. The entire training process for the CNN-FCM model took approximately two and a half days on a single NVIDIA Titan XP GPU, [18].

4 **Results and Discussion**

4.1 Results of Brain Tumor Segmentation using CNN-FCM Model

In this section, we present the results of processing MRI brain data, which includes the original MR input data, preprocessing steps, and tumor area segmentation using a convolutional neural network combined with the fuzzy c-means model. Figure 4 and Figure 5 demonstrate that the CNN-FCM model can effectively segment tumor areas from various MRI brain images. One of the key advantages of this approach is its ability to process MRI data without technical issues while achieving strong tumor area segmentation performance. The results illustrated in Figure 4 and Figure 5 indicate that the proposed method enhances the segmentation accuracy across all regions in the MRI images. Consequently, the predicted segmentation masks for the tumor boundaries align closely with the ground truth. This improvement is attributed to the CNN-FCM model's focus on normalized pixel intensity rather than local dependencies, allowing for more global information processing.

• Figure 4:

- (a) Original BRATS 2017 FLAIR images
- (b) Preprocessing results of BRATS 2017 FLAIR images
- (c) Tumor-marked area results of BRATS 2017 FLAIR images
- (d) Tumor-segmented zone results of BRATS 2017 FLAIR images
- Figure 5:
- (a) Original BRATS 2017 T1-T2 weighted images
- (b) Preprocessing results of T1-T2 weighted images
- (c) Tumor-marked area results of T1-T2 weighted images
- (d) Tumor-segmented area results of T1-T2 weighted images



(a) (b) (c) (d) Fig. 4: Segmentation results of CNN-FCM model using slices of each BRATS2017 FLAIR MRI modality



(a) (b) (c) (d) Fig. 5: Segmentation results of CNN-FCM model using slices of each BRATS2017 T1-T2 weight MRI modality

4.2 The Performance of the CNN-FCM Model

In this aspect, In this section, we present the experimental results along with a discussion of the findings. The implementation of the CNN-FCM model followed a series of steps: dataset collection, data augmentation, data splitting, model building, pre-training, and actual training. Each step is detailed in the following paragraphs, providing comprehensive information based on our implementation. The BRATS 2017 dataset comprises 3,000 MRI images, including FLAIR and T1-CE scans, representing three different types of brain tumors: gliomas, meningiomas, and pituitary tumors, along with images of healthy brain tissue. The dataset was categorized into three segments: 70% allocated for training, 15% designated for testing, and 15% reserved for validation. The model implementation is divided into two main stages: (1) model training and (2) model application. During the data partitioning process, we face the challenge of data imbalance, which occurs due to the limited diversity within the dataset. To mitigate this problem, we use data augmentation techniques such as image rotation and image flipping. Therefore, the BRATS 2017 dataset is divided into two subsets: a training set containing 80% of the total images (2400 images), and a test set containing 20% (600 images). These metrics are consistent with the dataset specifications. Furthermore, a CNN-FCM model is comprehensively used for tumor segmentation. The model is built using Google Colab and includes convolutional and pooling layers and the fuzzy cmeans method. The training process is divided into two stages: (1) pre-training and (2) actual training. The pre-training stage involves setting the fuzzy cmeans parameters in the model, including IF, THEN, AND rules, and the convolutional neural network. After the pre-training is completed, we enter the actual training phase, where the BRATS 2017 image dataset is processed for 120 epochs. Each epoch represents an iteration in which the training images are fed to the convolutional neural network, thus improving its ability to learn from the data. The performance of the hybrid CNN-FCM model was evaluated using five metrics: accuracy, sensitivity, specificity, overall DICE, and recall. The analysis shows that this new hybrid model has strong performance and achieves remarkable results, as shown in Figure 6(a), 6(b), 6(c), 6(d), and 6(e).





Fig. 6: Performance metrics of CNN-FCM model on BRATS 2017 dataset; (a) graph of accuracy metric; (b) graph of sensitivity metric; (c) graph of specificity metric; (d) graph of overall dice metric; (e) graph of recall metric

4.3 Evaluation Performance of CNN-FCM Model

The assessment of the CNN-FCM model includes a comparison with contemporary leading models, such as CNN-NADE, CNN-ResNet50, CNN-TL, CNN-SR-FCM, and CNN-GAN hybrid models. Each of these models employs the same BRATS 2017 dataset and is evaluated using consistent metrics, which encompass accuracy, sensitivity, specificity, overall dice, and recall.

Table 1. Comparison of the CNN-FCM model with
recent models using different metrics based on the
BRATS 2017 dataset

DIAI 5 2017 dataset						
Model	Accurac y%	Sensitivit y%	Specificit y%	Over all Dice %	Recall %	
CNN- NADE	93.2	85.7	91.3	92.53	91.6	
CNN- Resent 50	91.3	93.1	90.6	92.8	88.8	
CNN- TL	87.6	92.7	93.2	93.6	92.4	
CNN- SR- FCM	91.5	89.7	92.3	93.1	89.8	
CNN- GAN	90.6	88.4	91.3	89.5	90.4	
CNN- FCM	96.5	95.21	94.8	93.7	94.1	

To compare and analyze the output of the CNN-FCM model, this study evaluates the performance of

various recent convolutional neural network (CNN) methods for brain tumor segmentation using the BRATS 2017 database. Table 1 presents the performance metrics of these CNN models alongside the hybrid CNN-FCM model, with all models assessed using the same dataset. The experimental results indicate that the neural autoregressive distribution estimation with convolutional neural network (CNN-NADE) achieves accuracy. sensitivity, specificity, overall dice, and recall values of 93.2%, 85.7%, 91.3%, 92.53%, and 91.6%, respectively. The CNN-ResNet50 model vields scores of 91.3%, 93.1%, 90.6%, 92.8%, and 88.8%. The CNN with transfer learning (CNN-TL) records values of 87.6%, 92.7%, 93.2%, 93.6%, and 92.4%. The fuzzy C-means with super-resolution and convolutional neural network with extreme learning machine (CNN-SR-FCM) achieves results of 91.5%, 89.7%, 92.3%, 93.2%, and 93.6%. The CNN with generative adversarial networks (CNN-GAN) produces scores of 90.6%, 88.4%, 91.3%, 89.5%, and 90.4%. In contrast, the CNN-FCM model demonstrates superior performance, with metrics of 96.5%, 95.21%, 94.8%, 93.7%, and 94.1%. The comparative analysis reveals that the proposed CNN-FCM model outperforms other recent hybrid CNN architectures in terms of accuracy, sensitivity, specificity, overall dice, and recall. This evaluation concludes that the hybrid CNN-FCM model represents a robust approach for accurate glioma tumor segmentation, leveraging automatic deep CNN techniques combined with the fuzzy c-means principle to effectively utilize complementary volumetric contextual information, resulting in enhanced performance.

4.4 Ablation Study of CNN-FCM Model

To evaluate the effectiveness of the key components in our CNN-FCM model, we conducted ablation studies and presented the quantitative results in Figure 7. Panel (a) illustrates the ROC curve for the BRATS 2017 dataset, where the CNN-FCM model achieved an impressive ROC value of 0.97. This performance surpasses that of the CNN-NADE model, which reached 0.93, followed by the CNN-ResNet50 model at 0.87, the CNN-TL model at 0.83, the CNN-SR-FCM model at 0.77, and the CNN-GAN model at 0.66. Panel (b) displays the PR curves for different models on the BRATS 2017 dataset. A more convex PR curve towards the upper right indicates a better segmentation effect, which visually confirms that the CNN-FCM model outperforms the recent CNN-NADE, CNN-ResNet50, CNN-TL, CNN-SR-FCM, and CNN-GAN models across the entire BRATS 2017 dataset. This ablation study, utilizing criteria such as ROC and PR values on a unified BRATS 2017 dataset, demonstrates that the proposed model significantly outperforms previous hybrid CNN models.



Fig. 7: Ablation study of CNN-FCM model on whole BRATS2017 dataset; (a) comparison of ROC curves of different models; (b) comparison of PR curves of different models

5 Conclusion

In this study, we propose a novel model called the CNN-FCM, which integrates a convolutional neural network (CNN) with the fuzzy c-means (FCM) algorithm to address issues of inaccurate segmentation rates and varying input image shapes.

By combining the advanced capabilities of CNNs with the traditional FCM approach, our model demonstrates superior performance in brain tumor segmentation. We evaluated the CNN-FCM model using the BRATS 2017 dataset, and the experimental results reveal impressive segmentation accuracy. Compared to recent hybrid CNN models such as CNN-NADE, CNN-ResNet50, CNN-TL, CNN-SR-FCM, and CNN-GAN, the CNN-FCM model achieved higher overall performance across metrics including accuracy, sensitivity, specificity, overall dice, and recall. Ultimately, this innovative technique not only provides tumor segment masks that closely align with expert delineations for all grades of glioma but also facilitates faster diagnosis and treatment planning for patients.

Declaration of Generative AI and AI-assisted Technologies in the Writing Process

During the preparation of this work the authors used QuillBot AI / Grammar Checker in order to revised grammars problems in paper. After using this tool/service, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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Isselmou Abd El Kader: Corresponding Author, Wrote metholdoy and implementation of experiments Jingfei He: Wrote the Abstract and conclusion Guizhi Xu: Technical help Danil Vodolazskii: Wrote the literature survey Shivansh Singh: Wrote the Introduction Rujun Li: Technical Help Yunge Duan: Language revision

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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APPENDIX



Fig. 3: Architecture of proposed CNN-FCM model