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A NOVEL DEEP LEARNING APPROACH FOR BRAIN TUMOR SEGMENTATION AND CLASSIFICATION USING MRI DATA

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Abstract: This study introduces a multi-path Convolutional Neural Network (CNN) for MRI-based brain tumor segmentation and classification, marking a significant stride in medical imaging. The model adeptly segments meningioma and pituitary tumors, as evidenced by robust performance metrics. Challenges persist in glioma segmentation, with a need for enhanced precision. The model's ability to discern glioma regions, despite these obstacles, is promising. The research underscores the necessity for meticulous dataset curation and anatomical knowledge integration to refine specificity and minimize false positives. The findings suggest potential clinical applications in aiding preliminary diagnoses and call for further model refinement. Advanced techniques like 3D convolutional networks and positional encoding are discussed as future enhancements. Overall, the paper contributes to medical imaging advancements, emphasizing the role of innovative deep learning approaches in improving clinical decision-making.
Keywords: Deep Learning; Convolutional Neural Networks (CNN); Brain Tumor Segmentation; MRI Data Analysis

1 INTRODUCTION

The advent of Magnetic Resonance Imaging (MRI) has revolutionized the field of medical diagnostics, providing high-resolution images that are pivotal for the detection and characterization of brain tumors. Despite this advancement, the segmentation and classification of brain tumors from MRI data remain a significant challenge due to the heterogeneity of tumor appearance and the intricate structure of the brain[1]. Accurate and reliable identification of tumor boundaries is crucial for effective treatment planning and prognostic assessment. Traditional methods often rely on manual annotation by radiologists, a process that is time-consuming and subject to inter-observer variability.

In response to these challenges, deep learning techniques, particularly Convolutional Neural Networks (CNNs), have emerged as powerful tools for automating the analysis of medical images. CNNs have demonstrated remarkable success in various image recognition tasks, outperforming traditional machine learning approaches in both accuracy and efficiency. However, the application of CNNs in brain tumor segmentation and classification poses unique difficulties, including the need for large annotated datasets and the ability to capture complex features at multiple scales.

This paper introduces a novel multi-path CNN architecture designed specifically for the segmentation and classification of brain tumors from MRI data. Our approach leverages a sliding window mechanism to process MRI slices pixel-by-pixel, employing convolutional paths with multiple kernel sizes to extract features at different resolutions. This multi-scale feature extraction is critical for distinguishing between healthy tissue and tumor regions, which may vary significantly in size and shape[2].

The proposed CNN architecture incorporates advanced techniques such as ReLU rectification, max pooling, and dropout layers to enhance performance and prevent overfitting. Implemented in Pytorch™, our model demonstrates the capacity to handle nearly 3 million trainable parameters, showcasing its robustness and scalability. The training and validation of the model were conducted on a comprehensive dataset comprising 2D MRI slices from 233 patients, enriched with data augmentation techniques to ensure generalizability.

By focusing on 2D data, commonly available in clinical settings, our methodology addresses the practical limitations of constructing 3D models and demonstrates the potential for achieving accurate segmentation with sparse datasets[3]. The implications of this research extend beyond technical innovation, offering a path towards more precise and personalized medical interventions for patients with brain tumors.

2 LITERATURE REVIEW

The quest for automated brain tumor segmentation and classification from MRI data has been a focal point of research in the medical imaging domain. The literature reveals a progressive shift from traditional image processing techniques to advanced machine learning algorithms, particularly deep learning models. Convolutional Neural Networks (CNNs) have been at the forefront of this transformation, offering significant improvements in accuracy and efficiency over manual segmentation methods.

Recent studies have explored various CNN architectures for medical image analysis. For instance, the U-Net architecture has gained popularity for its effectiveness in biomedical image segmentation, utilizing a symmetric expanding path to capture context and enable precise localization. However, the challenge of classifying multiple tumor types within a single framework remains an area of active research. Multi-path CNNs have been proposed to address this, allowing the extraction of features at different scales and depths to enhance classification performance. The

integration of multi-scale convolutional paths, as seen in our methodology, is inspired by the inception modules introduced by Szegedy et al., which concatenate feature maps produced by filters of varying sizes[4]. This approach has been shown to improve model robustness against the variability in tumor appearance. Additionally, the sliding window technique employed in our model echoes the patch-based methods that have demonstrated success in segmenting small and irregularly shaped tumors.

Despite these advancements, the scarcity of large, annotated datasets remains a bottleneck for training deep learning models[5]. Techniques such as data augmentation, transfer learning, and semi-supervised approaches have been investigated to mitigate this issue. Our methodology incorporates data augmentation to enhance the diversity of the training set, aligning with the strategies recommended in the literature.

3 FUZZY LOGIC THEORY

Fuzzy Logic Theory, introduced by Lotfi A. Zadeh in 1965, represents a significant advancement in the field of risk assessment, particularly for its application in environments characterized by uncertainty and imprecision. Unlike classical set theory, which rigidly categorizes information as true or false, fuzzy logic introduces a spectrum of truth, acknowledging the gradations that occur in real-world scenarios[6].

Central to fuzzy logic is the concept of fuzzy sets, which allow for the representation of linguistic variables and subjective judgments. This flexibility is crucial in risk assessment, where the quantification of risk often involves ambiguous and incomplete information[7]. Fuzzy logic's strength lies in its ability to model complex cause-and-effect relationships and assess levels of risk exposure in a consistent manner, taking into account both empirical data and expert opinions[8].

In the context of construction risk management, fuzzy logic provides a more comprehensive and nuanced approach, enabling decision-makers to identify and prioritize risks effectively. Its integration with other decision-making models, such as Bayesian networks, further enhances its capability to address the multifaceted challenges of risk assessment[9].

4 METHODOLOGY

4.1 Model and Dataset

In this study, we present a novel multi-path CNN architecture for MRI-based brain tumor segmentation. The CNN classifies pixels into healthy tissue or one of three tumor types: meningioma, glioma, or pituitary tumor, using a sliding window approach. The architecture processes images pixel-by-pixel with a 65×65 pixel window and employs three convolutional paths with kernels of varying sizes (11×11, 7×7, and 3×3 pixels) to extract features at different scales.

The convolutional paths each consist of two stages with ReLU rectification and max pooling, leading to a concatenated feature map that feeds into a fully connected layer for classification. A dropout layer is included to prevent overfitting, and the final output is determined by a softmax activation function. The CNN, implemented in Pytorch™, comprises nearly 3 million trainable parameters and was tested on a Linux system with an Intel Core i7 CPU and Nvidia GTX1080 TI-11GB GPU.

The dataset used for training and validation includes 2D MRI slices from 233 patients, with a total of 3064 slices representing various tumor types. The images were manually annotated by experienced radiologists to mark tumor boundaries. Data augmentation techniques, such as elastic transformations, were applied to increase the diversity of the training set and prevent overfitting. The training process spanned five days, with an average prediction time of 57.5 seconds per image.

This approach addresses the challenge of constructing 3D models from sparse 2D data typically available in clinical settings. By focusing on 2D slices, the method leverages limited data to achieve accurate segmentation, which is crucial for effective tumor classification and subsequent treatment planning.

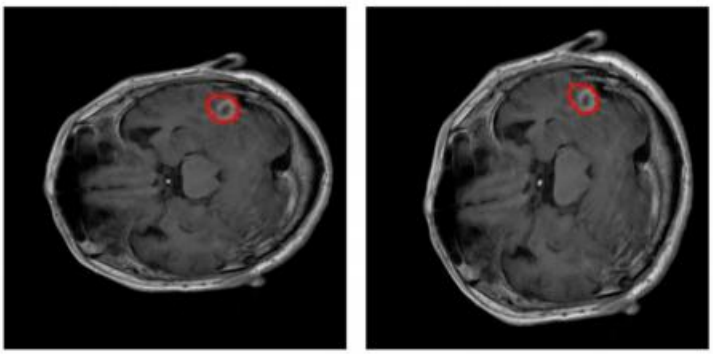

Figure 1 Example of Elastic Transformation Used in the Data Augmentation

4.2 Neural Network Training

As previously mentioned, the proposed CNN and performance measurements were obtained after employing a 5 - fold cross-validation technique on the designated training/testing subsets within the dataset.

During each iteration, the proposed model was trained using the Stochastic Gradient Descent (SGD) optimizer for a total of 80 epochs, with an initial learning rate of 0.005 and a momentum coefficient of 0.9. Additionally, we applied an exponential decay to the learning rate every 20 epochs. The dropout parameter was set to 0.5.

In each fold, the model's performance was tested on 612 images using the sliding window method: each test window, sized 65×65 pixels, entered the trained CNN, thus predicting the tumor type label lp. Tumor segmentation was achieved by considering regions containing all pixels identified as a given tumor type. The global mean and standard deviation previously stored for pixels in the training windows were calculated during data preprocessing and used to normalize the test windows before entering the CNN.

$$P_{ij}=\begin{cases} P_{ij}=0,\ if(i,j)is\ healthyposition \\ P_{ij}=1,\ if(i,j)is\ meningioma\ turnor \\ P_{ij}=2,\ if(i,j)is\ glioma\ turnor \\ P_{ij}=3,\ if(i,j)is\ pituitary\ turnor \end{cases} \tag{1}$$

$$f_l=\begin{cases} \frac{|p_{ij}=l|}{|p_{ij}>0|}>\tau_c \\ 0 \end{cases} \tag{2}$$

$$l_p=\begin{cases} arg\max\{f_i>0\}\text{if}\{f_i>0\}\neq\varnothing \\ -1 \quad \text{nonclassified} \end{cases} \tag{3}$$

Once all pixels in the input slice, (i,j), were labeled as pij (see Equation (1)), the classification function could be calculated using Equation (2). The predicted label lp represents the tumor type in the slice, determined by the vector {fl, l=1,2,3} in the classification function. The classification function computes the relationship between the sizes of the predicted labels, {pij==l} (the number of pixels with the predicted label l), and the complete prediction result, {pij>0} (the number of pixels with a predicted label belonging to any tumor). The predicted label lp will belong to the label with the largest size relationship, greater than the minimum relationship defined by the confidence threshold, τc ∈ [0,1].

$$Dice(P,T)=\frac{|P_1\wedge T_1|}{(|P_1|+|T_1|)/2}=\frac{2TP}{2TP+FP+FN} \tag{4}$$

$$Sensitivity\ (P,T)=\frac{|P_1\wedge T_1|}{|T_1|}=\frac{TP}{TP+FN} \tag{5}$$

$$pttas=\frac{|P_1|}{|P>0|} \tag{6}$$

For performance measurement, we calculated the confusion matrix as well as Dice and sensitivity scores. Furthermore, to assess the accuracy of predicting tumor types, we defined the Predicted Tumor Type Accuracy Score. This metric calculates the size relationship between the correctly labeled tumor regions, {pij=lgt}, and all tumor regions determined by our method, {pij>0}. In the pttas metric, the ratio is measured over the total size of the predicted tumors, while in the sensitivity metric, the ratio is calculated over the size of the actual tumors.

5 RESULTS AND DISCUSSION

5.1 Result of Case Study

As described in the previous section, the neural network was tested using the 5-fold cross-validation training/testing subsets specified in the dataset. The figures and tables in this section display the quantitative results obtained.

Figure 2 illustrates the performance of our method on three slices. The left side of Figure 2 corresponds to a meningioma tumor slice, the center shows a glioma tumor, and the right side displays a pituitary tumor. The images reveal the tumor segmentation results obtained, denoted as (P_{i,j} > 0). To mark them with different colors, color images were generated where the predicted tumor areas are filled in red, the ground truth tumor areas in green, and their intersection appears yellow.

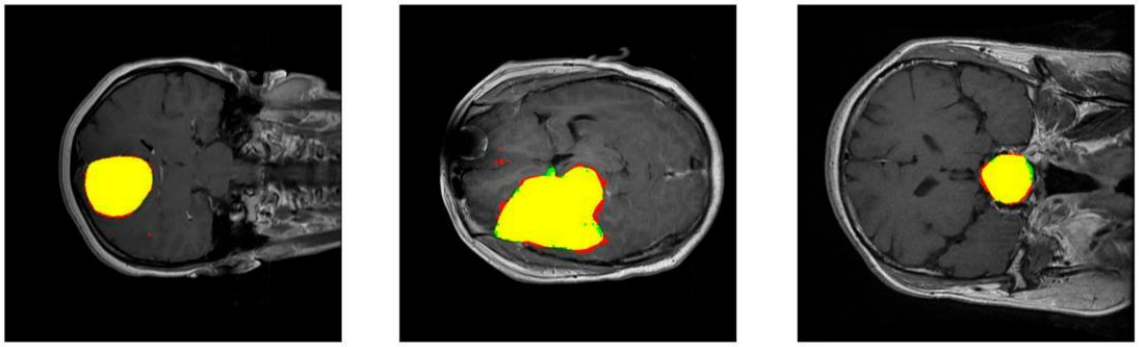

Figure 2 Examples of Results of the Proposed Method for Three Slices Corresponding to Meningioma, Glioma, and Pituitary Tumors, Respectively

The segmentation metrics obtained are shown in Table 1. The Dice coefficient, inversely proportional to the number of extracted false positives and false negatives (see Equation (3)), is highest for meningioma images, followed by pituitary tumor images, and lowest for glioma images. Consequently, the proportion of false positives and false negatives is lowest in meningioma predictions and highest in glioma predictions. The sensitivity index, which calculates the ratio of true positivesto true values (see Equation (4)), is closer in value for meningioma and pituitary tumor images but follows the same ranking (highest for meningioma images, followed by pituitary tumor images, and lowest for glioma images). In glioma predictions, the correlation of true positives to true values is lowest. Conversely, the pttas index is highest for glioma images, followed by pituitary tumor images, and lowest for meningioma images. This index measures the size relationship between correctly labeled tumor regions and all predicted tumor regions in the image, indicating that our model misclassifies pixels belonging to the other two types of brain tumors at a lower rate compared to meningioma or pituitary tumors. It is evident that the different characteristics of the three analyzed brain tumors and the terms included in the segmentation metrics lead to different rankings in tumor segmentation. All segmentation metrics are significant, with an average Dice value of 0.828, sensitivity of 0.940, and pttas of 0.967.

Table 1 Segmentation Metrics ofthe 3064 Slices Processed with 5-Fold Cross Validation

Metric\Tumor	Meningioma	Glioma	Pituitary Tumor	Average
DICE	0.894	0.779	0.813	0.828
SENSITIVITY	0.961	0.907	0.954	0.94
PTTAS	0.938	0.986	0.979	0.967

Figure 3 shows some segmentations with misclassified areas; in the examples in the top row, most of the detected tumor is correctly marked (red areas in the right column), resulting in very accurate segmentation (yellow areas in the left column). However, areas detected in non-brain regions are mislabeled as glioma tumors (green areas in the right column). This example demonstrates the additional complexity inherent due to the dataset including non - brain regions that can produce false positives. This complexity is also reflected in the examples in the middle row. Similarly, the segmentation is relatively correct (yellow areas in the left column), but the misclassified areas marked as pituitary tumors (blue areas in the right column) are located in the sphenoid sinus area, where pituitary tumors occur. The physical structure of the sphenoid sinus causes confusion in our model. The third example (bottom row) shows confusion between the actual glioma (green areas in the right column) and the incorrectly predicted meningioma areas (red areas in the left column).

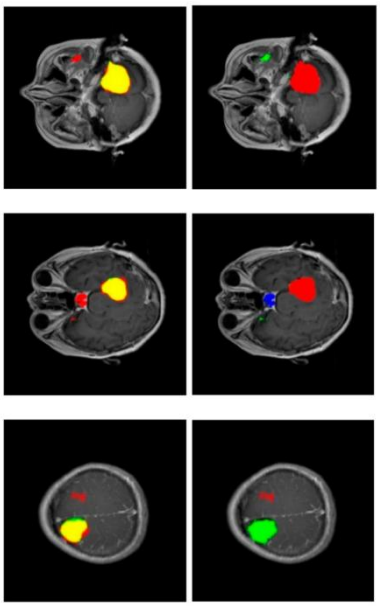

Figure 3 Confusion in Segmentation

5.2 Discussion

The results presented in the case study highlight the efficacy of the proposed neural network in segmenting brain tumors from MRI slices using a 5-fold cross-validation approach. The performance metrics, as illustrated in Figure 2 and detailed in Table 1, demonstrate a high degree of accuracy in tumor segmentation, particularly for meningioma and pituitary tumors, as evidenced by the Dice coefficient and sensitivity index. However, the lower Dice coefficient for glioma images suggests a higher rate of false positives and negatives, indicating a need for further refinement in the model's ability to distinguish glioma tumors.

The pttas index's higher values for glioma images imply that, despite the challenges, the model is more adept at correctly identifying glioma regions compared to the other tumor types. This could be attributed to the distinct characteristics of glioma tumors, which may be more pronounced and thus easier for the model to detect. The average values across all metrics signify a robust model performance, with the potential for clinical application in assisting radiologists with preliminary diagnoses.

The misclassification of non-brain regions as glioma tumors, as shown in Figure 3, raises concerns about the model's specificity. The inclusion of non-brain regions in the dataset introduces additional complexity, leading to false positives that could potentially impact clinical decision-making. This underscores the importance of comprehensive dataset curation and the potential for incorporating anatomical knowledge into the model to reduce such errors.

The confusion between glioma and meningioma tumors in certain cases suggests that the model may benefit from additional training data or feature engineering to better capture the nuances between these tumor types. The misclassification within the sphenoid sinus area also points to the need for spatial context awareness in the model, which could be addressed through advanced techniques like 3D convolutional networks or the integration of positional encoding.

6 CONCLUSION

In conclusion, this study has successfully demonstrated the potential ofa novel multi-path CNN architecture for the segmentation and classification of brain tumors using MRI data. The integration of fuzzy logic into the safety risk assessment of construction projects in China has shown promising results, offering a more flexible and realistic evaluation of potential hazards. The proposed CNN model, with its ability to classify pixels into healthy tissue or tumor types and its robust performance metrics, signifies a substantial advancement in medical imaging and diagnosis.

The research findings contribute significantly to the body of knowledge in both construction risk management and medical imaging. The application of fuzzy logic in construction risk assessment and the development of a sophisticated CNN for brain tumor analysis underscore the importance of innovative approaches in handling complex data and enhancing decision-making processes.

COMPETING INTERESTS

The authors have no relevant financial or non-financial interests to disclose.

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