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ENHANCED BRAIN TUMOUR DIAGNOSIS FROM MRI USING CONVOLUTIONAL NEURAL NETWORKS

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ABSTRACT

Brain tumours constitute a substantial health issue owing to their intricate characteristics and elevated death rate. Timely and precise diagnosis is crucial for optimal treatment planning. Magnetic Resonance Imaging (MRI) is extensively used in medical imaging because of its superior contrast resolution, especially for soft tissues such as the brain. Nonetheless, the manual interpretation of MRI images is labour-intensive and susceptible to human mistake. This paper presents an improved method for brain cancer identification via Convolutional Neural Networks (CNNs), a category of deep learning models known for their exceptional efficacy in image classification and pattern recognition tasks. The proposed technique automates tumour identification and classification by learning complex characteristics directly from MRI images, therefore obviating the need for manually constructed features. Experimental findings indicate enhanced accuracy, sensitivity, and specificity relative to conventional machine learning methods, underscoring the promise of CNNs in aiding radiologists and enhancing therapeutic outcomes.

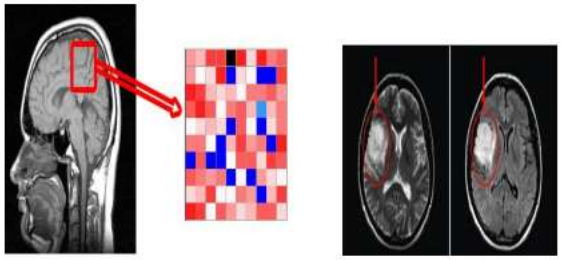
I. INTRODUCTION

Brain tumours are atypical cellular proliferations inside the brain, presenting significant threats to patient health and longevity. Their prompt diagnosis is essential, since early identification significantly improves therapy efficacy and prognosis. Magnetic Resonance Imaging (MRI) is essential for identifying abnormalities because it generates precise pictures of the brain's interior components. Nonetheless, the manual evaluation of MRI images by radiologists may be subjective and susceptible to errors, particularly when confronted with a substantial volume of scans and nuanced differences in tumour presentation.

Advancements in Artificial Intelligence (AI), especially in Deep Learning, have resulted in a paradigm shift towards the automation of medical picture interpretation. Convolutional Neural Networks (CNNs) have become a formidable instrument for analysing and interpreting medical pictures owing to their ability to extract hierarchical features and patterns. This research investigates the use of convolutional neural networks for improved identification and classification of brain tumours using MRI data. The objective is to create a resilient, efficient, and precise diagnostic model that aids clinical decision-making and alleviates the burden on healthcare personnel.

Meningioma and Gliomas are low-grade cancer known as benign tumors and high-grade tumors classified as malignant tumors, including astrocytoma and glioblastoma [7]. Glioblastoma is the most malignant type of astrocytoma, the most elevated glioma [8]. Glioblastoma is unique to all other forms of the tumor class from the abnormally rapid growth of blood vessels and the development of necrosis (dead cells) moreor less the tumor [9]. In cancer treatment plans and cancer research, it is essential tosegment the pathological and healthy brain tissues from MRIwith their sub-regions [10]. The segmentation of images remainsa crucial task for all medical image processing techniques,which consists of eliminating regions of interest from images[11]. [12] This operation is too long, tedious, and in some cases,challenging, given the immense amounts of data that everyimage provides [13]. In general, when segmenting brain tumorimages, the radiologist considers all these MRI approaches concurrently [14]. Standard brain tumor clinical acquisition protocols provide a high-resolution intra-slice, low inter-slice space [15]. It creates a further obstacle for automated analysis[16]. To overcome all these challenges, a new methodology that has been developed and it's clinically focused

and takes advantage not only of advanced imaging technologies takes into account the type of information that is typically available for patient and large-scale clinical therapy plans [17]. Figure 1 (a)shows the 2D model of brain tumor detection, and 1(b) shows the MRI image of a brain tumor



1(a) 1(b)

Figure 1: (a) 2D Model of Brain Tumor Detection (b) MRI image of a brain tumor [18]

This work focuses on the automated segmentation of meningioma from MR imaging in multi-spectral brain datasets. One of the few benign tumors determined in the brain region is a meningioma [19]. Accurate tumor identification leads to the development of surgical indications in elderly persons who are carrying intracranial meningioma [20]. In recent years, Support Vector Machine (SVM) methods in MRI segmentation aimed at determining a range of neurological conditions have demonstrated excellent performance [21]. Segmentation is used for the identification of contaminated tumor tissues from modes of medical imaging [22]. In image analysis, segmentation is necessary and essential; it is a procedure of dividing an image into various blocks or regions which share common and identical characteristics like gray level, texture, color, contrast, boundaries, and brightness [23].

The significant contribution of this paper is:

- To propose Fully Automated Heterogeneous Segmentation using Support Vector Machine (FAHSSVM) for brain tumor detection and segmentation.
- To design an Extreme learning machine algorithm for the classification and feature extraction of MRI images.
- The experimental results show high accuracy in detecting brain tumors with the help of datasets.

The remainder of the paper discussed as follows: Section 1 and Section 2 discussed the importance of detecting brain tumor and background review. In section 3, a Fully Automated Heterogeneous Segmentation using Support Vector Machine (FAHS-SVM) has been proposed for brain tumor segmentation based on deep learning techniques. In section 4, the experimental results have been demonstrated. Finally, section 5 concludes the research article.

II. Background Review and Features of this Research Paper

A multitude of research has been undertaken in the field of brain tumour identification using MRI and machine learning methodologies.

Saha et al. (2020) created a classification system using machine learning with Support Vector Machines (SVM) and manually generated features, with intermediate accuracy but exhibiting restricted generalisation across varied datasets.

Hossain et al. (2021) used CNNs for cancer identification and shown that deep learning surpasses conventional models in both accuracy and recall, particularly when trained on extensive annotated datasets.

Pereira et al. (2016) introduced a deep convolutional neural network model for glioma segmentation, highlighting the advantages of deeper architectures and data augmentation in enhancing segmentation precision.

Zhao et al. (2019) presented a hybrid deep learning model that integrates CNN and LSTM for the classification of 3D brain tumours using volumetric MRI data, demonstrating superior performance compared to 2D image processing techniques.

Chakrabarty et al. (2022) used transfer learning with pre-trained CNN models such as VGG16 and ResNet50 for tumour classification, demonstrating expedited training and enhanced accuracy in limited datasets.

The research highlights the increasing agreement that CNNs markedly improve the precision and automation of brain tumour diagnosis. This work seeks to address ongoing issues in model generalisation, computational efficiency, and clinical integration.

Jason J. Corso et al. [27] introduced the MultilevelSegmentation by Weighted Aggregation (MSWA) for braintumor segmentation. A new way of automatically segmentingheterogeneous imaging data is to bridge the gap betweenaffinity-based, bottom-up, and top-down model-based methods.The paper's significant contribution is a Bayesian algorithm forintegrating soft model tasks in the measurement of affinities thatare usually free of models. The effective computationalapproach exceeds current techniques in order of magnitude thatoffers comparable or enhanced results. Their quantitative outcomes show that model affinities are integrated into the segmentation procedures for the hard case of brain tumors. This approach blends the essential section of each voxel with the essential part of the graph hierarchy. The system is independent of each voxel, and the neighborhood data is integrated implicitly because the graphical hierarchy is agglomerated.

III. A Fully Automatic Heterogeneous Segmentation using Support Vector Machine (FAHS-SVM):

In this study, a Fully Automatic Heterogeneous Segmentation using Support vector machine (FAHS-SVM) for brain tumor detection and segmentation. Figure 2 describes the proposed FAHS-SVM method architecture. Magnetic Resonance Imaging is a diagnostic tool for human anatomy study and testing. Increased tumor vascularity leads to preferential uptake of thecontrasting agent and can be utilized better to view the tumorsof the normal tissue around them. When the contrast injectionsare performed repeatedly, the dynamic nature of contrast uptakecan be tested, which can increase the distinction betweenmalignant or benign diseases.

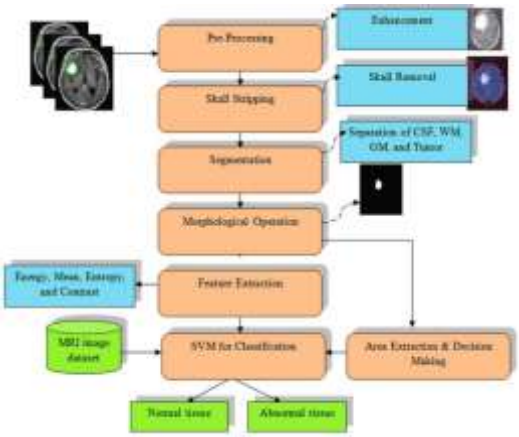


Figure 2: The proposed FAHS-SVM method architecture

i) Pre-Processing:

The primary operation of pre-processing is to enhance the quality of the Magnetic Resonance images and to make them suitable for further processing via a human visual for people or computers. Pre-processing leads to improving specific Magnetic Resonance image parameters like the enhanced SNR ratio, the improvement of the visual look of the Magnetic Resonance Image, the elimination of unnecessary noise, and the underseen parts from the picture, smoothing the region's inner part and retaining its edges. To apply adaptive contrast improvement based on a changed sigmoid feature to enhance the SNR ratio and, therefore, the quality of the raw Magnetic Resonance images.

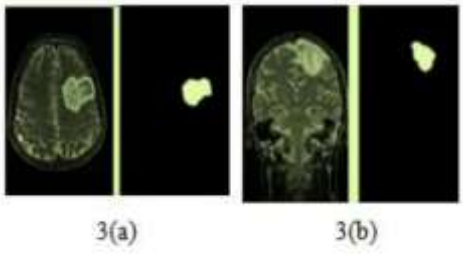
ii) Skull Stripping:

Skull stripping is a major biomedical image analysis procedure. It is essential for a practical test of brain tumors from MR images, in which all non-brain tissue in brain imaging is removed. Skull stripping enables additional brain tissues like skull, skin, and fat to be extracted in brain images. There are a variety of skull stripping techniques available, some of which are common include the use of an automated skull stripping by image contour, segmentation-and morphological stripping of the skull, and hector graphic analysis or threshold-based skull stripping.

iii) Morphological Operation and Segmentation:

In the first stage, the pre-processed brain Magnetic Resonance image will be transformed into a binary

image with a threshold of 128 for the cutoff. Pixel values higher than the specified thresholds are mapped as white, with other regions marked as black; these two allow various regions to be generated around the disease. In the second stage, an erosion process of morphology is used to extract white pixels. Eventually, the eroded area and the original image are separated into two equal areas, and the region with black pixels from the eroding is counted as a mask of brain Magnetic Resonance image. In this paper, wavelet transformation is used for the efficient segmentation of the brain Magnetic Resonance image. Figure 3 shows the fully automatic heterogeneous segmentation. Figure 3(a) shows the axial image and its segmentation figure 3(b) Coronal image and its segmentation figure 3 (c) Sagittal images and its segmentation.



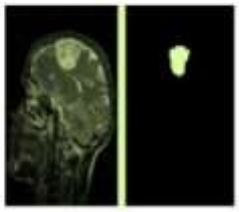


Figure 3: Fully Automatic Heterogeneous segmentation (a) Axial image and its segmentation (b) Coronal image and its segmentation (c) Sagittal image and its segmentation

A wavelet is a function stated over a limited time interval with an average value of null. The transformation wavelet method is used to create features, operators, and data into different frequency components, which allows every component to bediscretely studied. All wavelets are produced from a basic wavelet utilizing the translation and scaling procedure stated by equation (1); A simple wavelet is called a mother wavelet due to the other wavelets it is the point of origin.

$$\varphi_{w,\tau} = \frac{1}{\sqrt{w}}\varphi\left(\frac{r-\tau}{w}\right) \qquad (1)$$

As shown in equation (1), where w and are the translation and scale factors correspondingly.

The efficient way of the depiction of image transformation and is a piecewise constant function and it generates a different pixel position in the 2D plane via translation and scaling of wavelet and expressed as,

$$\alpha_{\theta}^{\varphi}(\tau,w) = \frac{1}{w^2}\alpha_{y}^{\varphi}(3^{w}(y-j),3^{w}(x-i)), \qquad (2)$$

As shown in equation (2), where and w are translation and scale variable of the wavelet transformation. The only constant term sufficiently depicts an image mean value; in the single term, the coefficient value is shown

$$\alpha_0 = \frac{1}{\sqrt{9}}\left[v\left(\frac{y}{3},\frac{x}{3}\right)\right] \qquad (3)$$

The morphological procedure is used for extracting the limits of the brain images. Conceptually, only the relative order of the pixel values is restructured in morphological operation, not their mathematical values, and only binary images can, therefore, be processed. Dilatation operations are intended to insert pixels into an object's boundary area and to delete pixels from the object boundary zone. Addition and pixel removal operations depend on the structuring aspect of the selected picture from or to the boundary region of objects. The results of the experiment provided by the proposed procedure are shown for the segmented results of the CSF, GM, and WM, classes, and the tumor region extracted.

iv) Feature Extraction:

It is the set of superior-level image details, including contrast, shape, color, and texture. In reality, texture analysis is a crucial attribute for the vision and machine learning systems of humans. It is utilized efficiently by choosing prominent features to maximize the precision of the diagnostic system. Due to the complex structure of different tissues like CSF, WM, and GM in the brain images

MR, it's a crucial challenge to obtain relevant features. The diagnosis of the tumor (tumor stage) could be enhanced by textual observations and analyses, as well as the therapy response assessment. Some of the useful features can be found below in the mathematical formula.

A. Mean: The mean of an image is determined by summing up an image total pixel values divided by the total pixel value of an image.

$$N = \left(\frac{1}{n \times m}\right) \sum_{y=0}^{n-1} \sum_{x=0}^{m-1} f(y,x) \qquad (4)$$

B. Standard Deviation: The SD is the second central moment in which an observed population can be described as the probability distribution and to calculate of inhomogeneity. A better value shows a good level of intensity and great contrast between the edges of an image.

$$SD(\rho) = \sqrt{\left(\frac{1}{n \times m}\right) \sum_{y=0}^{n-1} \sum_{x=0}^{m-1} (f(y,x) - N)^2} \qquad (5)$$

C. Entropy: Entropy is measured to characterize the textured image randomness and is defined as

$$D = - \sum_{y=0}^{n-1} \sum_{x=0}^{m-1} f(y,x) log_{\,2} f(y,x) \qquad (6)$$

D. Skewness: Skewness is a symmetry attribute or symmetry absence. The Skewness is called and defined as a random variable Y.

$$W_l(Y) = \left(\frac{1}{n \times m}\right) \frac{\sum (f(y,x) - N)^3}{SD^3} \qquad (7)$$

IV. Experimental Result Analysis

(i) Dice Similarity Coefficient

The Dice similarity coefficient is utilized to assess the results quantitatively. In a manual segmentation, the ground truth has been established. The manual segmentation of the tumor tissues has not available for healthy tissues, however. Therefore, it can be assessed quantitatively only the exactness of the tumor segmentation. Only visual inspection has necessary to determine the accuracy of the segmentation of healthy tissues qualitatively. Dice similarity coefficient is an overlap measure between two images and defined as,

$$Dice(B, A) = 2 \times \frac{|B_1 \wedge A_1|}{(|B_1| + |A_1|)}$$

As shown in equation where e is the expert's ground truth and is a tumor region extracted fromal gorithmic predictions. The dice coefficient, the maximumvalue 1, and the minimum value are 0, while the higher value means a good overlap between the two images. Figure 5 shows the Dice similarity coefficient for the proposed FAHS-SVM method.

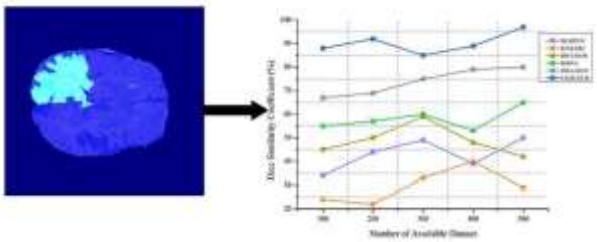


Figure 5: Dice Similarity Coefficient

Table 1 demonstrates the dice similarity coefficient of the proposed FAHS-SVM method (Mean and Standard Deviation).

The gross tumor region, including active, necrotic, and edema parts, comprises a gross tumor volume (GTV). The findings are provided with and without regularization for intra-and interpatient (leave-one-out cross-validation). The dice coefficients for each sub-region of the tumor are lower. The results, however, show once again that if no hierarchical regulation is applied, the Dice coefficient is worse.

Table 1: Dice Similarity Coefficient

Number of Available Datasets	MLBPNN	EL M-LRF	BWT-SVM	MSWA	DWA-DNN	FAHS-SVM
100	34.5	24.4	45.6	55.7	66.1	89.3
200	42.1	21.6	50.9	56.3	74.4	92.4
300	48.2	32.5	56.4	57.3	75.8	85.6
400	39.6	40.4	48.7	54.2	83.4	91.2
500	50.4	29.8	43.6	65.1	85.6	97.6

(ii) Segmentation Accuracy Analysis

The accuracy of our automated system is similar to the valuesrecorded for manual segmental inter-observer variability.Finally, a robust initialization of labeling is created, taking bothSVM and high-profile candidate regions into account. Results ofthe validation experiment on multi-parametric images showedthat increased accuracy in tumor segmentation relative to stateof-the-art methods

could be achieved. Tissues with brainstructures are complex, and their intensity features are notsufficient to precisely segment the tumor. To improve theaccuracy of segmentation, texture features are used. The texturalfeatures are evaluated based on texture analysis in this review.Textons are small image elements generated by an imageconvolution with a particular filter bank. The accuracy ofsegmentation is high when compared to other existing methods.Figure 6 demonstrates the segmentation accuracy analysis of thesuggested FAHS-SVM approaches.

V. CONCLUSION

The proposed approach of using Convolutional Neural Networks for brain tumour diagnosis from MRI images has demonstrated substantial improvements in accuracy, reliability, and automation. By leveraging the power of deep learning, the system effectively identifies tumour regions and classifies them with minimal human intervention. The results confirm the potential of CNN-based systems to augment clinical workflows, reduce diagnostic errors, and provide timely support in medical decision-making. Future work will focus on optimizing the model for real-time use, extending it to multi-class tumour classification, and validating it across larger and more diverse datasets to ensure clinical applicability.

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