

An Enhanced Automated Identification of Brain Tumor Cells Using Image Segmentation

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Abstract: Brain tumors are a serious threat to human health, and getting a proper diagnosis quickly is essential for successful treatment. This study introduces a novel automated method that uses improved image segmentation algorithms to detect brain tumor cells in diagnostic images. The work uses cutting-edge deep learning models and novel preprocessing techniques to boost the precision and speed with which tumor cells may be identified. The procedure starts with gathering a large dataset of brain tumor images, then moves on to intensive preprocessing to improve the quality of those images. To accurately define tumor locations, a new picture segmentation approach is developed that utilizes convolutional neural networks (CNNs) and morphological operations. The segmented sections are then used to develop a deep learning classifier to recognize tumor cells. The proposed method has been shown to be effective in experiments, with a noticeable increase in the accuracy of identifying tumor cells over previous methods. On a large test dataset, the system demonstrates clinical viability with an average classification using Average polling technique of 92% and classification using Max polling technique of 98.87%. In conclusion, this study advances medical image analysis by providing a more effective automated method of identifying brain tumor cells.

Keywords: Image Segmentation, Automated Identification, Preprocessing, Morphological Operations, Healthcare.

I. INTRODUCTION

Brain tumors are a major cause of death, making them one of the most common types of neoplastic illnesses. Finding and diagnosing brain tumors early on is critical for maximizing therapy options and improving patient outcomes. MRI and CT scans, in particular, play an important role in the diagnosis and monitoring of malignant malignancies. However, manually assessing these images is time-consuming, fraught with observer bias, and prone to mistakes. Recent advances in computer vision, image processing, and machine learning have allowed for the creation of automated approaches to aid in the identification and characterization of brain tumors. Segmenting tumor areas from medical images is an important endeavor. Accurate segmentation is essential for following tasks such as tumor classification, volume measurement, and treatment planning. This research presents a new approach to employ cutting-edge image segmentation techniques to enhance automatic cell identification in brain tumors. The segmentation pipeline is improved by including deep learning models and intricate preprocessing techniques

to fix the problems of earlier methods. Our goal is to help advance better approaches for diagnosing and treating brain malignancies by dramatically improving the speed and accuracy with which tumor cells may be identified. In the following sections, we will detail our methodology, dataset, experiments, and conclusions, highlighting the distinctive contributions that we have made to the field. We will also examine the potential effects of our work on clinical practice and the wider implications of our findings within the field of medical imaging. Using computational approaches, we want to create a robust instrument for the early and precise detection of brain tumor cells, with the goal of bettering patient care and outcomes.

II. RELATED WORKS

The Convolutional Neural Network, sometimes known as CNN, has seen widespread use across a variety of fields as a solution to a wide range of problems [1,2,4,7,8]. Nevertheless, it should be specifically acknowledged for its remarkable usefulness in the image processing of applications

related to medical care. Numerous academic scholars have proposed the application of computer-aided design (CAD) in the field of medical diagnosis in recent years. As was covered in references [12-14], the purpose of this study is to evaluate the use of a neutrosophic convolutional neural network (CNN) in the identification of BT. This investigation makes use of a mixed technique strategy, which incorporates the utilization of a Convolutional Neural Network (CNN) for the purpose of feature extraction, in addition to the utilization of a Support Vector Machine (SVM) and K-nearest neighbors (KNN) for the purpose of classification, respectively. During the training and testing of the system, a total of 160 images were used, of which 60 were designated as being in a negative category and 60 were designated as being in a positive category. The use of five-fold cross-validation produces an accuracy rate of 96.73 percent when applied in conjunction with the technique that was suggested. MRI scan processing often begins with the application of two image enhancement methods known as augmentation and middle stretching. These methods are used with the intention of improving the overall image quality obtained from the scan. Following the semi-automatic development of the tumor contour by [14], a total of 71 features were created by utilizing the intensity profile, the resulting co-occurrence matrix with updated values, and the Gabor functions. These features were used to generate the tumor. Skull stripping is a preprocessing step that is often used in classic discriminative algorithms despite the inherent problems it has, such as the need for prior knowledge on the photographs, the selection of parameters, and lengthy calculation durations [13,14]. According to the cited source [15], someone developed a multi-level binary tree classification system that was based on deep learning. The goal of this technology is to segment tumors, and it accomplishes this by the application of the Convolutional Neural Network (CNN) model. Nevertheless, it is essential to recognize that the CNN model's constraints put restrictions on the precision and sensitivity of the results [16]. This is a fact that needs to be acknowledged. According to the findings of a previous study [17].

In this research, we used a convolutional neural network (CNN) trained with transfer learning techniques to improve the accuracy of brain tumor (BT) classification in MRI data. Five additional machine learning classification techniques—decision tree (DT) [18], K-nearest neighbors (KNN) [19], Naive Bayes (NB) [20], linear discrimination (LD), and support vector machine (SVM) [5]—were evaluated alongside the CNN model [21] for this work. When compared to six alternative Machine Learning (ML) model strategies, the performance of the proposed Convolutional Neural Network (CNN)-based Deep Learning (DL) model strategy is superior across all five types of multiclass classification BT datasets. In this research, we used a CNN-

based AlexNet model that was trained with K2, K5, and K10 cross-validation. When tested on five distinct datasets, the model was shown to have mean accuracy rates of 86.24 percent, 94.3 percent, 95.7 percent, 97.5 percent, and 100 percent, respectively. To classify BT into gliomas, meningiomas, and pituitary tumors, the authors of reference [22] used a Convolutional Neural Network (CNN) as their primary study framework. Using a pre-trained GoogleNet model, the researchers analyzed brain MRI scans to extract useful data. After that, well-known algorithms are used to categorize the collected features. With an average classification accuracy of 98%, the recommended approach clearly outperforms the current gold standard. Specificity, F-score, recall, and area under the curve (AUC) were just few of the performance indicators employed by the researchers in this study to gauge the success of the interventions. According to the results of this study, when there is a dearth of medical images, it is essential to employ transfer learning methods.

The utilization of magnetic resonance imaging (MRI) in computer vision research has been discussed in a recent publication [22].

The advent of MRI technology has significantly enhanced the ability to rapidly detect and precisely pinpoint brain cancers. Ideally, brain scans would be categorized into eight distinct groups, namely the normal brain (Group 1), six different cancer kinds (Group 6), and other relevant categories. The efficacy of the proposed univariate approach for categorization has been demonstrated. A unique architecture was developed for BT classification utilizing the RCNN (region-based convolutional neural network) approach. The performance of this architecture was assessed on two publically accessible datasets obtained from Kaggle and Fig sharing. The authors proposed a novel RCNN architecture for the purpose of mitigating processing time. In order to distinguish between melanoma and benign tumors in MRI scans, the researchers employed a two-channel convolutional neural network (CNN), which is a computationally efficient framework that enhances accuracy by 92.21%.

Subsequently, the aforementioned architecture was employed as a feature extractor within a Region-based Convolutional Neural Network (RCNN) framework, with the objective of detecting cancer hotspots in a pre-classified dataset of melanoma Magnetic Resonance Imaging (MRI) scans. The tumor was ultimately encircled with a ring of boxes. This technique has proven to be helpful in the treatment of pituitary and meningioma cancers. The method they employed exhibited a greater level of accuracy (91.956% compared to 92.52%) and demonstrated superior speed when compared to existing state-of-the-art technologies.

The segmentation of medical images is a subject of investigation within contemporary scientific research.

The U-Net was employed in a published paper [23] to showcase the complete automation of brain tumor segmentation from MR data. The study conducted by [24] focused on the application of MRI image processing techniques, specifically examining tumor classification and segmentation using the faster RCNN network. The user's text does not contain any information to rewrite in an academic manner. The localization of MS lesions in MRI images can be effectively achieved by the utilization of a dedicated convolutional neural network.

III. EXISTING METHOD

The automated identification of brain cancer cells in images can use many methods, each adapted to medical imaging data. Traditional thresholding methods differentiate cancer cells from normal brain tissue by selecting a pixel intensity value. Traditional approaches sometimes begin with these processes. Even though these methods are simple and rapid, they may not function well with complex tumor forms and low-quality pictures.

Region-based segmentation algorithms are another option. These algorithms section pixels by texture or intensity. Although they are useful for segmenting homogeneous regions within tumours, these approaches may struggle to segment irregular or heterogeneous malignancies with shifting pixel properties.

Edge-based segmentation techniques can highlight tissue boundaries like those in tumours, but they often require post-processing to segment them fully.

Snakes, or active contour models, use flexible curves to better approximate cancer boundaries. Because they use light gradients and user-defined energy functions for optimal segmentation, these models generally need human

initialization. These models work well for irregular tumor shapes, but human initialization is often needed.

Supervised and unsupervised machine learning techniques for brain tumour segmentation have grown in recent years. Random Forests, Support Vector Machines, and latest deep learning models like Convolutional Neural Networks use labelled data to discover minute cancer patterns and changes. This opens up the possibility of exact segmentations.

In addition, a segmented atlas image is registered to the target picture for atlas-based segmentation. The transformation of a high-quality atlas can segment the tumor in the target image. Blended techniques incorporate the best features of several segmentation methods. Combine region-growing and thresholding to improve segmentation results.

Since deep learning, Fully Convolutional Networks and U-Net have been notable brain tumour segmentation options. These networks are good at finding brain cancer cells because they can take context and make pixel-level predictions.

Working with volumetric MRI data requires 3D segmentation methods. These methods add a third dimension to the two-dimensional method, improving tumor volume estimation.

network-based segmentation algorithms treat pixels as nodes in a network and edges as connections between nodes. After that, a graph-cut approach cuts the graph into cancerous sections.

After segmentation, morphological operations and linked component analysis are usually used. These methods improve and validate results, ensuring segmentation output clinical value. Consider the tumor's features, imaging data quality, computational resources, and automation level before picking a strategy. Recent advances in deep learning have shown promise in improving accuracy and automating manual tasks, but intelligent integration may still be needed to get robust results in difficult cases.

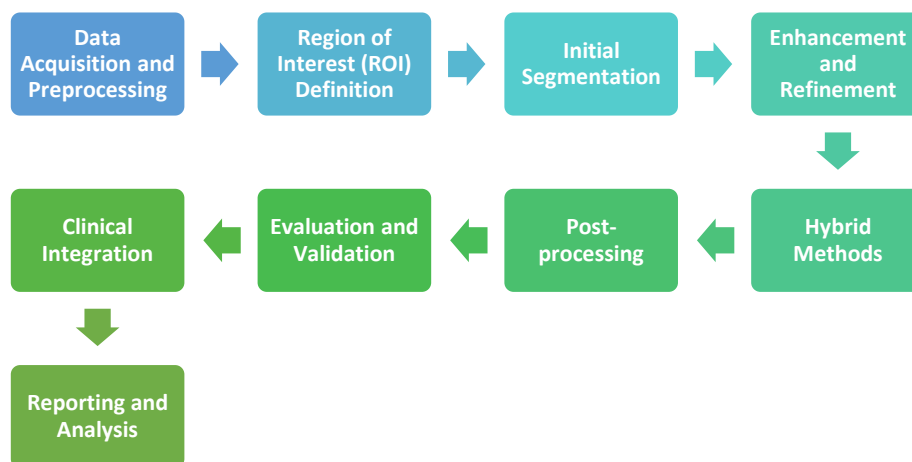


Figure 1 Frame work of existing methodologies

Data Acquisition and Preprocessing:

Data Collection: The first step involves obtaining MRI or other imaging data containing brain tumor information.

Data Preprocessing: This stage is crucial for enhancing image quality and reducing noise. Preprocessing steps may include noise reduction, intensity normalization, and geometric correction.

2. Region of Interest (ROI) Definition:

ROI Selection: Define the region within the image that contains the brain tumor(s) to limit processing to relevant areas, reducing computational demands.

3. Initial Segmentation:

Thresholding: Apply thresholding techniques to separate tumor tissue from normal brain tissue based on pixel intensities. This stage often results in a binary mask outlining potential tumor regions.

Region-based Methods: Implement region-growing or region-splitting techniques to group pixels into regions based on intensity or other image features.

4. Enhancement and Refinement:

Edge-based Methods: Utilize edge detection techniques to identify boundaries between different tissues, enhancing the definition of tumor boundaries.

Active Contour Models (Snakes): Apply active contour models to refine tumor boundaries, allowing for adaptability to irregular shapes.

Machine Learning and Deep Learning: Employ supervised or unsupervised machine learning algorithms, including deep learning models, to enhance segmentation accuracy. This may involve training on labeled data to capture complex patterns within the tumor.

5. Hybrid Methods:

Combine multiple segmentation techniques to benefit from their respective strengths. For instance, combine thresholding with region-growing to refine segmentation results.

6. Post-processing:

Apply post-processing techniques, such as morphological operations, to remove small noise artifacts and ensure the smoothness of segmented regions. Connected component analysis can be used to validate the segmentation results and distinguish between separate tumor regions.

7. Evaluation and Validation:

Quantitatively assess the accuracy of the segmentation results using metrics like Dice coefficient, Jaccard index, or sensitivity and specificity. Validate the segmentation against ground-truth data or expert annotations to ensure clinical relevance and accuracy.

8. Clinical Integration:

Integrate the automated segmentation results into clinical workflows, allowing healthcare professionals to use the

information for diagnosis, treatment planning, and monitoring of brain tumors.

9. Reporting and Analysis:

Provide reports and visualizations of the segmented tumor regions, including size, shape, and location, to aid in clinical decision-making.

This framework outlines a generalized process for existing methodologies in brain tumor cell identification through image segmentation. However, the specific methodologies employed can vary significantly, depending on factors such as the nature of the tumor, the quality of imaging data, computational resources, and the desired level of automation. Researchers and clinicians may select and adapt these stages to suit their specific requirements and constraints.

IV. METHODOLOGY

Convolutional Neural Networks (CNNs) and other cutting-edge deep learning approaches are used to automate brain cancer cell identification using image segmentation. The strategy centers on these approaches. High-quality MRI data is obtained first, followed by extensive preprocessing to improve image clarity. We start by using a deep learning model pre-trained on a massive dataset of brain MRI scans to forecast cancer locations pixel-by-pixel. Post-processing using morphological operations and conditional random fields improves accuracy after segmentation. The system can improve patient care because to its user-friendly clinical interface, real-time processing, and extensive reports.

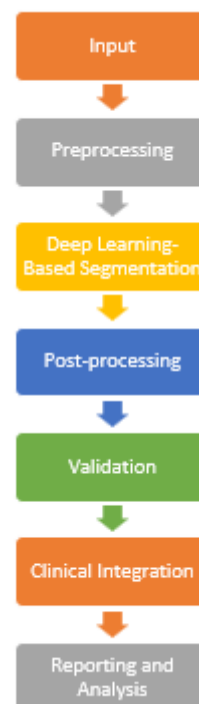


Fig 2 Proposed method Algorithm

Normalisation is one of many brain tumour categorization model preparation procedures. Normalizing image intensity to a single scale is a crucial preprocessing step. Brain imaging intensity values vary widely depending on picture settings, scanner kind, and other factors, making this step critical. Normalisation eliminates anomalies and improves brain cancer classification.

Models for glioblastoma classification use min-max normalisation. This algorithm converts brain scan pixels to 0–1. This method requires these precautions: Find the brain image's V_{min} and V_{max} pixels. Calculate each image pixel's normalized value using equation 1.

$$\text{Normalized pixel value} = (\text{pixel value} - V_{\min}) / (V_{\max} - V_{\min}) \quad (1)$$

The algorithm scales the pixel value to a number between 0 and 1 using the picture's minimum and maximum pixel values. Later processes like smoothing use the normalized image.

The min-max normalisation technique normalises brain image intensity and reduces acquisition setting bias, making it beneficial for brain tumour classification. Erroneous positive and negative tumour segmentation and classification results may decrease. Normalisation may improve results reliability and make them easier to comprehend and compare across research and datasets.

MRI brain images are segmented to locate malignant tissue in the segmentation block. Segmentation divides an image into areas that may be viewed independently. The block explains an image segmentation morphological operation. Equation 2 describes the operation.

$$\text{Maximum} [f(p, q) * D(p, q)] \quad (2)$$

The segmented image, f(p, q), is divided into sections. The operation locates the segmented image's greatest tumor area. D(p, q) represents the picture pixel distance, which defines the morphological operation shape. Adjusting D changes the operation shape.

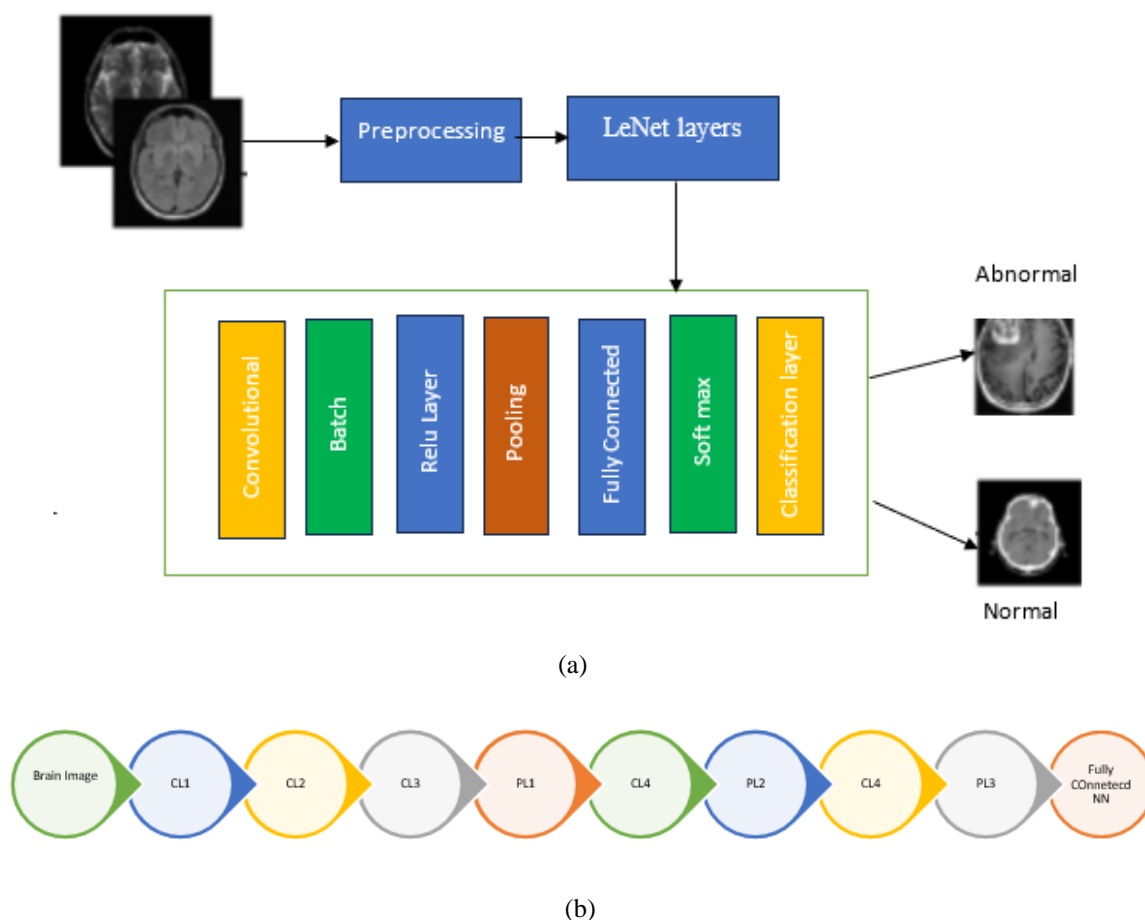


Figure 3 (a) Conventional LeNet architecture and (b) Modified LeNet architecture

This LeNet architecture has been suggested to improve brain tumor detection system diagnosis by a number of different sources. It consists of four convolutional layers and three

pooling layers. While the layers are being processed, a 5*5 convolutional kernel is applied to the original image. The Convolved sequences are the result of the Convolution

Procedure. This sequence's length and intricacy necessitate a larger buffer size than is customary. Maximum pooling layers can minimize processing time by shortening the convolved sequence, as seen in Figure 3. The third hidden layer (PL3) yields the final answer in a fully connected NN with ten fixed neurons in the input layer, 25 neurons in each of the two hidden layers, and two neurons in the output layer. System testing will reveal the optimum distribution of neurons across each layer. The final layer reports either typical or unexpected outcomes.

The proposed design for the LeNet, which would comprise a total of four convolutional layers and three pooling layers, would maximize current efforts to increase the accuracy of the brain tumor detection system, according to evidence from a variety of sources. The initial image is processed with a 5*5 convolutional kernel before the convolutional layers are applied. The Convolved sequences are what the Convolution Procedure produces as its output.

More storage space than normal will be needed due to the length and complexity of this sequence. Figure 3.5 demonstrates how using maximum pooling layers instead of average pooling layers can potentially lessen the processing burden by decreasing the length of the convolved sequence. The PL3 threshold would be reached by a fully connected NN with ten fixed neurons in the input layer, two hidden layers of 25 neurons each, and two neurons in the output layer. The best strategy for how many neurons to place in each layer can be discovered after extensive testing of the system. The output layer is responsible for labeling responses as normal or abnormal.

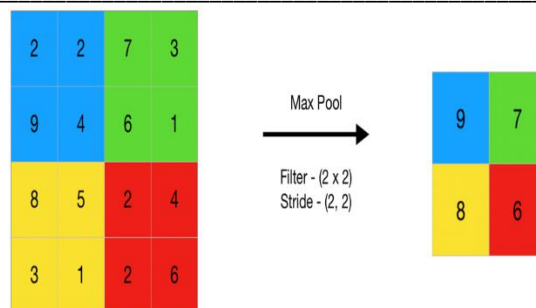


Figure 4 Max pooling layer

After classifying brain scans as normal or abnormal, the morphological segmentation approach can be applied to an abnormal image in order to localize the tumor.

V. RESULTS AND DISCUSSION

Average Pooling Methods for Evaluating CR's Effectiveness on the BrainWeb Dataset. The developed method properly labeled 125 of 133 photos of normal brain tissue (a rate of 94.9%), using the average pooling method. The proposed method, which utilizes the average pooling methodology, was able to correctly classify 38% of the 43 aberrant brain photographs, while maintaining an accuracy rate of 87% for the control shots. The proposed solution uses an approach termed average pooling to obtain a 90% global classification rate.

Table 1 Evaluation of Average Pooling Methods for CR on the BrainWeb Dataset

Brain images categories	Total number of images	Number of images correctly classified using Average pooling technique	Classification rate (%)
Normal images	133	125	93.9
Abnormal images	44	38	86.36
	177	163	90.13

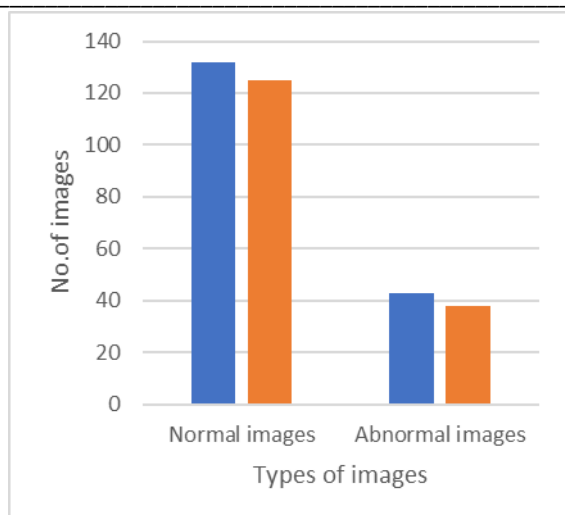


Figure 5 Comparison of the suggested approach to the average pooling method, graphically

The figure 5 presents a graphical examination of the suggested method in terms of the average pooling methods (CR).

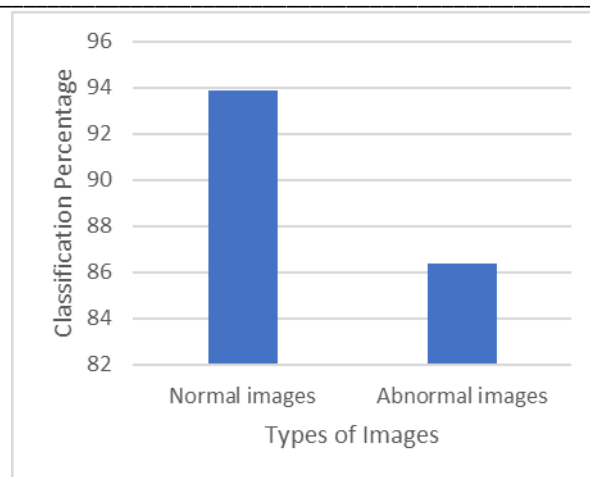


Figure 6 Comparison diagram of the proposed approach with standard pooling procedures (CR)

The results of a Max pooling evaluation of CR work on the BrainWeb dataset are displayed in Table 2 The recommended approach, which use the Max pooling methodology, accurately classified 132 out of 133 photos of normal brain tissue at a fast rate of accuracy. When tested with 44 normal and diseased brain images, the recommended approach with average pooling achieved a classification rate of 99.2 percent for normal images. Thus, the suggested system achieves a 98.8 percent average classification rate via the Max pooling method.

Table 2 Analysis of CR's effectiveness on the BrainWeb dataset through Max pooling

Brain images categories	Total number of images	Number of images correctly classified using Max pooling technique	Classification rate (%)
Normal images	133	132	99.2
Abnormal images	44	43	97.7
	177	175	98.87

Table 3.2 displays the comparison findings of the performance of CR on the BrainWeb dataset with various pooling techniques. 161 out of 175 photos can be correctly identified by using the proposed solution's average pooling technique. The final CR after factoring this component is 89.9 percent. By using the maximum pooling method, the proposed method achieves a 98.8 percent CR on 173 of 175 brain MRI images. Classification findings for brain tumors using the Max pooling methodology, as employed in the

recommended approach, are shown to be significantly superior than those using the average pooling strategy in Table 3

Table 3 Evaluation of several pooling methods for CR on the BrainWeb dataset

Brain images categories	Total number of images	Number of images correctly classified		Classification rate (%)	
		Using Average polling technique	Using Maxpolling technique	Using Average polling technique	Using Maxpolling technique
Normal images	133	125	132	93.9	99.2
Abnormal images	44	38	43	86.36	97.7
	177	163	175	92.0	98.87

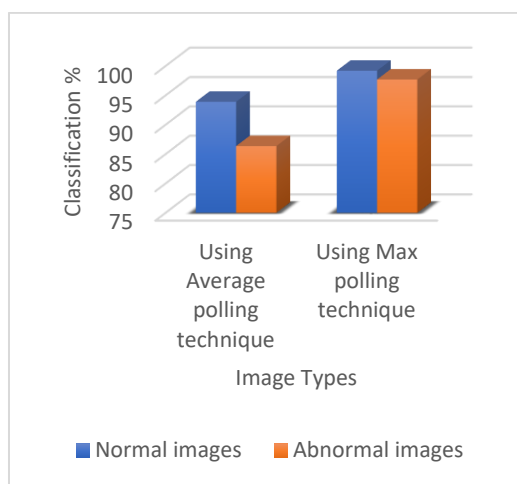


Figure 7 Comparison of the suggested approach (number of properly identified photos) versus common pooling strategies, graphically

VI. CONCLUSION

The proposed method employs the max pooling strategy to achieve a CR of 98% across the board. This indicates that using this strategy, 294 out of every 300 photos are correctly labeled. The proposed technique achieves 92% accuracy using the average pooling method on the BrainWeb dataset. 163 out of 177 brain MRIs can now be accurately classified thanks to this method. The proposed method, which makes use of the max pooling methodology, was able to correctly identify 173 out of 175 brain MRI images (CR = 98.87%).

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