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Research Article

Ensemble Deep Learning Technique for Detecting MRI Brain Tumor

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The classification process of MRI (magnetic resonance imaging) is frequently used for making medical diagnoses for conditions including pituitary, glioma, meningioma, and no tumor. For this reason, determining the type of MRI and its quantity are significant and valuable measurements that reveal the brain's state of health. To segment and classify brain analysis, laboratory personnel employ manual examination via screen; this requires a lot of labour and time. On the other hand, the devices used by specialists are not practical or inexpensive for every doctor or institution. In recent years, a variety of computational algorithms for segmentation and classification have been developed with improved results to get around the issue. Artificial neural networks (ANNs) have the capability and promise to classify in this regard. The purpose of this paper is to create and put into practice a system for classifying different types of MRI images of brain tumor samples. As a result, this paper concentrated on the tasks of segmentation, feature extraction, classifier building, and classification into four categories using various machine learning algorithms. The authors used VGG-16, ResNet-50, and AlexNet models based on the transfer learning algorithm for three models to classify images as an ensemble model. As a result, MRI brain tumor segmentation is more precise because each spatial feature point can now refer to all other contextual data. In the specifics, our models outperformed every other published modern ensemble model in the official deep learning challenge without any postprocessing. The ensemble model achieved an accuracy of 99.16%, a sensitivity of 98.47%, a specificity of 98.57%, a precision of 98.74%, a recall of 98.49%, and an $F1$-score of 98.18%. These results significantly surpass the accuracy of other methods such as Naive Bayes, decision tree classifier, random forest, and DNN models.

1. Introduction

In the era of electronic health records and information technology, health experts will give people excellent medical care [1]. This study examines the challenges associated with segmenting and managing dysfunctional normal tissues, such as brain tissues including GM (grey matter), detecting WM (white matter), and CSF (controlling cerebrospinal fluid) using magnetic resonance (MR) imaging techniques and images. It utilizes a support vector machine learning algorithm and a feature extraction which is a preprocessing technique for analysis [2–4]. This type of tumor is characterized as an aberrant and uncontrolled proliferation of cancer cells or an expanding lattice [5]. A brain tumor is defined by the excessive and uncontrolled growth of cancerous or malignant cells. Brain tumors may be categorized into two types: benign neoplasms and malignant neoplasms [6]. Benign brain tumors in patients are characterized by a uniform structure and the absence of active malignancy cells. Malignant brain tumors in patients exhibit structural heterogeneity, including many types of actively proliferating cancer cells. Gliomas and meningiomas are examples of benign tumors, which are characterized by low-grade growth and development [7].

Glioblastoma and astrocytoma are both high-grade growth tumors that are classed as malignant tumors [8].

The World Health Organization (WHO) and the American Brain Tumor Association (ABTA) adopt a widely established categorization method that distinguishes distinct kinds of benign development and malignant tumor growth using grade I and grade IV scales [9]. Benign malignancies are classified as phases below grade I and grade II glioma development on this scale. Different types of malignant tumor growth are classified below grade III growth and are rated as IV glioma growth.

Tumors classified as grade I and II exhibit contrasting growth rates, with grade I tumors characterized by sluggish growth and grade II tumors characterized by fast growth [10]. If a low-grade brain tumor is left untreated, it will advance to a high-grade brain tumor, ultimately developing into a malignant type characterized by irregular and uncontrolled development. Patients diagnosed with various types of grade II gliomas may need regular monitoring by magnetic resonance imaging (MRI) or computer tomography (CT scans) at intervals of 6 to 12 months [11]. Brain tumors may impact individuals of all ages, and the specific consequences on the body might differ across individuals. Gliomas, which are benign tumors characterized as low-grade (I and II) and uncontrolled growth, can be cured through complete surgical intervention. On the other hand, malignant brain tumors of grades III and IV require various forms of radiotherapy, chemotherapy, or a combination of both treatments [12].

The term malignant glioma encompasses both type III and IV glioma, which are also referred to as anaplastic astrocytoma. Anaplastic astrocytoma is a tumor of intermediate grade that exhibits irregular or unusual development characteristics and has a greater proliferation rate compared to typical low-grade cancers [13]. Glioblastoma is the most perilous kind of astrocytoma seen in individuals, and it is classified as the highest-grade glioma within this group. Glioblastoma is characterized by aberrant and unregulated angiogenesis, resulting in the rapid development of various blood vessels, as well as the presence of uncontrolled necrosis around the tumor segment in the patient [14]. Glioblastoma, a grade IV tumor, is an aggressive and deadly kind of tumor that grows rapidly and spreads easily. Unlike other tumor groups, it may be detected using various medical imaging techniques via the process of segmentation, which helps identify contaminated tumor tissues [15]. Classification is a process that involves dividing an image into distinct blocks based on shared characteristics, such as colour, form, growth, structure, contrast, brightness, development, border, and grey level in the patients [16]. This is a notable advancement in the image processing procedure. The process of distinguishing various types of tumor tissues, such as edema and necrotic cell formation, from normal brain tissues and healthy tumors, is referred to as brain tumor segmentation. This involves categorizing the different developmental stages of white matter (WM), grey matter (GM), and CSF using MR images or other imaging techniques [17]. The study in [18] addresses the inefficiencies and error-prone nature of manual brain tumor diagnoses, which rely heavily on the variable expertise of radiologists. The authors propose an automated method using deep learning to enhance the speed and accuracy of tumor detection from MRI images. Their methodology begins with preprocessing the images to improve visual quality, followed by employing a deep learning model trained to categorize brain images based on tumor presence and type. This approach not only aims to minimize human error by automating diagnosis but also enhances scalability, making it feasible for handling large datasets in extensive health monitoring systems. In [19], it is based on deep feature mining of high-quality regions in MRI images, where they increase the recognition accuracy of the tumor in the diagnostic stage. The complexity and variability in size, shape, and appearance of brain tumors call for patient-specific treatment plans [20]. The authors believe that the manual detection of the brain tumor inside the human body is an error-prone, inefficient activity. This method highly depends on the expertise of radiologists. In this work, they try to make an advanced automated classification system using deep learning that attempts to overcome the drawbacks through performance better than the existing one, which could be achieved due to the effect of the use of enhanced image processing technique and data augmentation. This, in turn, would allow the possibility of finer determination of location for classification of the tumor and hence would offer a new standard of accuracy for MRI imaging in the diagnosis of brain tumors.

This paper stands as one of the very important milestones in the domain of medical imaging because it presents an ensemble model for MRI brain tumor segmentation that increases the efficiency of segmentation and provides more accurate results. Pooling spatial and contextual features generally performs better than traditional approaches in segmentation for more accurate results. The automations by the system, therefore, reduce handling manually and further accelerate the diagnostic process, which, in this situation, "fast" means everything for "time" in medical conditions. Another big advantage is in terms of cost-effectiveness, which enables many more underresourced facilities worldwide to take advantage of the technology, therefore not being overly dependent on manual examinations and special hardware. That kind of bold application of transfer learning, for instance, the adoption of established models such as VGG-16, ResNet-50, and AlexNet, is pointing to a very bold approach to medical imaging. The strategy in general sense tends to boost up the generalization and performance of the model without overly customization of the same to the particular dataset. These models have, in the end, set benchmarks above other state-of-the-art methods in a certain deep learning challenge, hence ensuring their practical efficacy in real-world applications without further post-processing. This is very essential, bearing in mind that it will contribute effectively to the enhancement and improvement of the boosting of medical diagnostics reliability, especially in the detection of brain tumors from MRI images. The paper is organized starting with an introduction in first section, followed by a background and literature review in second section. It then progresses into the methodology section in third part, continues with the results, and concludes with the conclusion.

2. Comprehensive Theoretical Foundations

2.1. Finding and Identification of Brain Tumor in MRI Imaging. MRI images of the brain are processed with a median filter, and morphological segmentation and tumor extraction methods are used to look at brain tissue [15]. This method works well to get a clear MRI image of the growth. This article talks about how a neural algorithm can be used to find the tumor area in brain images taken by magnetic resonance imaging (MRI). The captured image is then used with the grey-level co-occurrence matrix (GLCM) method to figure out the features. Neural networks and segmentation systems are used to find tumors. Magnetic resonance imaging (MRI) and patient-controlled analgesia (PCA) are both used to get useful knowledge and features. The best rate of discovery is about 96.8%, and the normal rate is about 88.3%. Rajesh and his colleagues suggested using a probiotic neural network (PNN) to sort MRI data into groups that would help us see brain tumors better [21–23]. PNN suggests that the process of giving brain tumor names should be done with more care and sensitivity. Sushmita and Lalit created an unsupervised learning system to look at positron emission tomography (PET) images of people's brains [24]. MRI images are thresholded, denoised, and tumor separated before they are analyzed [25]. The GLCM method, which is commonly used in image processing, is used to find and keep the brain's structure. A brain system called the self-organizing system (SOM) is also formed, determined, and then mapped using this method.

2.2. Brain Tumor Types. When the rate of cell division goes up without the rate of neural cell death going down, one gets tumors. Brain growth can have serious effects on the whole body, even the head, and can cause many health issues. Every day, the number of people with brain tumors keeps going up [23]. Brain tumors, like all other medical problems, need to be found quickly to be treated properly. The magnetic resonance imaging (MRI) method is also used to find brain cancers early on. Magnetic resonance imaging, or MRI, is a safe medical process that does not involve giving the patient any drugs. It also uses very little radiation and does not subject the patient to any kind of radiation. Axial, coronal, and sagittal image patterns are all part of a normal MRI scan. Three types of images can be used together with MRI to get more detailed information about the tumor's shape, tissue makeup, and thickness [26]. Three different ways can be used to do three-dimensional phase MRI scans. Using the single-sequence MR imaging method for 3D brain MRI scans might not be able to tell the difference between these two types of tumors in living tissue. There are two types of magnetic resonance imaging (MRI) sequences: T1-weighted and T2-weighted. It is possible to find brain cancers that have spread into cerebrospinal fluid using T1-weighted MRI. T2-weighted MR imaging uses contrast to easily see the opposite side's disease, which is important. Nearby brain tumors can be found. That is why tumors are given names that describe the type of cell they are made of. Tumors are most often found in the brain and pituitary gland. The brain and spinal cord are the main parts of the nervous system that are affected by glioma. Gliomas start in the brain cells that support nerve cells. The brain tumor grows in the dura mater, which is the tissue that covers the brain. It starts in the dura mater. One of the most common types of brain tumors in people is this one. About 15 to 20 percent of the time, brain tumors are found [23]. A pituitary tumor grows in the pituitary gland, which controls other glands' functions and keeps hormones in balance. It also affects part of the menstrual cycle. When T1-weighted MRI is used to tell the difference between groups of brain tumors, it can be ineffective and lead to wrong diagnoses [27]. Deep learning (DL) and image recognition algorithms are now used in new MRI computer diagnosis tools to cut down on time and mistakes. The method for recognizing objects is a form of AI called "deep learning," which makes use of multilayer neural networks. Deep learning can learn from the same kinds of data as machine learning algorithms, like text, images, and movies [26]. It can also learn from data that are used in more standard ways. It is important to keep in mind, though, that these methods have very different ways of fixing problems. The study's goal is to create a web-based app that uses a correct T1 MRI scan to correctly group glioma, meningioma, and pituitary limbs by using deep learning methods. Thanks to the creation of web-based tools, it is now easy for doctors and health scientists to find brain tumors. Often, this web-based software can help doctors figure out what kind of brain tumor a person has by putting it into groups like glioma, meningioma, and pituitary tumors. The test results show that all the factors that were measured can accurately tell the difference between the different types of brain tumors in the training dataset. All of the measures, except for sensitivity and major or comorbid complications (MCCs) for meningioma, had scores of 91% or higher. This model uses a convolutional neural network (CNN) to correctly find different kinds of brain tumors [28, 29] during the testing and planning stages. Currently, the CNN is carrying out a novel research study through which it aims to diagnose brain cancer by using standard MRI scans. This research study plans to bring a major improvement in diagnostic accuracy by using modern imaging methods and artificial intelligence. Deep learning methods were used in this study to look at 3400 T1-weighted scans of the same people. As a result, the images were put into 233 different designs, 3000 of which were unique. The improved method gives an average accuracy of 96.14% and 98.8% when used on two different datasets. In [30], the research was centered on bolstering assistance for young pediatric brain tumor survivors. Its primary objective was to identify key issues and enhance available resources for these individuals, drawing insights from an online survey. Although specific findings from the study are not explicitly mentioned here, the overarching aim involved comprehending the needs of these survivors and devising strategies to facilitate their reintegration into daily life posttreatment. Notably, the study underscored the significance of furnishing pertinent information and support to aid in educational and vocational decisions, recognizing the distinctive hurdles encountered by this demographic in their posttreatment journey. In [31], the authors proposed a radiogenomic classification method

for predicting the methylation status of the MGMT promoter using multiomics fused feature space. The approach aims to facilitate the least invasive diagnosis of this status through mpMRI scans. The research, published in Scientific Reports, presents a novel method that integrates radiomics and genomics data to improve diagnostic accuracy and reduce the need for invasive procedures in identifying MGMT promoter methylation status. In [32], the authors introduced an intelligent ultra-light deep learning model designed for the detection of multiclass brain tumors. The proposed model is aimed at enhancing the efficiency and accuracy of brain tumor detection processes. Published in Applied Sciences, the study presents a novel approach leveraging deep learning techniques to classify different types of brain tumors. This model holds promise for improving diagnostic procedures and ultimately aiding in the early detection and treatment of brain tumors. The study focuses on leveraging convolutional neural networks (CNNs) for the accurate classification of brain tumor types based on MRI images. The research involves tasks such as feature extraction, data augmentation, and training of the CNN model. By employing deep learning techniques, the proposed approach aims to enhance the classification accuracy of brain tumors, which is crucial for effective diagnosis and treatment planning [33].

2.3. Method for Detection. A review of real-world studies shows that being able to easily find brain tumors is very important when lives are at risk [23, 34]. Figure 1 shows a useful way to find brain tumors. It starts with getting an image and then moves on to preparation, extraction, and segmentation. Using a machine learning program to identify features and classify them is a popular way to find cancer in MRI images.

The dataset used in the study [31] for the task of radiogenomic classification in predicting MGMT promoter methylation is at times hard to be availed and has also turned to be cumbersome due to restrictions encountered with source websites. This implies that the experiment of this study might have utilized the 2021 RSNA Brain Tumor Challenge dataset (BraTS-2021) since it consists of multiparametric MRI (mpMRI) imaging, which includes fluid-attenuated inversion recovery (FLAIR), T1-weighted, T1-weighted with contrast enhancement, and T2-weighted images. For this reason, this dataset is broadly used in the field to develop and test models related to brain tumor segmentation and classification, including those tied to radiogenomic classifications. In [29], the study was conducted on fluid-attenuated inversion recovery (FLAIR) MRI brain images to develop an automated segmentation system. The dataset might contain MRI scans with both a tumor core and edema, segmented by superpixels, based on the extremely randomized trees for the classification algorithm. These datasets were very important for the development and validation of algorithms, aiming at the identification and delimitation of the abnormal cerebral tissue associated with the neoplasm. In [13], the empirical evaluation used three datasets, each presenting its own challenges and opportunities for insights. The first was a Digital Imaging and Communications in Medicine (DICOM) series of 22 images showing tissues with tumors but lacked corresponding validation ground truth images. The second, provided by BrainWeb, featured sets of fully simulated 3D brain MR images from various imaging sequences, with emphasis on 13 out of 44 T2-weighted images characterized by 1 mm slice thickness, 3% noise, and 20% intensity nonuniformity. The final dataset, compiled from expert radiologists, included a comprehensive collection of 135 images across all modalities from 15 patients, enhanced with ground truth images to allow direct comparison between the automated algorithm and expert manual analysis. This range of datasets ensured comprehensive validation of the algorithm, from simulated settings to real-world clinical scenarios.

2.3.1. Image Acquisition Stage for MRI. In the first step, MRI images of the brain are collected. These images are also used as data for the system's editing step [24]. During this step, examples of different kinds of images are gathered to make sure they are useful. It is promised that performance measures will be managed after the image capture and development phase [35]. A magnetic resonance (MR) study of a healthy brain is shown in Figure 2. All of the images show that there is no growth. The dataset of actual images from Hiwa Cancer Hospital in Sulaymaniyah is divided into four main categories: pituitary, glioma, meningioma, and nontumorous, and a total of 3,650 images are used in this paper.

2.3.2. Preprocessing. Preprocessing makes an image more useful by making some of its parts better before it goes through more processing [26]. The following steps are taken before the MRI images are processed: MRI images are not coloured images, rather they are grey-level images, and Figure 3(a) shows the first step of normalization. After that, a median filter is used on the image. Look at Figure 3(b). A filter was used to get rid of the noise so that a more in-depth study could be done. Figure 3(c) shows the Canny edge recognition method. For image segmentation, it needs an image that has been edited to find edges. In Figure 3(a), the input image from the database contains blare and artifacts. Figure 3(b) shows the input image after being filtered with a median filter before image conversion. In Figure 3(c), the image is converted to a greyscale shadow image for further processing. Figure 3(d) demonstrates the enhanced image quality, ensuring accurate segmentation. In Figure 3(e), the image is segmented using a template-based K-means algorithm. Finally, in Figure 3(f), the tumor is detected from the segmented image and marked in red [26]. There is a certain image in the basin division result diagram where all the items and tools are given different numbers on a set scale. The pixels in the first object are given the value of 1, while the pixels in the second object and all the ones that come after it are given the value of 30. Figure 3 is an image that shows different ways that MR scans of the brain have been prepared for analysis.

2.3.3. Feature Extraction. When a program takes in a lot of data and boils it down to a small set of features, this is called "reducing to a feature vector" [36, 37]. The process of turning data into a set of features is called feature extraction.

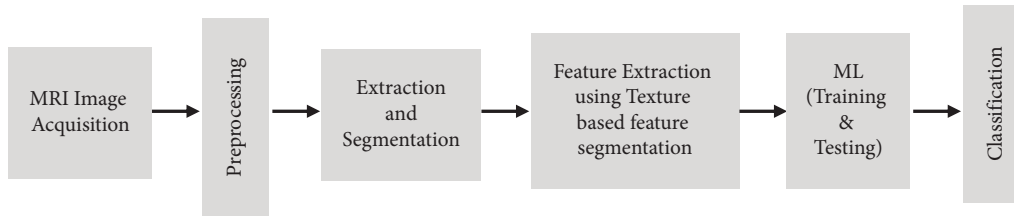

Figure 1: Usable method for brain tumor detection in MRI imaging.

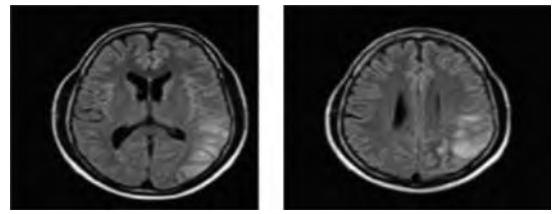

Figure 2: Brain MR image (samples) [24].

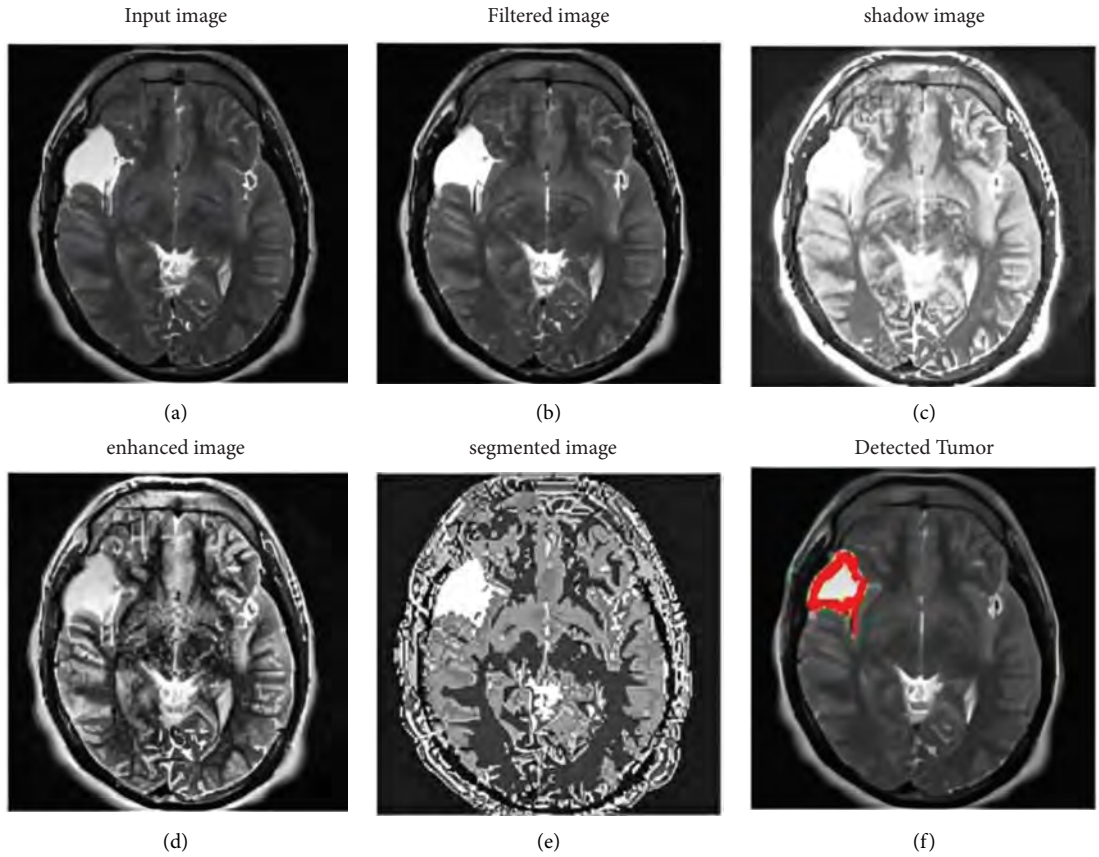

Figure 3: Stages in preprocessing of MRI images: (a) original image, (b) filtered image, (c) shadow image, (d) enhanced image, (e) segmented image, and (f) detected image [26].

The method used for tissue segmentation is to pull out the forms of the tissue's features, which are then shown in the segmented MR image [38]. To get rid of these unique traits, the GLCM method works very consistently and quickly [39, 40], GLCM tools are very good at figuring out how to separate textures. Because they can use fewer grey levels, which leads to better total classification, they are widely used for growth and identification [38]. Grey level and co-occurrence (GLC) measurement features are used to tell the difference between normal and abnormal behaviour [41]. The layout gives details about how things are arranged on the ground. When it comes to classifying images, using spatial information with the grey colour is more important. Grey-level co-occurrence matrix (GLCM) quantifies texture in an

image when comparing a pair of pixels having some values (grey levels) at a given spatial orientation. This, therefore, helps in identifying the distribution and relationship that does exist between the neighboring pixels, hence aiding an easier way of analyzing the texture of an image. In medical imaging, such as MRI, GLCM is useful in studying the texture patterns; this greatly helps to differentiate between healthy tissue and diseased tissue. This is because different tissues and pathological conditions have unique texture characteristics. Principal component analysis (PCA) is a statistical procedure to convert a set of observations that possibly show correlation between variables to a set of values of linearly uncorrelated variables. Variance scaling finds wide use in image processing and other sections of data analysis to underline variation and bring out strong patterns in the dataset. PCA retains most of the original variability in data; it only reduces the dimension of the data so that it could be easily understood and visualized. In this context, PCA is applied to bring down data complexity, enabling an easy location of important features in, for example, MRI images. Self-organizing map (SOM) is a computational technique used in the visualization and interpretation of high-dimensional data. SOM uses artificial neural networks to reduce the high dimension of data to a small dimension, so it gives a greatly simplified two-dimensional representation from many complex patterns. One domain area of image processing that SOM finds use in is pattern recognition. The third one is in finding features within images, and the last one is clustering similar images. For example, the SOM will help to classify the different kinds of tissue or clusters of cells according to characteristics for the diagnosis or analysis of the different diseases in medical imagining.

2.3.4. Classification. Multilayer perceptron (MLP) and Naive Bayes (NB) methods are sometimes used to recognize patterns in brain images [42], which help people learn and make it easier for them to make decisions. For this method to work, we need to build an artificial neural network (ANN) [43] with many layers that are in charge of connecting inputs to an output variable. After that, the output variable is fed into one or more lower stages until the right answer is found. There is a firing process for each cell in the MLP [44]. A feedback loop is not a feedforward loop because it does not have any return [38]. Achievement goals that are in line with real results lead to learning, which improves bond skills [45]. Because of bad reviews, this method is made fun of by calling it "backward pathogenesis." The objective is to lower the total weights as much as possible to lower the mistake rate for each edge. Figure 4 shows the preprocessed image, which is the result of all the steps that were given. The image that was segmented with k-means is shown in Figure 4(a), and the image that was segmented with c-means is shown in Figure 4(b). The image with hard lines is shown in Figure 4(c), and the image with features taken out is shown in Figure 4(d).

3. Method

The researchers in this study apply the steps presented in Figure 5 to separate brain tumors and pull out their features. This process has several steps, such as preprocessing, image segmentation, morphological image processing (which includes erosion and dilation), brain tumor feature extraction (which includes structure, spatial features, momentary changes, simultaneous matrix, contrast, homogeneity, entropy, energy, correlation, colour moments, and intensity characteristics), and classification types.

To make a collection, a short program was created. A Microsoft Excel file is used to store the data for each shape, along with numbers and layer traits. As a result, a list of 22 traits is made, which are fed into the classification methods.

A new set of data called feature vectors is made by pulling out important features from MRI images of brain tumors. Next, a method called a classifier is used to turn the feature vector into a set of classes. Making classification models from a set of data in a planned way is what a classification strategy is. This study looks at transfer learning as a group method, focused on the decision tree (DT), convolutional neural network (CNN), and random forest (RF) classification methods in particular. These methods are used to sort brain tumors into different groups, as seen in Figure 6. Each approach uses a learning method to find the model that best matches the link between the set of features and the raw data's class name. In Figure 6, one can see how the sorting method works.

3.1. Convolutional Neural Network (CNN). Nineteen layers make up the 1D CNN model. There are four convolution layers, two removal layers with a drop rate of 0.5, and two fully linked layers. Researchers use cross-validation to make certain model factors better, like the number of complexity levels, filters, and epochs.

Table 1 shows the CNN layers and presents what they do. By adding a 13th layer to the CNN model, the regional and local feature map can be recovered using 10 filters on a single convolution layer. Edges, such as straight and wavy lines, and other features in the raw information are found by filters. To utilize MRI images with a 1D convolutional neural network (CNN), the process includes preprocessing the images to normalize pixel values and reduce noise, extracting crucial features like edges and textures, and then flattening the images into a one-dimensional format. This transformation allows the features to be input into the CNN, which consists of convolutional, pooling, and dense layers for extracting patterns, reducing dimensionality, and performing classification tasks. The model is then optimized and validated to ensure it achieves high accuracy and performance, making this approach suitable for environments where computational resources are limited or rapid processing is required.

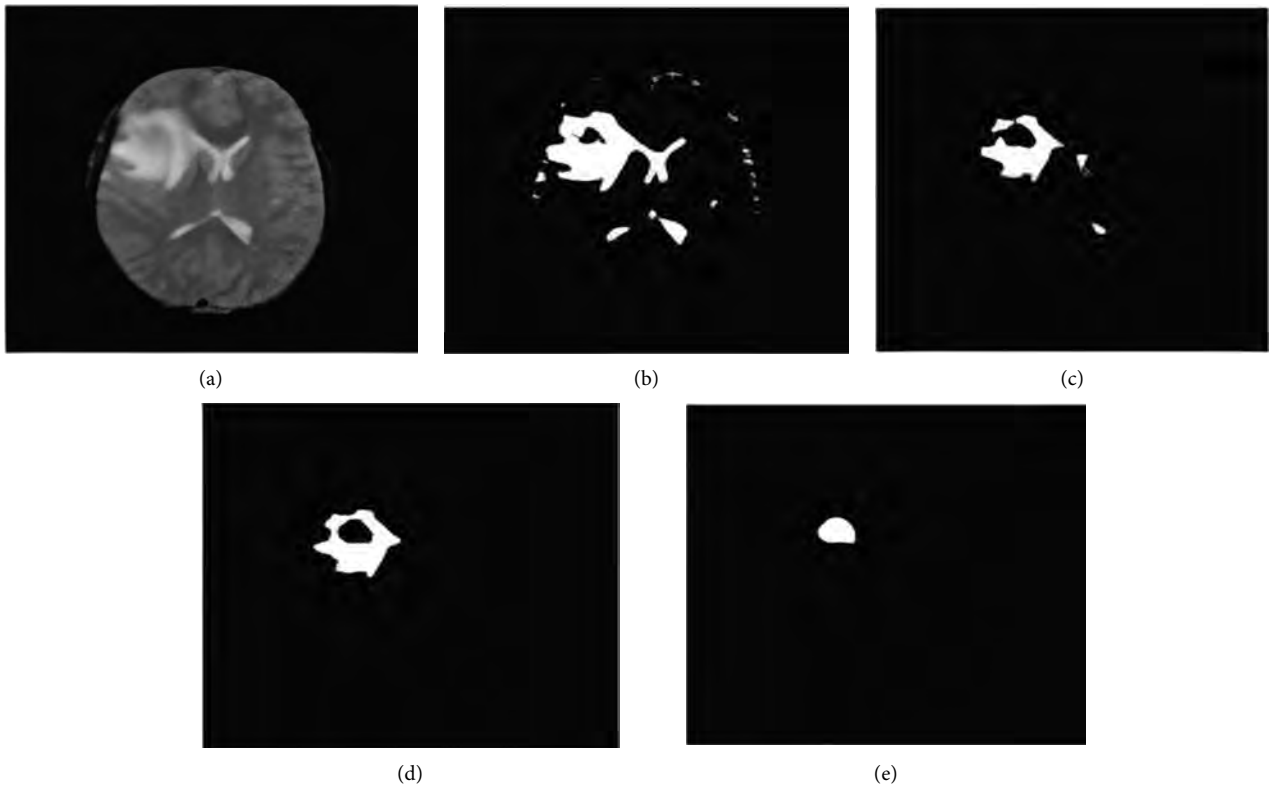

Figure 4: Classification for different MRIs: (a) original image, (b) by k-means segmentation, (c) by fuzzy c-means segmentation, (d) clear border, and (e) feature extracted image.

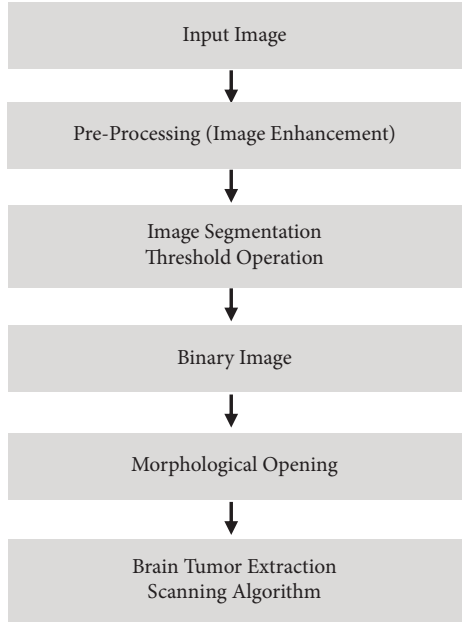

Figure 5: Proposed step of segmenting brain tumor.

An automated machine learning system has four primary components: input data, preprocessing, feature extraction, and classifier. This format is sufficiently equitable for the categorization of brain tumors using MRI. Figure 7 displays the suggested methodology for classifying brain tumors in MRI scans in this research. Below is the structured framework for design with provided details, with the objective to design a 1D convolutional neural network (CNN) model structure that classifies the MRI image into its respective categories. This model follows a series of preprocessing, convolution, and fully connected layers with an objective of making sure effective processing and

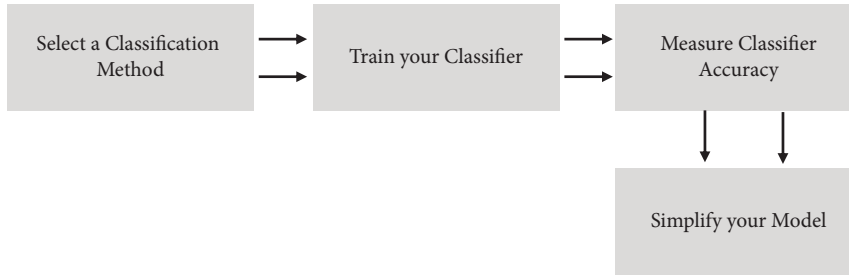

Figure 6: The block diagram of the classification process.

Table 1: Detailed explanation of the 1D CNN architecture.

No. of layers	Names	Explanation
1	Inputs	Depends on the input with "zero center" normalization
2	Layer 1	20 convolutions layers of size 7 with (1) paddings same
3	Batch normalization 1	Batch normalization 1
4	ReLU, clipped	ReLU activation with clipped ceilings at 5
5	Dropout	Dropout 50%
6	Layer 2	20 convolutions layers of size 9 using (1) length, "same" padding
7	Batch normalization 2	Batch normalization 2
8	Leaky ReLU	ReLU with a leaky scale of 0.01
9	Layer 3	30 convolution layers of size 5 with (1) stride, "same" padding
10	Batch normalization 3	Batch normalization 3
11	Softmax activation function	Softmax
12	Dropout	Dropout 50%
13	Layer 4	10 convolution layers of size 3 with (1) stride, "same" padding
14	Batch normalization 4	Batch normalization 4
15	ReLU	ReLU
16	Completely connected first	60 layers connected
17	Completely connected second	Two layers that are fully connected
18	Softmax activation function	The last fully connected layer's activation function
19	Classification layer	The output

classification from MRI data preprocessed from initial CSV file inputs. The workflow starts from the image acquired from MRI, which gets pushed into the system. Further preprocessing includes standardization of the images and noise reduction. This step is of utmost importance in the aspect of preparing the images for effective feature extraction, considering the variability in MRI imaging conditions. The 1D CNN model contains different convolution stages (depicted by red bars in Figure 7). These are the layers of convolution that help in the acquisition of fine details required for proper classification. After these, the fully connected layers (green) include the features found in the stages of convolution. This is a very important layer since it synthesizes data into the shape of data that is actually going to be used by the classifier. Highlighted in the transition from convolutional to fully connected layers is a funneling of information from broad feature detection to specific output determination. Final classification in 4 well-defined classes shows how the model can be able to classify MRI findings in potentially very different medical diagnostic classes.

3.2. Transfer Learning. Transfer learning (TL) is a type of machine learning that leverages knowledge gained from solving one problem and applies it to a different but related problem. Recent years have seen the creation of many transfer learning methods that use deep neural networks. These have been successfully used in computer vision, reinforcement learning, and natural language processing [46, 47]. The authors look into how to use transfer learning to classify the MRI into different groups by fine-tuning several deep convolutional neural network (CNN) designs that were learned on the datasets. Due to the smaller amount of the dataset used compared to MobileNet, transfer learning works well in this case. Features taken from models that have already been trained are sent to an eight-output unit through a fully linked layer. By fine-tuning the feature generator, we can use what we already know about new and specific features from looking at MRI images. This method makes the whole training process easier and faster than starting from scratch and training the model that way [48]. The combination model in Figure 8 is made up of three transfer learning models: VGG-16, ResNet-50, and AlexNet. The ImageNet collection was used to train the model. In a network model, there are layers of integration, layers of complexity, and layers of fully linked layers. These new fully connected layers were taken out and replaced with thick layers to sort MRI brain tumors into groups for this work's current use of the updated VGG-16 model. It was necessary to tune the model before it could connect all of its layers. To stop the ResNet-50 model from fitting too well, batch

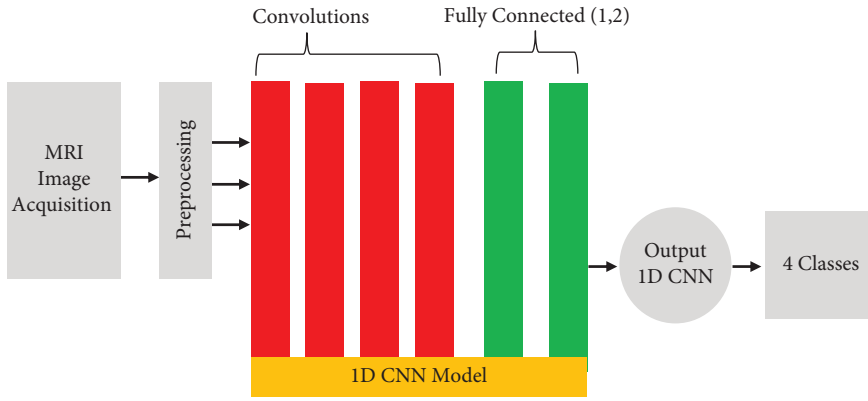

Figure 7: 1D CNN model proposed technique.

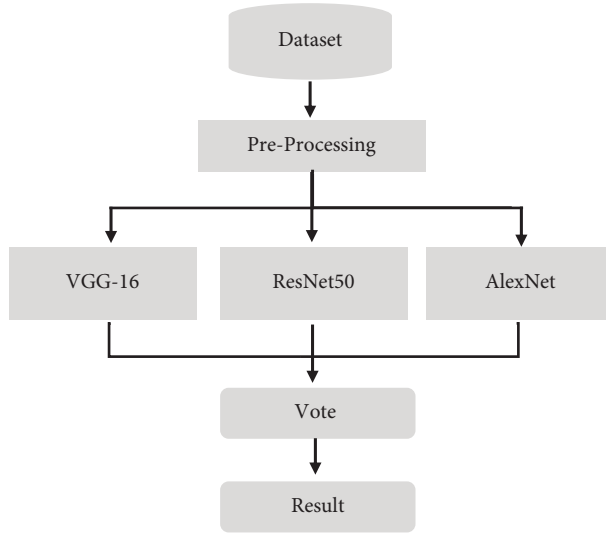

Figure 8: The block diagram of the Ensemble transfer learning classification process.

normalization and maximum pooling were added as layers on top of the levels of complexity that had already been learned. There are 50 levels in the ResNet-50 network, which is used to sort the first group. All but the last layer of the ResNet model were set to be frozen. This was done so that weights gained from earlier data could be used to train new features and sort ECG beat patterns into groups. There is a 1000-way software predictor, five convolution layers, one top layer, and three fully linked layers that makeup AlexNet. For a binary classification task, the model was trained for 100 iterations, and for a multiclass classification task, it was trained for 30 iterations. The Matplotlib tool was used to make graphs of the measures that were found. Figure 9 shows how the suggested method would be used.

The authors fixed the first convolutional and pooling layers for all three models. That most probably meant that the following were supposed to learn how to detect generally useful features of the image—common other tasks in image classification: edges, textures, and shapes.

3.2.1. Modification and Fine-Tuning. We fine-tune the final layers of more task-specific models given to the problem of brain tumor classification. All of this usually translates to replacing the last fully connected layers with new layers that have the same number of output classes (e.g., different types of tumors). Then, some MRIs with classified tumors are used to train the modified models from scratch, where new layers are added, frozen, or fine-tuned at a lower learning rate to generalize the features with respect to MRI images.

3.2.2. Specific Task Adaptation. Modified networks learn from MRI images to recognize what features belong to which type of brain tumor. They are learned through training by changing the weight of networks according to features that could be extracted from MRI images using the labeled dataset. Utilizing transfer learning techniques with models such as VGG-16, ResNet-50, and AlexNet reduces the training time required for models of deep learning and provides still accurate and efficient classification of brain tumors from MRI images with reduced computational resources that researchers usually have. These are of major advantage for two reasons: first, brain tumor imaging is complicated, and secondly, because large labeled MRI datasets are relatively rare.

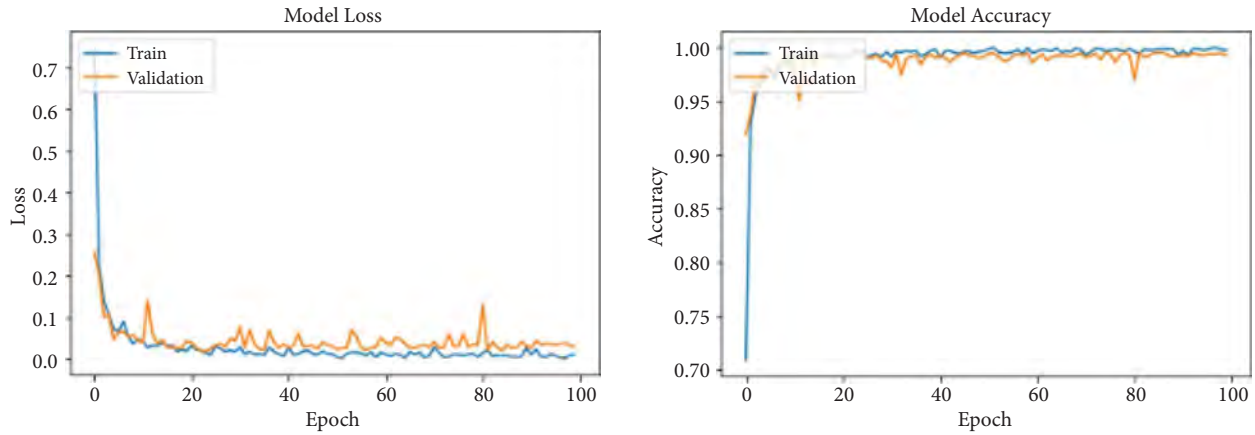

Figure 9: Accuracy of the Ensemble model.

This paper, therefore, employs a comprehensive set of performance evaluation measures to evaluate the efficacy and accuracy of segmentation of this challenging set of images. For this reason, the measures are of immense importance in ascertaining the accuracy of the segmentation process and accuracy of classification models (1D CNN, transfer learning models which include VGG-16, ResNet-50, and AlexNet). These performance measures used in this research include the following:

Accuracy: The number of correct predicted instances divided by the total instances. This is important in understanding how efficient the classification algorithms are in general.

Precision: It is also known as positive predictive value, and it refers to the measure of the ratio of correctly predicted positive observations to all observations that were predicted to be positive. Therefore, if the precision is high, it translates to low numbers of false positives. This is very key in medical imaging for the reduction of false alarms.

Recall (sensitivity): It tells what proportion of actual positives was identified correctly. In the case of brain tumor detection, high recall is very essential since most of the malignant tumors need to be correctly identified.

$F1$-score: The $F1$ value in the $F1$-score is basically the harmonic mean of precision and recall. It tells us that the $F1$ measure is useful when the distribution of classes has an imbalance and reflects equal weightage of precision and recall.

Specificity: This shows the proportion of actual negatives that are correctly identified. High specificity will, therefore, mean its prediction that the model is good at correctly identifying those patients who do not have a brain tumor.

4. Results and Discussion

To ensure equitable distribution, each category will initially contain 912 images, with the dataset separated into 80% for training and 20% for testing. To determine the beginning weights of the classifier, they make use of a random gradient descent technique that has a velocity of 0.9 [29]. For this investigation, a Lenovo computer equipped with a 1.90 GHz central processing unit (CPU) and a 10th generation Intel Core i5 10400 processor is used. This machine, which has 16 gigabytes of random access memory (RAM), has Windows loaded on it—the programming language known as Python was used in the process of creating this model. Tools for deep learning are used by the Python 3.9.10 framework to construct and test models. An initial learning rate of 0.001 is seen at the beginning of the instructional procedure. There is a 0.1-point decrease in the value for every seven periods. After a total of 25 epochs, training becomes complete when the model reaches a consensus. During the training process, the authors make use of techniques that are referred to as "data augmentation" to cope with the limited quantity of information that is accessible. This enables the model to react well to novel circumstances. Several typical image modifications are included in the training set. These modifications include rotating the image by sixty degrees and spinning it randomly in both the horizontal and vertical axes. The characteristics were extracted hierarchically, beginning with the input layer and working their way up through the buried layers until they reached the final classification output layer. The image that was supplied was altered in terms of its quality so that it would conform to the specifications of the model. When the learning rate was increased, the process of learning proceeded more quickly. When it comes to classification jobs, the completely connected layer is responsible for transforming the shape of the feature map into the required shape. A further step in the process of multiclass classification is the activation function. The cost of the model that has already been trained is reduced by the use of a cost function that is referred to as continuous cross-entropy. Choosing the meta-parameters of our strategy was made easier by the use of an algorithm. When compared to all of the many optimization strategies that were investigated, the RMS prop produced the best results.

It is not the same thing to evaluate the accuracy of the models that have been gathered. The lowest degree of accuracy that AlexNet can achieve is 85.6%, whereas the

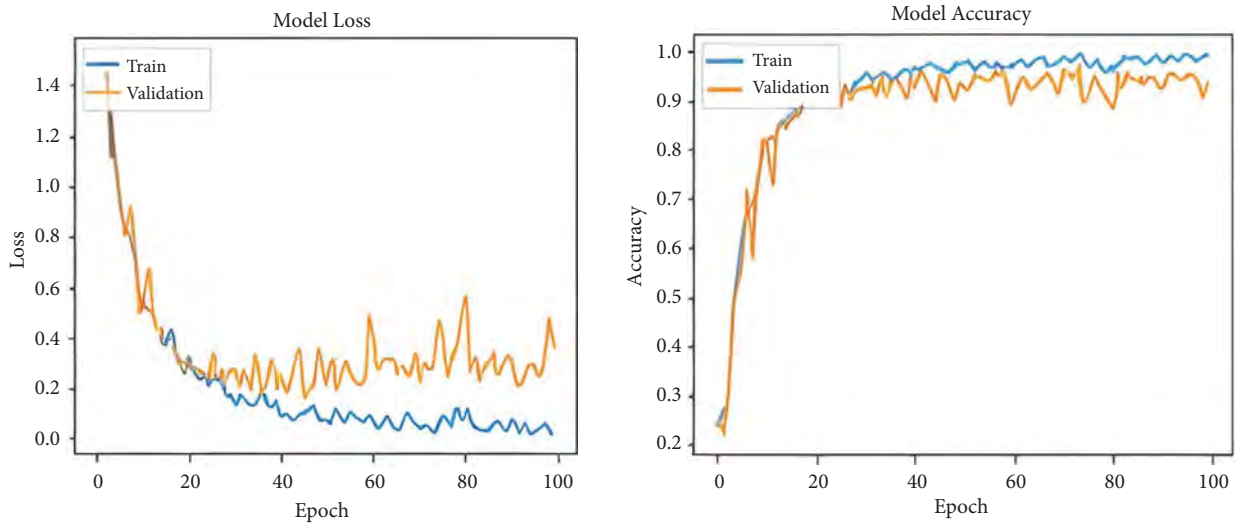

Figure 10: Accuracy of the CNN 1D model.

Table 2: Comparison of the proposed models.

Method	Accuracy (%)	Sensitivity	Specificity	Precision	Recall	*F*1-score
MLP [12]	98.6	—	—	—	—	—
Naive Bayes [12]	97.6	—	—	—	—	—
DNN [17]	96.97	—	—	97.0	97.0	97.0
Decision tree classifier (DT)	89.21	75.02	92.25	79.52	75.03	90.04
Random forest (RF)	90.54	90.94	95.58	92.39	90.98	96.52
CNN 1D	96.3	95.85	96.57	94.35	94.25	97.35
Ensemble model	**99.16**	**98.47**	**98.57**	**98.74**	**98.49**	**98.18**
MGMT-PMP system + RA [30]	96.94	—	—	—	—	0.96
UL-BTD [32]	98.46	—	—	—	—	—

maximum level of accuracy that ResNet-50 can achieve is 99.16%. As can be seen in Figure 8, VGG-16 accurately predicted the outcome 96.51% of the time. The decision tree (DT) model indicates that there is 89.21% truth in it. It is estimated that the random forest (RF) model is accurate ninety-five percent of the time. It is shown in Figure 10 that the convolutional neural network (CNN) model is capable of achieving an accuracy of 96.3% without the need for any external tools. On average, the best audit findings are provided by average numbers. The categories are shown in the table. Twenty percent of the data will be saved for testing, while eighty percent will be used for training.

Table 2 presents a comparative analysis of different machine learning and deep learning models used for detecting brain tumors. The models evaluated include multilayer perceptron (MLP), Naive Bayes [12], deep neural network (DNN) [17], decision tree classifier (DT), random forest (RF), convolutional neural network (CNN) 1D, an ensemble model, MGMT-PMP system + RA [30], and UL-BTD [32]. The ensemble model achieves the highest accuracy at 99.16%, suggesting that it is the most effective model for this task. Following closely are MLP and UL-BTD with accuracies of 98.6% and 98.46%, respectively. The decision tree classifier shows the lowest accuracy at 89.21%, indicating that it is less reliable compared to the other models. The ensemble model demonstrates exceptional performance with a sensitivity of 98.47% and specificity of 98.57%. This indicates that the ensemble model is highly effective at correctly identifying both tumor cases and nontumor cases. Random forest also performs well, with a sensitivity of 90.94% and specificity of 95.58%, making it a robust alternative. The ensemble model again stands out with a precision of 98.74% and recall of 98.49%, showcasing its robustness in accurately identifying true positive cases. In contrast, the decision tree classifier has lower precision (79.52%) and recall (75.03%), indicating a higher number of false positives and false negatives. The ensemble model achieves the highest *F*1-score at 98.18%, followed by CNN 1D at 97.35% and random forest at 96.52%. The decision tree classifier, with an *F*1-score of 90.04%, shows that while it performs adequately, it is not as effective as other models in balancing precision and recall.

5. Conclusion

Rapid diagnosis in brain tumor conditions is vital for potentially saving lives, a principle that underscores our research. Our ensemble deep learning model demonstrates its potential for lifesaving applications by providing faster and more accurate diagnoses. Different from other models due to its complex architecture that uses multiple convolution techniques in each layer, this model excels in processing and

classifying complex medical data. Our approach involves training on a diverse set of classes, utilizing neural networks to categorize medical imagery efficiently. The ensemble model, in particular, showcases superior performance, demonstrating significant progress despite the challenges of classifying multiple diseases. By adding more data, extending training durations, and fine-tuning several parameters like learning rates, epochs, hidden classes, and activation functions, we have seen marked improvements in outcomes. Our findings, through comprehensive testing across various performance metrics, reveal that our model surpasses traditional methods in accuracy, sensitivity, and specificity, affirming its value in real-world medical applications. This advancement signals our commitment to enhancing diagnostic processes, ultimately aiming to improve patient outcomes in the battle against brain tumors [49–52].

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

References

[1] S. Goswami and L. K. P. Bhaiya, "Brain tumour detection using unsupervised learning based neural network," in *Proceedings of the International Conference on Communication Systems and Network Technologies, CSNT 2013*, pp. 573–577, Gwalior, India, April 2013.

[2] T. Rajesh and R. S. M. Malar, "Rough set theory and feed-forward neural network based brain tumour detection in magnetic resonance images," in *Proceeding of the International Conference on Advanced Nanomaterials & Emerging Engineering Technologies*, pp. 240–244, Chennai, India, July 2013.

[3] S. Rajeshwari and T. S. Sharmila, "Efficient quality analysis of MRI image using preprocessing techniques," in *Proceeding of the IEEE Conference on Information and Communication Technologies, ICT 2013*, pp. 391–396, Thuckalay, India, April 2013.

[4] T. A. Assegie, R. L. Tulasi, and N. K. Kumar, "Breast cancer prediction model with decision tree and adaptive boosting," *IAES International Journal of Artificial Intelligence*, vol. 10, no. 1, pp. 184–190, 2021.

[5] R. Jader and S. Aminifar, "Fast and accurate artificial neural network model for diabetes recognition," *NeuroQuantology*, vol. 20, no. 10, pp. 2187–2196, 2022.

[6] P. Gadpayleand and P. S. Mahajani, "Detection and classification of a brain tumour in MRI images," *International Journal of Emerging Trends in Electrical and Electronics (IJETEE)*, vol. 5, no. 1, 2013.

[7] M. Shasidhar, V. S. Raja, and B. V. Kumar, "MRI brain image segmentation using modified fuzzy c-means clustering algorithm," in *Proceedings of the International Conference on Communication Systems and Network Technologies, CSNT 2011*, *2011 International Conference on Communication Systems and Network Technologies*, pp. 473–478, Katra, India, June 2011.

[8] K. Sharma and N. Kaur, "Comparative analysis of various edge detection techniques," *International Journal of Advanced Research in Computer Science and Software Engineering*, vol. 3, no. 12, pp. 617–621, 2013.

[9] J. Selvakumar, A. Lakshmi, and T. Arivoli, "Brain tumour segmentation and its area calculation in brain MR images using K-mean clustering and Fuzzy C-mean algorithm," in *Proceeding of the IEEE-International Conference on Advances in Engineering, Science and Management, ICAESM-2012*, pp. 186–190, Nagapattinam, India, March 2012, https://ieeexplore.ieee.org/abstract/document/6215996/metrics#metrics.

[10] R. F. Jader, S. Aminifar, and M. H. M. Abd, "Diabetes detection system by mixing supervised and unsupervised algorithms," *Journal of Studies in Science and Engineering*, vol. 2, no. 3, pp. 52–65, 2022.

[11] X. Xuan and Q. Liao, "Statistical structure analysis in MRI brain tumour segmentation," in *Proceedings of the 4th International Conference on Image and Graphics, ICIG 2007*, pp. 421–426, Chengdu, China, August 2007.

[12] K. Sharma, A. Kaur, and S. Gujral, "Brain tumor detection based on machine learning algorithms," *International Journal of Computer Application*, vol. 103, no. 1, pp. 7–11, 2014.

[13] N. B. Bahadure, A. K. Ray, and H. P. Thethi, "Image analysis for MRI based brain tumor detection and feature extraction using biologically inspired BWT and SVM," *International Journal of Biomedical Imaging*, vol. 2017, pp. 1–12, 2017.

[14] M. W. Nadeem, M. A. Al Ghamdi, M. Hussain et al., "Brain tumor analysis empowered with deep learning: a review, taxonomy, and future challenges," *Brain Sciences*, vol. 10, no. 2, p. 118, 2020.

[15] D. V. Gore and V. Deshpande, "Comparative study of various techniques using deep learning for brain tumour detection," in *Proceeding of the International Conference for Emerging Technology (INCET)*, pp. 1–4, Belgaum, India, June 2020.

[16] R. Jader and S. Aminifar, "Predictive model for diagnosis of gestational diabetes in the kurdistan region by a combination of clustering and classification algorithms: an ensemble approach," *Applied Computational Intelligence and Soft Computing*, vol. 2022, pp. 1–11, 2022.

[17] H. Mohsen, E.-S. A. El-Dahshan, E.-S. M. El-Horbaty, and A.-B. M. Salem, "Classification using deep learning neural networks for brain tumors," *Future Computing and Informatics Journal*, vol. 3, no. 1, pp. 68–71, 2018.

[18] M. Aamir, Z. Rahman, Z. A. Dayo et al., "A deep learning approach for brain tumor classification using MRI images," *Computers & Electrical Engineering*, vol. 101, Article ID 108105, 2022.

[19] M. Aamir, Z. Rahman, W. Ahmed Abro, U. Aslam Bhatti, Z. Ahmed Dayo, and M. Ishfaq, "Brain tumor classification utilizing deep features derived from high-quality regions in MRI images," *Biomedical Signal Processing and Control*, vol. 85, Article ID 104988, 2023.

[20] K. Kamnitsas, C. Ledig, V. F. J. Newcombe et al., "Efficient multi-scale 3D CNN with fully connected CRF for accurate brain lesion segmentation," *Medical Image Analysis*, vol. 36, pp. 61–78, 2017.

[21] S. K. Chandra and M. K. Bajpai, "Effective algorithm for benign brain tumour detection using fractional calculus," in *Proceeding of the TENCON 2018 2018 IEEE Region 10 Conference*, pp. 2408–2413, Jeju, Korea (South), October 2018.

[22] S. W. Kareem, R. Z. Yousif, and S. M. Jihad Abdalwahid, "An approach for enhancing data confidentiality in Hadoop," *Indonesian Journal of Electrical Engineering and Computer Science*, vol. 20, no. 3, pp. 1547–1555, 2020.

[23] A. Triayudi and I. Fitri, "Comparison of the feature selection algorithm in educational data mining," *TELKOMNIKA (Telecommunication Computing Electronics and Control)*, vol. 19, no. 6, pp. 1865–1871, 2021.

[24] J. Seetha and S. S. Raja, "Brain tumor classification using convolutional neural networks," *Biomedical and Pharmacology Journal*, vol. 11, no. 3, pp. 1457–1461, 2018.

[25] J. Cheng, W. Huang, S. Cao et al., "Enhanced performance of brain tumor classification via tumor region augmentation and partition," *PLoS One*, vol. 10, no. 10, Article ID e0140381, 2015.

[26] M. K. Islam, M. S. Ali, M. S. Miah, M. M. Rahman, M. S. Alam, and M. A. Hossain, "Brain tumor detection in MR image using superpixels, principal component analysis and template based K-means clustering algorithm," *Machine Learning with Applications*, vol. 5, Article ID 100044, 2021.

[27] G. Litjens, T. Kooi, B. E. Bejnordi et al., "A survey on deep learning in medical image analysis," *Medical Image Analysis*, vol. 42, pp. 60–88, 2017.

[28] L. Szilagyi, L. Lefkovits, and B. Benyo, "Automatic brain tumor segmentation in multispectral MRI volumes using a fuzzy c-means cascade algorithm," in *Proceeding of the 12th International Conference on Fuzzy Systems and Knowledge Discovery (FSKD)*, pp. 285–291, Zhangjiajie, China, August 2015.

[29] M. Soltaninejad, G. Yang, T. Lambrou et al., "Automated brain tumour detection and segmentation using superpixel-based extremely randomized trees in FLAIR MRI," *International Journal of Computer Assisted Radiology and Surgery*, vol. 12, no. 2, pp. 183–203, 2017.

[30] M. Bonanno, C. J. Bourque, L.-A. Robichaud et al., "Prioritizing solutions and improving resources among young pediatric brain tumor survivors: results of an online survey," *Current Oncology*, vol. 30, no. 9, pp. 8586–8601, 2023.

[31] S. A. Qureshi, L. Hussain, U. Ibrar et al., "Radiogenomic classification for MGMT promoter methylation status using multi-omics fused feature space for least invasive diagnosis through mpMRI scans," *Scientific Reports*, vol. 13, no. 1, p. 3291, 2023.

[32] S. A. Qureshi, S. E. A. Raza, L. Hussain et al., "Intelligent ultra-light deep learning model for multi-class brain tumor detection," *Applied Sciences*, vol. 12, no. 8, p. 3715, 2022.

[33] H. H. Sultan, N. M. Salem, and W. Al-Atabany, "Multi-classification of brain tumor images using deep neural network," *IEEE Access*, vol. 7, pp. 69215–69225, 2019.

[34] J. R. Fink, M. Muzi, M. Peck, and K. A. Krohn, "Multimodality brain tumor imaging: MR imaging, PET, and PET/MR imaging," *Journal of Nuclear Medicine*, vol. 56, no. 10, pp. 1554–1561, 2015.

[35] G. M. Shivakumarswamy, P. V Akshay, T. A. Chethan, B. H. Prajwal, and S. V Hande, "Brain tumour detection using Image processing and sending tumour information over GSM," *International Journal of Advanced Research in Computer and Communication Engineering*, vol. 5, no. 5, pp. 179–183, 2016.

[36] A. R. Mirza and M. Sah, "Automated software system for checking the structure and format of ACM SIG documents," *New Review in Hypermedia and Multimedia*, vol. 23, no. 2, pp. 112–140, 2017.

[37] T. Kalaiselvi, P. Nagaraja, and P. Sriramakrishnan, "A simple image processing approach to abnormal slices detection from MRI tumor volumes," *The International Journal of Multimedia & Its Applications*, vol. 8, no. 1, pp. 55–64, 2016.

[38] R. Kumar and K. J. Mathai, "Brain tumor segmentation by modified k-mean with morphological operations," *International Journal of Innovative Research in Science, Engineering and Technology*, vol. 6, no. 8, pp. 16191–16198, 2017.

[39] A. Mukaram, C. Murthy, and M. Z. Kurian, "An automatic brain tumour detection, segmentation and classification using MRI image," *International Journal of Electrical, Electronics and Computer Systems*, vol. 6, no. 5, pp. 54–65, 2017.

[40] S. Patel and D. Rao, "Brain tumor detection in MRI images with new multiple thresholding," *Journal of Network Communications and Emerging Technologies (JNCET)*, vol. 7, no. 6, pp. 34–39, 2017.

[41] A. Pawar, Y. Zhang, Y. Jia et al., "Adaptive FEM-based nonrigid image registration using truncated hierarchical B-splines," *Computers & Mathematics with Applications*, vol. 72, no. 8, pp. 2028–2040, 2016.

[42] R. F. Jader, M. H. M. Abd, and I. H. Jumaa, "Signal modulation recognition system based on different signal noise rate using artificial intelligent approach," *Journal of Studies in Science and Engineering*, vol. 2, no. 4, pp. 37–49, 2022.

[43] M. Havaei, F. Dutil, C. Pal, H. Larochelle, and P.-M. Jodoin, "A convolutional neural network approach to brain tumor segmentation," in *Proceeding of the Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries, Chsm*, pp. 195–208, Springer, Cham, January 2016.

[44] S. Pereira, A. Pinto, V. Alves, and C. A. Silva, "Deep convolutional neural networks for the segmentation of gliomas in multi-sequence MRI," in *Proceeding of the Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries, Chsm*, pp. 131–143, Springer, Cham, January 2016.

[45] K. Kamnitsas, C. Ledig, V. F. Newcombe et al., "Efficient multi-scale 3D CNN with fully connected CRF for accurate brain lesion segmentation," *Medical Image Analysis*, vol. 36, pp. 61–78, 2017.

[46] D. Yi, M. Zhou, Z. Chen, and O. Gevaert, "3-D convolutional neural networks for glioblastoma segmentation," *Computer Vision and Pattern Recognition*, pp. 1–8, 2016, http://arxiv.org/abs/1611.04534.

[47] O. H. Salman, M. F. A. Rasid, M. I. Saripan, and S. K. Subramaniam, "Multi-sources data fusion framework for remote triage prioritization in telehealth," *Journal of Medical Systems*, vol. 38, no. 9, pp. 103–123, 2014.

[48] S. M. R K Al- Jumur, S. Wahhab Kareem, and R. Z Yousif, "Predicting temperature of Erbil City applying deep learning and neural network," *Indonesian Journal of Electrical Engineering and Computer Science*, vol. 22, no. 2, pp. 944–952, 2021.

[49] S. Kareem and M. C. Okur, "Bayesian network structure learning using hybrid bee optimization and greedy search," in *Proceeding of the 3rd International Mediterranean Science and Engineering Congress (IMSEC 2018)*, pp. 1–7, Adana-turkey, October 2018.

[50] S. W. Kareem and M. C. Okur, "Pigeon inspired optimization of bayesian network structure learning and a comparative evaluation," *Journal of Cognitive Science*, vol. 20, no. 4, pp. 535–552, 2019.

[51] B. Badawi and M. C. Okur, "A fuzzy multi-layer color QR code decoder algorithm," *International Journal of Advanced Trends in Computer Science and Engineering*, vol. 8, no. 1, pp. 131–137, 2019.

[52] S. W. Kareem and M. C. Okur, "Evaluation of Bayesian network structure learning using elephant swarm water search algorithm," *Handbook of Research on Advancements of Swarm Intelligence Algorithms for Solving Real-World Problems*, pp. 139–159, 2020.