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RESEARCH ARTICLE

Brain Tumor Segmentation Based on Convolutional Neural Network and Integration of Deep and Shallow Features

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ABSTRACT

Segmentation of Brain tumors refers to one of the most challenging problems in analyzing a medical image. To establish accurate brain tumor region delineation, brain tumor segmentation is used. Feature extraction refers to one of the basic steps in the processing of an image that aids classification. Various features' kinds are extracted from MRI images. The traditional classifiers of Machine learning need hand-crafted features that are time-consuming and susceptible to errors made by humans. Against this, Deep learning is too powerful in terms of feature extraction and has already been extensively applied for the aims of classification. The presented technique combines multiple feature extraction strategies (integrating deep and shallow features). Thus, shallow methods extract image features manually and based on prior knowledge from the image using image processing methods. Deep approaches use machine learning and neural networks to automatically extract image information. The proposed method of this paper for image segmentation is based on the combination of the PSO evolutionary algorithm with the K-means clustering algorithm. For image processing, the K-means algorithm works perfectly. In the presented technique, PSO is applied to identify the optimum centers of the cluster. K-means algorithm outcome depends on the basic solution and has good convergence. In Google Colab, the proposed model used the Python programming language to diagnose precision, accuracy, sensitivity, error matrix, and receiver operating characteristic (ROC). Outcomes illustrate that the presented model has a high performance in brain tumor diagnosis. That obtains an accuracy of 87.94% and an average precision of 88.35%.

Keywords: Brain tumor classification, Deep learning, Feature extraction, Image classification, Machine learning, Segmentation

Introduction

Tumors in the brain are growths caused by abnormal brain cell proliferation and loss of the brain's regulatory systems. Brain strain and elevation caused by head tumors can affect one's physical well-being.[1]

Various artificial intelligence (AI) algorithms aid pattern identification in machine vision and can be divided into two types: supervised and unsupervised. Supervised algorithms, which use labeled data to train models that predict the class of input images, are further classified into parametric and non-parametric methods.[2]

Machine learning (ML), a form of artificial intelligence, allows computers to discover patterns and make judgments without requiring human intervention. Algorithms are trained by being exposed to a variety of circumstances, which helps them refine their understanding with additional data, resulting in increased accuracy. Deep learning, an extension of machine learning, outperforms shallow neural networks by using complex algorithms that mimic human cognitive processes. These algorithms, which build deep neural networks, mimic the logical structure of the human brain, allowing them to derive conclusions by processing data.[3]

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Unlike their traditional counterparts, deep learning models have an innate ability to extract features, a process that has historically been difficult. This proficiency can be attributed to the architecture's ability to intuitively recognize relevant features, eliminating the necessity for explicit feature engineering.[4]

The fundamental area of study in the field of medical imaging is early tumor segmentation, since it helps physicians determine which course of action is appropriate for the patient's condition. More than 120 different forms of brain tumors have been identified by medical researchers during the past few decades.[1] Treatment success and improved patient outcomes depend on early detection and proper brain tumor segmentation. A patient's ability to receive a good course of treatment and see results depends on an early and accurate diagnosis. A magnetic resonance image (MRI) provides comprehensive information about the location and size of a tumor. For medical professionals, evaluating a sizable volume of medical data generated by various sources has proven to be a difficult task. Manual brain tumor segmentation is a laborious and error-prone procedure, especially when the tumors don't have regular shapes, sizes, or appearances.[5]

MRI image Segmentation makes gliomas and surgery planning detection simple. However, manual brain tumor segmentation is subjective and prone to mistakes because of high variability in their location, form, and structure. In addition, the intensity inhomogeneity exists in MRI images from similar orders. Practitioners and investigators are working on important automated techniques for appropriately detecting tumor kind and phase. In the current era, deep learning (DL) methods are extensively applied through diversified rules such as management, life, and social science, biological science, and engineering.[6]

Machine learning refers to a DL level such as a large-scale neural network with several attributes and layers. DL bulk includes frameworks of neural networks. Accordingly, deep neural networks have become famous. Learning includes several important diverse node levels cascade for feature extraction and manipulation. Machine learning provides a higher research level with relatively appropriate abilities achieved from medium-access features, while lower layers learn fundamental features near the input of data. the framework generates a powerful and modular classification model well fitted for assessing and gathering appropriate knowledge from huge data amounts and info achieved from a lot of resources. Strategies of DL are grouped as supervised, semi-supervised/unsupervised. In supervised learning, a network is created by the containers' group. Each reasonable performance serves as a dataset of training for the consideration parameters confirmation technique. Applying basic labels, a technique predicts the expected result labels. Segmentation strategies include learning algorithms and might be applied for identifying faces and signage, converting audio to text, etc.[7]

Researchers have found over 120 distinct forms of brain tumors over the last few decades. The success of the treatment and the enhancement of the patient's outcomes are ensured by an early and accurate diagnosis of the tumor and its appropriate division in the brain. Although magnetic resonance imaging (MRI) may accurately determine the location and size of tumors, evaluating large amounts of heterogeneous medical data from many sources can be difficult for professionals.[8] Brain tumor segmentation by hand is a tedious and error-prone procedure, particularly when the tumors have non-uniform sizes, forms, and appearances.[4]

The diagnosis and planning of gliomas are aided by MRI image segmentation. However, because brain tumors vary greatly in terms of location, form, and structure, as well as in terms of the intensity of MRI images, manual brain tumor segmentation is prone to inaccuracy. Doctors and researchers are working on automated techniques to precisely identify the kind and stage of tumors. Deep learning (DL) techniques are now widely applied in many domains, such as biology, engineering, social sciences, and management science.[9]

Deep learning techniques have shown great promise in medical image analysis, particularly in the segmentation of brain tumors. However, depending solely on abstract and deep traits could have drawbacks. Surface features (e.g., texture and intensity gradient) might convey essential information that is missed by deep learning-only models, particularly when tumors have irregular forms and intensity variations. This problem may result in subpar segmentation performance, particularly in intricate scenarios when the tumor detection process heavily relies on these surface features.

On the other hand, surface learning approaches and conventional image processing methods (such edge detection and texture analysis) are highly efficient at obtaining these low-level characteristics, but they might not work well when applied to vast and intricate datasets.

The study suggested method is novel in that it combines surface and deep data for brain tumor segmentation. Surface data (such as texture, intensity, and local gradients) provide specific and detailed information that can more correctly detect tumor boundaries, while deep learning algorithms extract high-level, abstract features that explain complicated patterns. By combining these two methods, the tumor is more fully and thoroughly represented, leading to more precise segmentation.

The study approach leverages surface characteristics to enhance deep features, in contrast to deep learning models that solely depend on abstract features. Surface features, for instance, aid in the detection of minute histological alterations and the delineation of tumors in MRI images, which are typically overlooked by exclusively deep models. By using a hybrid technique, a model is produced that can both uncover smaller information that are crucial to enhancing the segmentation process and generalize to complex scenarios.

Furthermore, MRI picture intensity heterogeneity is not adequately handled by the majority of deep learning techniques now in use, which results in incorrect tumor boundary detection. These issues are significantly lessened and result in a more reliable and precise segmentation of brain tumors when surface features are integrated.

Manual tumor segmentation from pictures requires a significant amount of processing time and may produce erroneous findings. Automatic segmentation techniques of brain tumors are gaining popularity as a tool for doctors to diagnose and treat tumors, as well as researchers to investigate brain processes. Despite this, segmentation remains difficult due to the brain tumor's variable shape and appearance. The points raised above prompted us to conduct a review of brain tumor segmentation approaches. After reading and analyzing various papers of research on brain tumor segmentation and classification, most strategies take anyone's operation into account (feature extraction, segmentation, classification) to diagnose brain tumors. Segmentation of brain tumors is a really hard function since this includes big data amount for a test. Several factors exist like soft-tissue boundaries, restricted acquisition time, patient movement, and big tumor kinds' number with differing forms and kinds.[8] So, brain tumor segmentation and classification applying MRI images refers to a large research domain. In segmentation, an image is shared in sections given the pixels have the same features. Likely, image classification refers to achieving various info levels processed from MRI images. Normally, doctors and professionals get the infected region from MRI images in hospitals by applying manual segmentation. From previous studies, this is obvious that some algorithms are concentrating on anyone from feature extraction, segmentation, and classification. Most strategies lack the appropriate MRI image pre-processing and suitable feature extraction. The proposed method of this paper for image segmentation is based on the combination of the K-means clustering algorithm with the PSO evolutionary algorithm. The K-means algorithm is ideal for image processing. In the proposed method, PSO is used to find the optimal cluster centers. K-means algorithm outcome depends on the basic solution and has good convergence. The major contributions of the proposed method are listed as below.

1. Integration of deep and shallow features, so that shallow methods extract image features manually and based on previous knowledge from the image with image processing methods. Deep methods extract image features automatically through machine learning and neural networks.
2. In the proposed method for image segmentation, the combination of K-means clustering algorithm with PSO evolutionary algorithm is used.
3. Simulations are conducted to demonstrate the superiority of proposed method over some existing up-to-date works in performance metrics.

Literature review

The various analyses were carried out applying DL methods to automatically segment and diagnose brain tumors. The present part discusses different present brain tumor diagnosis methods in this domain.

Brain tumor segmentation algorithm process given the DL

Over the years, a lot of experts from different backgrounds have worked and are yet working in the image processing field, coping with different cancerous illnesses diagnoses, and classifications such as brain tumors and so on, also they have presented a lot of new ways for creating the best outcomes.

Aggarwal et al.[10] proposed the effective technique for brain Tumor segmentation given the Improved Residual Network (ResNet). Present ResNet could be developed by keeping whole accessible connection links' details through developing projection shortcuts. Such details are fed to later steps, because of what improved ResNet obtains higher precision and could raise the pace of the learning process.

Khairandish et al.[11] performed Hybrid technique, on brain MRI images to diagnose and group tumors. The implemented system uses supervised hybrid CNN and SVM techniques to classify brain pictures as benign and malignant tumors. The fundamental steps of preprocessing have been completed in order to normalize the input images, extract significant features using the Maximally Stable Extremal Regions

(MSER) technique, and segment the images using a threshold-based segmentation method. To group brain MRI pictures, the identified segmented features are fed into hybrid CNN and SVM algorithms.

Shehab et al.[12] proposed the Deep Residual Learning Network (ResNet)-based automated approach for brain tumor segmentation in order to overcome the gradient DNN problem. ResNets outperform their equivalent DNN in terms of accuracy and have the potential to expedite the training process. ResNets add a shortcut skip connection parallel to CNN layers in order to achieve this increase.

Vankdothu and Hameed[13] proposed a new automatic model for classification and diagnosis. The technique that is being given can be categorized into four groups: feature extraction, MRI image preparation, segmentation, and classification. To remove MRI image noise, an adaptive filter is applied during the image preprocessing stage. An enhanced K-means clustering (IKMC) algorithm is used to segment images, and gray level co-occurrence matrix (GLCM) is used to extract features. They used the DL model to classify different types of MRI pictures, such as non-tumors, gliomas, pituitary tumors, and meningiomas, after removing characteristics from the images. Recurrent convolutional neural networks were used to carry out the classification procedure (RCNN).

Chattopadhyay and Maitra[14] proposed the CNN algorithm for segmenting brain cancers from 2D MRIs, which is followed by DL methods and conventional classifiers. In order to properly train the model, writers have acquired a variety of MRI scans with distinct tumor sites, shapes, sizes, and image intensities. They have also cross-checked work using the SVM classifier and additional activation algorithms (softmax, RMSProp, sigmoid, etc.).

Agrawal et al.[15] proposed a functional framework for classifying and segmenting brain tumors using DL techniques. This work employs a 3D-UNet model for volumetric segmentation of MRI images, followed by CNN-based tumor classification. To establish model validity, the loss and precision graphs are displayed.

Raza et al.[16] proposed a hybrid deep learning model called DeepTumorNet that uses the primary CNN architecture to classify three types of brain tumors (BTs): meningioma, pituitary, and glioma. The GoogLeNet architecture model from CNN was used as a foundation. The final five GoogLeNet layers were removed in order to improve the hybrid DeepTumorNet approach, and fifteen new layers were introduced in their place. To increase the expressiveness of the model, authors also employed a leaky ReLU activation function in the feature map.

Ranjbarzadeh et al.[17] proposed a sophisticated and automated brain tumor segmentation system using four MRI sequence pictures, the improved CNN. The Improved Chimp Optimization Algorithm (IChOA) is used to determine the amounts of the whole weight and bias CNN models. To identify multiple possible current tumor fields, the four input images are normalized in the first stage. Next, the Support Vector Machine (SVM) classifier is used using IChOA to select the best features. Finally, the optimal CNN model receives the best-extracted features, which group all objects for brain tumor segmentation. The previously reported IChOA is then used to feature selection and hyperparameter optimization in a CNN model.

Pedada et al.[18] proposed the updated U-Net structure based on residual networks that employ sub-pixel convolution encoding at the decoder section and periodic shuffling at the basic U-Net. Compared to traditional resizing convolution, sub-pixel convolution includes more parameters, which allows for more robust modeling at comparable processing complexity and avoids de-convolution overlaps.

Anand et al.[19] proposed a single 3D encoder-decoder architecture to segment various components of brain tumors. They trained the model using smaller patches and hard mining. A reduced patch size allows us to deploy the model on a smaller GPU. The hard mining stage identifies hard examples during weight training of the loss function. They demonstrated using a fully convolutional neural network for brain tumor segmentation. Overall survival prediction is derived by combining generated segmentation maps with traditional machine learning algorithms.

The paper method builds upon these previous works by combining the strength of CNN architectures while addressing their limitations. Unlike some approaches that suffer from overfitting or require manual feature selection, our approach introduces automated feature extraction with regularization techniques such as dropout and batch normalization to improve generalization. Additionally, our system is designed to be computationally efficient, making it suitable for both 2D and 3D MRI data, without sacrificing accuracy.

The research methodology

The proposed method for classification of brain tumor images includes 4 distinct phases, i.e. image preprocessing, image segmentation, feature extraction, and classification. Each of these phases is described below. In Fig. 1 represents the main steps of the proposed method for classifying brain tumor images.

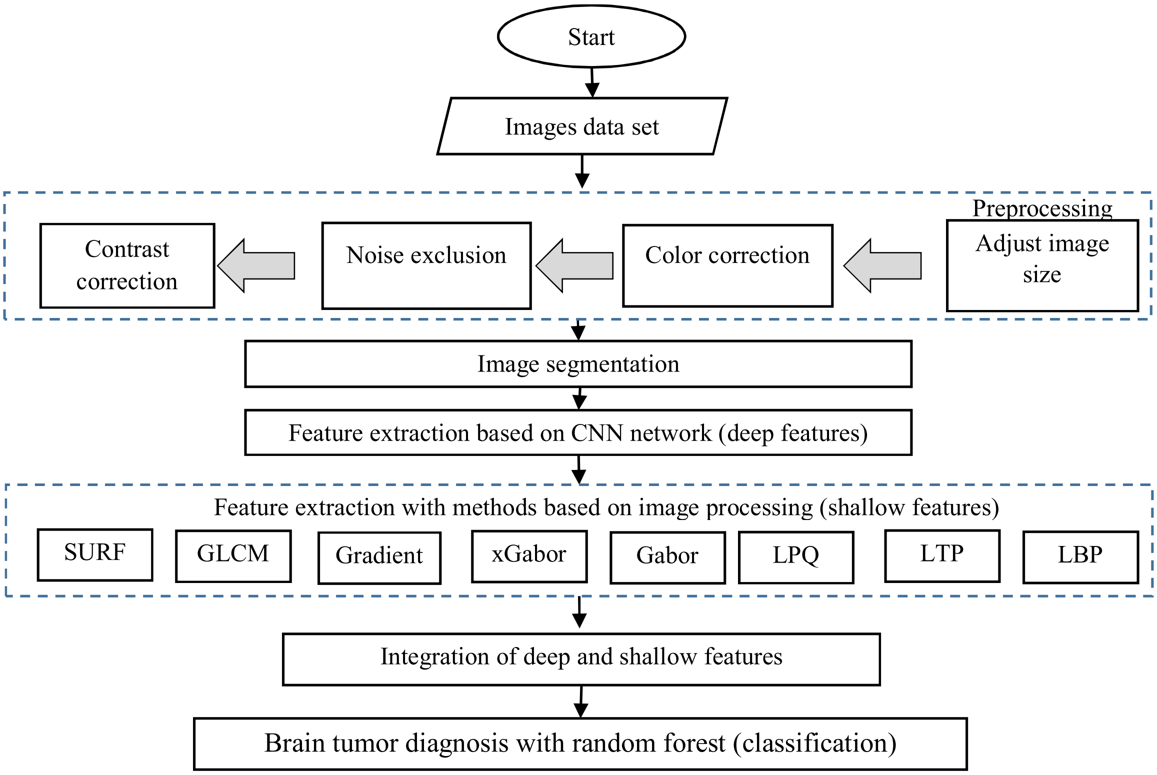

Fig. 1. Flowchart of the main stages of the proposed method.

Pre-processing phase

In brain tumor classification systems, image preprocessing is an essential step that helps get the images ready for further analysis, such as segmentation and classification. Preprocessing in a brain tumor image classification system is equivalent to the process of preparing brain tumor images for segmentation and classification. This process includes the following four steps:

- Adjusting the size of the image: the image should be set to a standard size so that it can be processed by the model.
- Color correction of the image: The color of the image should be corrected so that the colors look accurate and natural.
- Removal of image noise: any noise should be removed to enhance the quality of the image.
- Image contrast correction: Image contrast should be corrected to better reflect image details.

The process consists of multiple steps, all of which are significant to enhance the final results' accuracy and quality: image resizing, which is converting the images to standard dimensions so the machine learning model can process them correctly; this ensures the homogeneity of the images and prevents deviations caused by the different dimensions of the images; and image color correction, which is adjusting the colors of the images to make them appear more realistically and accurately. By enhancing visual perception and making it easier to discern important picture elements like tumor-containing areas from healthy tissues, color correcting helps. The next step is to remove the noise. The devices employed or the conditions of the image recording could be to blame for the sounds in the photos, which could interfere with the analysis of the images. The clarity and quality of the photographs are improved, and a more precise assessment is achieved, by eliminating noise. The last phase, image contrast correction, seeks to improve the contrast of images so that details may be seen more clearly. This aids in the model's ability to distinguish minute variations between various picture elements, such as the boundaries of a tumor and its surrounding tissues. Improved contrast makes it easier to identify important image elements for the model and improves the final results' accuracy.

Image pre-processing as a critical step ensures the correct evaluation of the images and the presentation of accurate results. Below are some of the advantages of image preprocessing:

- Strengthening the accuracy of the evaluation results: pre-processing of the images helps to improve the accuracy of the results. This is because pre-processing images helps to remove noise, correct color and improve contrast.
- Creating uniform images: pre-processing images helps to create uniform images. This because pre-processing images help in resizing, color correcting, and de-noising images.
- Reduction of evaluation time: Preprocessing of images helps to reduce evaluation time. This because image preprocessing helps prepare images and reduces the need for human evaluation of images.

In summary, image preprocessing is a critical step in the classification of brain tumor images. This process, ensures the correct evaluation of the images and the presentation of accurate results.

Image segmentation phase

Segmentation involves labeling pixels in medical images that divide the image into distinct segments. Each of these segments has uniform lighting levels. Observing tissues in medical imaging requires accurate detection of tissue boundaries. In addition, the segmentation of MRI images has many applications, such as identifying the anatomy of tissues, planning a doctor for surgery, discovering abnormal tissues such as tumors and wounds, examining the progress of diseases, diagnosing brain swelling, etc.[20] Identification and classification of brain tumors in MRI images are very important in medical diagnosis. This is because its accurate segmentation is critical for finding tumors, swelling, and dead tissue. For this reason, doctors must have an accurate automated computer system to provide this information. During brain surgery, access to such facilities is necessary to diagnose brain tumors. MRI images are used to detect and segment the tumor area using very accurate and fully automated methods.[21] Brain tumor segmentation methods can be classified into three classes based on the amount of human interaction required,[22] including manual segmentation, semi-automatic segmentation, and automatic segmentation.

In manual segmentation, human experts (trainees, radiologists, anatomists) apply not only the info presented in an image but also extra knowledge like anatomy. Manual brain tumor segmentation is sometimes accomplished on a single image with enhancement presented by an injected contrast agent. In semi-automatic segmentation, human operator intervention is needed. Mainly, actual communication between the user and computer is identified via input and output devices monitored by the user interface. In fully automated methods, computers perform tumor segmentation without human intervention. The fully automatic method combines human intelligence and previous knowledge in an algorithm. Automated segmentation requires a model to describe the size, shape, location, and appearance of the tumor, as well as provide a platform for applying the expected changes to these features.

There are two ways of automatic segmentation including supervised and unsupervised segmentation. In unsupervised segmentation, like when an image data is not labeled, an image is segmented applying clustering algorithms. No human help is presented. No labels exist for each training data subset. The full pixel vector set is presented in cluster analysis model shape and clusters are algorithmically identified. In supervised segmentation, an operator assigns texture numbers in the image given the image data. In supervised segmentation, appropriate training data choice is essential. It is due to that various training sets could cause big disparities in training time and potential differences in segmentation outcomes. Unsupervised techniques do not apply manually labeled training data. additionally, in unsupervised segmentation, the levels' number is automatically assigned by the algorithm. Such an algorithm recognizes clusters in the same numerical pixel shape.

The proposed method of this study for image segmentation is based on the combination of the K-means clustering algorithm with the PSO evolutionary algorithm. The K-means algorithm is ideal for signal and image processing. The reason is that the selection conditions provide the exact number of clusters needed for the segmentation of brain components. For this reason, three distinct clusters were defined as follows: the first cluster for the black background of the image with cerebrospinal fluid, the second cluster for the white matter, and the third cluster for the gray matter. In the proposed method, PSO is used to find the optimal cluster centers. K-means algorithm outcome depends on the basic solution and has good convergence. In this way, the PSO algorithm was applied to search for a solution. However, the achieved solutions are developed in every generation by one K-means algorithm iteration. PSO algorithm fitness function applied in the presented technique is the Otsu variable. Such a variable is applied to find the optimal threshold amounts given the image histogram. Otsu's technique is repeatedly applied for image segmentation.

One of the disadvantages of most clustering methods is the convergence of clustering to the local optimum. In other words, when the clustering algorithm minimizes the objective function, it stops at the local value of the objective function and does not achieve the optimal clustering result. Another problem of clustering algorithms is that the algorithm gets stuck between two types of clustering in the successive loops of the clustering procedure. Under these conditions, the algorithm is stuck in the reduction loop of the objective function and cannot achieve the optimal value. Clustering in a d-dimensional Euclidean space is equivalent to the segmentation process of an image with n pixels (points) into k pieces based on the similarity criterion. The i^{th} point is defined by the numerical value of the pixel.

If $D = (d_1, d_2, \ldots, d_n)$ is an image with n pixels, the objective of a clustering algorithm is to determine a partition $D = D_1 \cup D_2 \cup \cdots \cup D_k$. Each partition D_i corresponds to a cluster center c_i. Also, the set of cluster centers is defined as $C = (c_1, c_2, \ldots, c_k)$. Each pixel d_i is assigned to the closest cluster center. To find k cluster centers, the problem is defined in the form of minimization of an objective function based on image pixels and cluster centers. A popular function used to quantify segmentation goodness is the sum of intra-cluster distances as Eq. (1):

$$f(D, C) = \sum_{i=1}^{n} \min_{J=1,2,\ldots,K} D_*(d_i, c_i) \tag{1}$$

where $D_*(d_i, c_j)$ is the distance between two pixels of the image. The clustering problem tries to find optimal quality clusters (in the presence of many possible solutions).

The number of possible solutions is equal to the STIRLING number of the second type in Eq. (2):

$$\frac{1}{K!} \sum_{I=1}^{K} (-1)^{K-1} \binom{K}{i} i^N \tag{2}$$

The above relation proves that clustering is an NP-hard problem.

To solve this problem and reduce the time complexity, heuristic algorithms are used to find a good (not necessarily optimal) solution. The PSO algorithm was used in this study. In evolutionary algorithms such as PSO, the relationship between the algorithm and the objective problem, how to code and represent the solutions, and the fitness function should be investigated. In the process of clustering images for segmentation based on the particle swarm algorithm, the solution space is equal to the gray spectrum of the image, which must be mapped to the PSO understandable space. For this purpose, the centers of clusters as points in the search space was considered. In the proposed method, clustering brain MRI images with a gray spectrum of 0 to 255 in three clusters were investigated. The first cluster is considered for the black background of the image with cerebrospinal fluid. The second and third clusters are included for white matter and gray matter mapping, respectively. Therefore, a point of the search space is a 1×3 matrix with real values from 0 to 255. Each row of the matrix displays the value of a cluster center. In general, each particle in the PSO search space has n×m dimensions (variables). Also, m is the number of clusters and n is the number of data features. The variable n in the segmentation of gray and color images is equal to 1 and 3, respectively.

Evaluation of a point in the search space means calculating the value of the sum of squared error E for the coordinates of the cluster centers for all clusters as shown in Eq. (3):

$$E = \sum_{i=1}^{k} \sum_{y_j \in C_i} \left\| y_j - \omega_i \right\| \tag{3}$$

where k is the number of clusters, ω_i represents the center of the i^{th} cluster, y_j is the member of the i^{th} cluster. $\|y_i - \omega_i\|$ is the Euclidean distance between the cluster member and the cluster center obtained from Eq. (4):

$$\left\| y_j - \omega_i \right\| = \sqrt{(y_{j1} - \omega_{i1})^2 + (y_{j2} - \omega_{i2})^2 + \cdots + (y_{jn} - \omega_{in})^2} \tag{4}$$

where n is the number of data features. y_{jm} is the m^{th} feature belonging to the y_j cluster and ω_{im} is the m^{th} feature from the center of the i^{th} cluster. The membership of a data y_i in the i^{th} cluster is determined based on Eq. (5):

$$\left\| y_j - \omega_i \right\| \leq \left\| y_j - \omega_r \right\|, r = 1, 2, \ldots, k \tag{5}$$

This means that y_i has the smallest distance from the center of cluster ω_i compared to other clusters. The fitness function of the PSO algorithm is equal to the sum of squared errors E. In addition, the segments obtained by clustering using the Otsu algorithm should also be evaluated. For this, the minimum and maximum values of the gray spectrum are determined in each cluster. Subsequently, the threshold limit of each cluster or segment is obtained. Then these thresholds are fed to the Otsu algorithm and the segmentation quality is measured and optimized as a fitness function by PSO. The selected parameters for PSO and K-means algorithms are shown in Table 1.

Table 1. The parameters chosen for PSO and K-means algorithms.

Parameters	Values
Num-particle	100
Maxiter	50
Initial starting location	[0, 100, 200]
Input bounds	[(0, 255), (0, 255), (0, 255)]
N-cluster	3

Num_particles are the number of particles in PSO algorithm and the maximum iteration of the algorithm is equal to 50. N_clusters are the number of clusters in K-means algorithm. Initial experiments should be used to alter parameters like the particle count. These tests could involve running the model with varying particle counts (50, 100, or 150, for example) and noticing how these modifications affect the model's functionality. The ultimate decision might be based on how well accuracy, execution time, and outcome stability are balanced. These values Table 1 are obtained based on many experiments.

Feature extraction phase

Feature extraction in the segmentation of brain tumor images is equal to the process of converting an image into a set of numerical features. This process can be used to classify brain tumor images. Features can be visual features such as color, contrast, sharpness, and detail, or semantic features such as the object in the image. Feature extraction is one of the critical steps in the proposed method for classifying brain tumor images. This process needs the most information from the images to get a deep insight into the image and to reach the appropriate result in the regression. The number of features can reach hundreds, thousands to millions of items. There are various parameters for extracting these features such as shape, edge, color, texture, local, global, statistical, etc. However, feature extraction is completely application-dependent. In the proposed method, a combination of different feature extraction methods is used. In general, feature extraction methods are categorized into two classes as follows.

- Methods based on image processing (shallow features)
- Methods based on deep learning (deep features)

Shallow and deep feature extraction methods in image processing are two different approaches to extracting image features. Shallow methods extract image features manually based on their prior knowledge. Deep methods extract image features automatically through machine learning and neural networks. Features based on image processing methods (shallow features) include the following.

Shallow features

- **Local binary patterns**

This method was introduced in 2002 by Ojala[23] as a powerful descriptor for texture classification. The LBP method was defined as a fixed operator with a gray scale for local contrast measurement for texture analysis. The LBP operator labels gray-scale image pixels in a 3×3 neighborhood with a threshold of eight central pixels. Mathematically, the LBP operator for a pixel x_c is defined by the following Eq. (6):

$$LBP\left(x_c\right) = \sum_{p=0}^{P-1} \emptyset\left(I\left(x_p\right) - I\left(x_c\right)\right) \times 2^p \tag{6}$$

where $I(x_c)$ is the value of the central pixel, $I(x_p)$ is the value of its neighbors, P is the number of neighbors and $\emptyset(.)$ is the Heaviside step function. This function is a discontinuous and multi-objective function whose value is equal to one and zero for negative and non-negative numbers, respectively. The formula and shape of this function are shown in Eq. (7):

$$\emptyset\left(z\right) = \begin{cases} 1 & if\ z \geq 0 \\ 0 & if\ z < 0 \end{cases} \tag{7}$$

- **Local ternary patterns**

Tan and Triggs[24] introduced and designed a more advanced type of LBP as local triple patterns (LTP). This method is more resistant to noise than LBP. Similar to LBP, it uses a 3 × 3 neighborhood phase for coding. However, to encode the image, it uses a ternary threshold function instead of a step function. LTP relation and ternary threshold function are represented in Eqs. (8) and (9) respectively.

$$LTP\left(x_c\right) = \sum_{p=0}^{P-1} \mathcal{V}_T\left(I\left(x_c\right) - I\left(x_p\right)\right) \times 2^p \tag{8}$$

where T in $\mathcal{V}_T$ is the threshold value and $\mathcal{V}_T$ is the ternary threshold function defined as Eq. (9):

$$\mathcal{V}_T\left(a, b\right) = \begin{cases} 1 & if\ a \geq b + T \\ 0 & if\ b - T \leq a \leq b + T \\ -1 & otherwise \end{cases} \tag{9}$$

Also, to simplify the ternary function process, another function was introduced for LTP based on extracting two binary patterns and dividing them into positive and negative parts.

- **Local phase quantization method**

The local phase quantization (LPQ) method was introduced in 2008.[25] This operator is based on the quantization feature using the Fourier spectrum. The LPQ method uses the estimated information phase in M×M local neighborhood for each pixel with position x of image f. The local spectrum uses a discrete Fourier transform based on two or more dimensions and is defined as Eq. (10):

$$F(u,x) = \sum_{y\in N_x} f(x-y)\; e^{-j2\pi u^T y} = W_u^T f_x \tag{10}$$

where W_u^T is the basis vector of two-dimensional DFT with frequency u, f_x is an M×M vector containing neighborhoods for pixel x. The local Fourier coefficient is calculated on four different frequency points, including $u_1 = [a, 0]^T$, $u_2 = [0, a]^T$, $u_3 = [a, a]^T$ and $u_4 = [a, -a]^T$. Also, a is a fractional numerical frequency. The vector of each pixel is positioned as Eq. (11).

$$F(u,x) = [F(u_1,x), F(u_2,x),\ F(u_3,x),\ F(u_4,x)] \tag{11}$$

The information phase in the Fourier coefficient is calculated by the following Eqs. (12) and (13).

$$q_j = \begin{cases} 1, & if\ g_j \geq 0 \\ 0, & otherwise \end{cases} \tag{12}$$

where g_j is the jth component of the vector G(.):

$$G(X) = \ [Re\{F(x)\},\ Im\{F(X)\}] \tag{13}$$

- **Gabor filter**

Gabor filter[26] is a powerful tool to find the difference between images and has many applications in various research. Gabor filter can extract information from image texture in different scales. The Gabor filter used in image recognition is a linear filter whose response is a modulated sine with a Gaussian function (Gabor wavelet). This filter is realized by the combination of two-dimensional Gaussian functions. The Eq. (14) is used to apply the Gabor filter.

$$g(x,y,\theta,\phi) = e^{\frac{-(x+y)}{\sigma^2}} \times e^{2\pi\phi i(x\ \cos\ \theta\ +\ y\ \sin\ \theta)} \tag{14}$$

where σ, θ, and ϕ are standard deviation, spatial frequency, and rotation, respectively. Assuming that I(x,y) represents the image, the filter with the handwriting image in the feature extraction procedure is calculated as Eq. (15):

$$G(x,y,\theta,\phi) = \iint I(p,q)\ g(x-p,\ y-q,\theta,\phi)\ dp\ dq \tag{15}$$

Finally, the feature vector F_i is defined as Eq. (16).

$$F_i = \sum_x \sum_y \left| G\left(x, y, \frac{\pi.i}{n}, m\right)\right| \tag{16}$$

where i is the feature index, n is the number of angles and variables between 0 and 180 degrees.

- **xGabor filter**

This filter,[26] is a modified version of the Gabor filter providing distinct curves. Therefore, it performs better than the Gabor filter. The relation of this filter is presented in Eq. (17):

$$xg(x,y,\phi,r_x,\ r_y) = e^{\frac{-(x^2+y^2)}{\sigma^2}} \times \ sin\left(\phi.\ \frac{r_x.x^2 + r_y.\ y^2}{r_x +\ r_y}\right) \tag{17}$$

Where $r_x,\ r_y$ are the horizontal and vertical radii of the ellipse. ϕ represents the spatial frequency. To extract features by Gabor filter x, Eq. (18) is used.

$$XG(x,y,\phi,r_x,\ r_y) = \iint I(p,q) \times\ xg(x-p,\ y-q,\phi,r_x,\ r_y)\ dp\ dq \tag{18}$$

Also, the features are evaluated as Eq. (19):

$$F_i = \sum_x \sum_y |XG(x,y,\phi,r_x,r_y)| \tag{19}$$

- **Gradient feature**

Another feature extraction method is to use the gradient feature.[26,27] The Sobel filter filters an image vertically and horizontally by calculating this feature. Then the direction histogram of pixels in 24 cells containing the value is identified as a feature vector. Therefore, 24 final images are extracted from this filter. The direction is calculated by the Eq. (20):

$$direction = tan^{-1}\left(\frac{dy}{dx}\right) \tag{20}$$

- **Gray level co-occurrence matrix (GLCM)**

The co-occurrence matrix (GLCM) is a two-dimensional matrix that measures the probability of each pair of gray levels occurring in a certain distance and direction. GLCMs are powerful tools for texture analysis in images and can be used to extract various texture features.

- **Speeded Up Robust Features (SURF)**

This technique is a feature extraction method designed to identify local features in images. The SURF technique is based on the features of SIFT and is faster and more robust than SIFT. Scale inhomogeneous feature transform (SIFT) is a feature extraction method to identify local features in images. The SIFT technique detects features that are resistant to scaling, orientation, and lighting changes. SIFT uses three steps to identify features as follows.

1. Feature detection: This step uses a har filter to identify local features in the image. This feature highlights images and is resistant to scaling, orientation, and lighting.
2. Feature Description: This step uses a descriptor vector to describe the detected features. This feature vector has 128 dimensions that store information about the orientation and size of the feature.
3. Feature Selection: This step uses a feature selection algorithm to select important features from the identified features. This algorithm determines geometrically distinct features and provides a lot of information about the image.

SURF uses two distinct steps to identify features as follows.

Feature detection: This step uses a wavelet filter feature to identify local features in the image. These features highlight images and are resident for scaling, orientation, and lightning.

Feature description: This step uses a descriptor vector to describe the detected features. This feature vector has 128 dimensions that store information about the orientation and size of the feature.

Deep features

CNN has been applied in feature extraction techniques given DL (deep features). CNN refers to one of the essential DL techniques that robustly train countless layers. This very effective technique refers to one of the most common techniques in different computer vision applications.[28]

CNN networks were first introduced in 1970. Its first application was realized in 1998.[29] CNNs are like artificial neural networks. Indeed, artificial neural networks form the CNN network foundation. Such networks' kinds include neurons with learnable and adjustable weights and biases. Every neuron receives several inputs. After that computed weights' product in inputs. At last, by applying a function of transformation/nonlinear activation, this provides an outcome. The whole network presents a differentiable score function. The raw input image pixels and related group scores are located on both function sides. In the last layer, the fully connected layer, a cost function such as Soft max is embedded.

In the convolutional neural network, two steps are used for training, including the feedforward step and the backpropagation step. In the feedforward stage, input image/data is fed to the network. The convolution operation is done in every layer, such as product multiplication among every neuron input and the parameters, layer result is computed. To do so, the network result is compared to the proper answer by applying the error function, and the amount is assigned. Based on the calculated error rate, the operation of the post-propagation stage starts in the next stage. In this step, whole parameters are modified based on the effect used on an error made in a network. After updating parameters in a network, the feedforward stage begins again. Such a process goes on till network training is completed.

Basic CNN architecture includes three various layers' kinds, such as the fully connected layer,[30] the convolutional layer, and the pooling layer as below.

Convolution layer

The main block in CNN networks is the convolution layer. This layer performs most of the calculations and leads to the extraction of useful features from the input image. The operations performed in this layer are as follows. First, a filter with a certain size is defined. This filter is then applied to the input data matrix. The numbers in this filter are multiplied as weights in each of the rows. The sum of the values obtained from the multiplication operation is considered as the final output of the filter. In this way, a matrix with smaller dimensions is produced.[31,32]

Pooling layer

After the convolution layer, a pooling layer is usually inserted. This layer, known as the sub-sampling layer, is used to reduce the output of convolution neural networks. The pooling layer includes various functions such as Max Pooling and Average Pooling. The filter based on Max Pooling selects the highest value in the selected part of the filter. With the average function, the filter averages all values in the selected range. Like convolutional layers, adding layers is invariant (stable) to the change of location due to considering neighboring pixels in their calculations.[31,32]

Fully-connected layer

This layer is used for data classification and it has an input layer, a hidden layer, and, an output layer. The output of this layer is considered as a classification system result.[32,33] This layer usually uses the Softmax layer. A Softmax layer is used to map the information of the previous layer to an output. The Soft max function has a value between 0 and 1 determining the probability of assigning classified data to a specific label. Finally, the label with the highest value is considered the final label of the data.[34] In most cases, the soft-max function is used as Eq. (21).

$$f_i(x) = \frac{e^{x_i}}{\sum k^{e^{x_k}}} \tag{21}$$

Where x_i is the input value, k is the number of kernels and x is the rank vector. Also, f_i is the ith element of the output function f.

An architecture for feature extraction with CNN and initializing its parameters was developed parameters to evaluate the quality of images. The number of layers can produce better results. However, it cannot be said with certainty that more layers lead to better results. On the other hand, increasing the number of layers leads to an increase in calculations and operation time. As a result, after examining different architectures based on the trial and error method, an architecture with a specific number of layers will be presented to extract features of brain tumor images.

Integration of deep and shallow features phase

This approach uses a combination of shallow and deep features to integrate features. Put otherwise, this model first extracts several properties from MRI scans and then combines these features to use them for categorization. There's a combination of two kinds of deep and shallow features. Deep features are extracted using a convolutional neural network (CNN) model from a matrix containing shallow data. Dropout, Max Pooling, and Convolution layers are present in this model. Lastly, completely connected layers are created by flattening and entering the features extracted from the images. Deep and shallow features are given either in sequence or in parallel to the final classification model (which might be a Fully Connected layer or a Random Forest classifier). The model then predicts and classes using these features. This feature fusion combines two distinct worlds: deep features acquired via convolutional neural networks, and shallow features derived from traditional image processing methods. The model can make use of all the information present in the photos thanks to this hybrid technique, which also improves classification accuracy.

Data classification phase

Classification is a machine learning method that divides data into a set of target classes. The purpose of classification is to predict class labels for each data. A classification system is a system that divides data into different classes and can learn the relation between features and classe.[35]

The purpose of this phase is to classify the input data taken from the feature extraction stage. Each of these classes indicates the presence or absence of a brain tumor in the input images. In other words, the classification system identifies the patient's brain tumor based on the features obtained from LBP, LTP, LPQ, Gabor, xGabor, Gradient, GLCM, SURF, and CNN methods. So far, many classification systems have been introduced with different approaches. In most of these methods, a set of input samples belonging to different classes is needed as a training set. Based on the input samples, the classifier learns the process of separating the samples into their corresponding classes. In the proposed method, the features obtained for brain tumor images are fed to a classification model based on random forest as follows.

Random forest is a machine learning-based classification that uses a large number of decision trees. This method shows good resistance to data fluctuations by randomly selecting features and samples from the data set. Random forest first divides a data set into several subsets. It then trains a decision tree for each subset. It then combines the predictions from each decision tree to generate the final prediction.

Results and discussion

a) Simulation results

On Microsoft Windows 10, simulations have been run using Google Colab's Python programming language. The Intel®CoreTM i7-9750H CPU, operating at 2.60 GHz, is used for testing. It is equipped with 16.0 GB of RAM and an 8 GB Nvidia RTX 2070 GPU. The effectiveness of the proposed approach was demonstrated using five assessment measures. The analysis metrics that are employed are accuracy, precision, recall, specificity, and F1-score. The following are the mathematical expressions for entire measures in Eqs. (22) to (26):

$$Accuracy = \frac{TN + TP}{FP + FN + TP + TN} \quad (22)$$

$$\text{Precision} = \frac{TP}{TP + \text{FP}} \times 100 \quad (23)$$

$$Recall = \frac{TP}{TP + FN} \times 100 \quad (24)$$

$$\text{Specificity} = \frac{TP}{TP + \text{FP}} \times 100 \quad (25)$$

$$\text{F1} - \text{score} = 2 \times \frac{\text{Precision} \times Recall}{\text{Precision} + Recall} \times 100 \quad (26)$$

FP, FN, TP, and TN show False Positive, False Negative, True Positive, and True Negative.

Now, the proposed model evaluations are done by applying the BraTS 2020 dataset. Such a dataset is broadly identified for its complexity and relevance to brain tumor segmentation and serves as a powerful benchmark to gauge the performance of the framework. BraTS 2020 challenge set of data[36] includes 166 test multimodal brain MR, 369 training, and 125 validation cases. As shown in Fig. 2, each paper contains four MR images: fluid-attenuated inversion recovery (Flair), T1-weighted (T1), T2-weighted (T2), and post-contrast T1-weighted (T1ce). The overall dimensions of the MR images are 240 × 240 × 155, and the voxel spacing is 1 × 1 × 1mm3. Experts annotated necrotic, enhancing tumor (ET), peritumoral edema (ED), non-enhancing tumor core (NCR/NET), and ED voxel by voxel for each study. Annotations on training articles are normally available; however, for online assessments and the final segmentation competition, annotations for validation and test research are omitted, respectively.

Here, the aforementioned assessment variables were used to show the proposed approach's effectiveness.

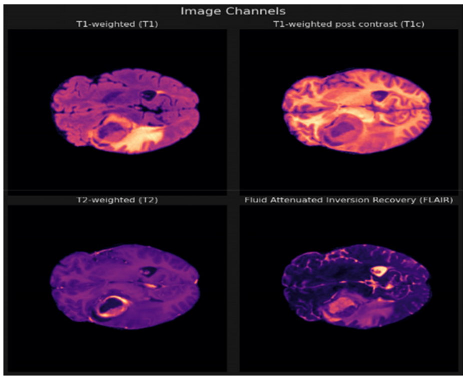

Fig. 2. Brain MRI with image channels.

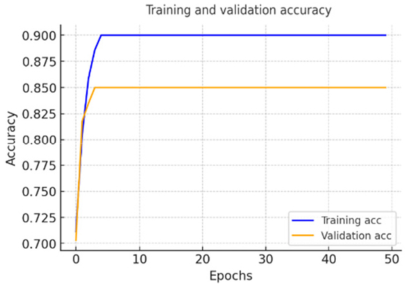

Fig. 3. Accuracy curves for the CNN.

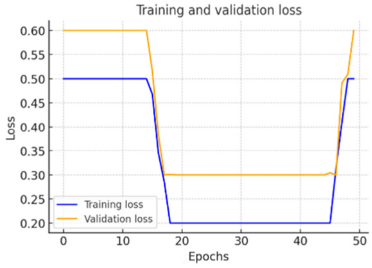

Fig. 4. Loss curves for the CNN.

The proposed model is trained and implemented. The training and testing accuracy curves for CNN are shown in Fig. 3. The training accuracy percentage is 100% at 50 epochs, whereas the testing accuracy percentage is 87.94%. These numbers indicate that, at 50 training epochs, CNN performs better than the testing and training dataset. CNN loss learning curves are displayed in Fig. 4. The rate of loss for testing is 0.066 while the rate of loss for training is 0 at 50 epochs.

In Table 2 shows the brain tumor classification report with specificity, Accuracy, F1-score, recall, and precision assessment metrics for a model of CNN in training and testing data. Here, the weighted Accuracy, recall, precision, specificity, and F1-score averages are respectively 87.94%, 88.25%, 88.35%, 87.61%, and 88.30%. Such amounts mean that the proposed model outperforms the testing and training dataset at 50 training epochs. Such outcomes are estimated from the matrix of confusion which is applied to the proposed model performance evaluation.

The Fig. 5 defines the matrix of confusion assigned given the CNN. Here, diagonal amounts are the accuracy of testing for grouping MRI images. Presented CNN for healthy accuracy is 0.45; the sick accuracy is 0.42. So, respectively classification errors of 0.066 and 0.064 for healthy and sick. These values indicate that the CNN produces fewer classification errors for healthy cases compared to sick cases.

One of the primary methods for assessing the effectiveness of a classification model is the ROC (Receiver

Table 2. Classification report for the proposed model.

Metrics	Accuracy	Recall	Precision	Specificity	F1-score
Values (testing)	87.94	88.25	88.35	87.61	88.30
Values (training)	100	100	100	100	100

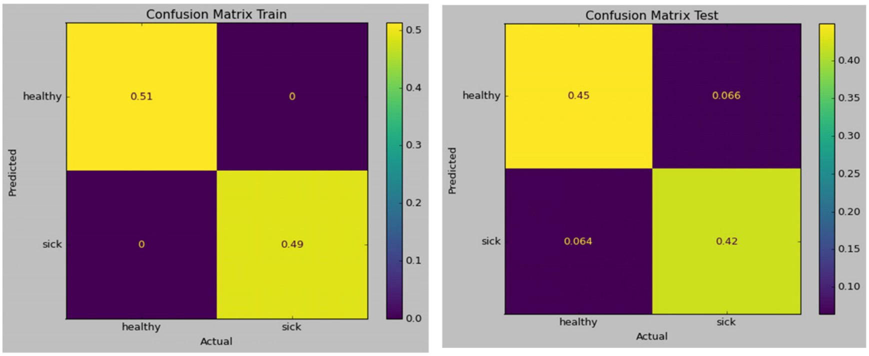

Fig. 5. Confusion matrix for CNN.

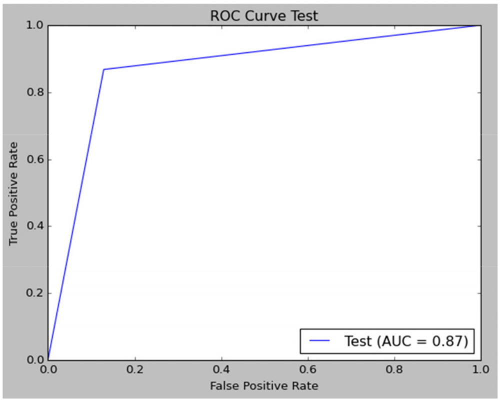

Fig. 6. Curves of the CNN.

Operating Characteristic) curve in Fig. 6, which is especially useful when the classified data comprises two groups (such as healthy and diseased). The True Positive Rate (TPR) and False Positive Rate (FPR) fluctuate at various decision threshold values, as depicted by this curve. The proportion of negative samples that are mistakenly categorized as positive is known as the false positive rate (FPR), and it is represented on the horizontal axis. This is a number that ranges from zero to one; the lower the number, the better the model has done in identifying negative samples. The true positive rate (TPR), or the ratio of correctly categorized positive samples to all positive samples, is represented by the vertical axis. The model's accuracy in identifying positive samples increases with the TPR value. The model's performance is shown by the blue curve in Fig. 6; the closer the curve is to the upper left corner of the curve, the more accurately the model can discriminate between positive and negative classes. Thus, based on TPR and FPR values at various thresholds, the provided model performs exceptionally well in distinguishing between those who are healthy and those who are ill, as indicated by the ROC curve and AUC value. The graph demonstrates how well the model consistently identified positive samples and greatly reduced the error rate (false positives). Fig. 6 shows the ROC curve, where healthy and sick tumor levels' domain are 0.87. The micro-average domain for the ROC curve is 0.87; so, which proves that the presented model obtains high performance given such curves. ROC curve is defined by true positive rate (TPR) to false positive rate (FPR). PR curve is a rate of precision and recall.

Normalized matrices of confusion, the curve of ROC illustrate that appropriate brain tumor patient classification is obtained by applying the presented model. In addition, the presented model had a low loss rate and high accuracy while testing and training. Table 3 defines an accuracy comparison obtained by previously published works[10,19] as well as this work. Here, the presented model obtained a max accuracy of 87.94% which is better than the last models. By combining deep and shallow features, the proposed model can capture both high-level semantic information (from deep layers) and fine-grained details (from shallow layers). This often leads to better segmentation accuracy, especially in complex or small tumor

Table 3. Comparison between previous works and the proposed work.

Reference	Model	Specificity	Recall	Testing accuracy (%)
Aggarwal et al.[10]	ResNet	92.3	73.65	87.9
Anand et al.[19]	CNN	–	–	45.2
Proposed method	CNN	87.61	88.25	87.94

regions, where either type of feature alone might not suffice. This approach can outperform models relying solely on deep features, which might miss fine details, or on shallow features, which might lack contextual understanding.

The limitations of our proposed method are as follows: while integrating deep and shallow features can improve segmentation accuracy by capturing both high-level and fine-grained details, it can also lead to feature redundancy, increased model complexity, and potential overfitting. When deep and shallow characteristics are combined, processing this information may need additional computational power due to the increased number of model parameters. Because the model must process and interpret a greater number of characteristics, this increase in complexity may result in a longer training period for the model. Furthermore, since each layer of the model needs to store and process a different set of information in memory, integrating these features can necessitate additional memory space. Future studies could focus on more effective feature selection or dimensionality reduction techniques to optimize the integration process. Exploring advanced fusion techniques or adaptive integration strategies that dynamically weigh the importance of different features could also be beneficial.

Conclusion

Using a combination of deep and shallow features, this paper presents a novel model that successfully groups two brain tumors from MRI image patients into "healthy" and "sick" groups, achieving a high testing accuracy of 87.94% in the image dataset. The proposed model efficiency is measured by the ROC curve, precision, recall, and F1-score; the Proposed model has a precision of 88.35, a recall of 88.25%, and an F1-score of 88.30%. The average domain under the ROC curve is 88% for healthy and sick levels for the model. Results illustrate that the presented technique could develop brain tumor diagnosis. The integration of deep and shallow features enhances the accuracy of brain tumor segmentation, enabling more precise identification of tumor boundaries. This can help radiologists and oncologists detect tumors at an earlier stage, improving the chances of successful treatment and patient outcomes. The present work was planned to be developed in the future by experimenting with wider sets of data and other tumor types. In conclusion, the offered framework might be performed as an effective system for doctors to provide acceptable medical treatment techniques for brain tumor diagnosis.

Authors' declaration

- Conflicts of Interest: None.
- I hereby confirm that all the figures and tables in the manuscript are mine. Furthermore, any figures and images, that are not mine, have been included with the necessary permission for re-publication, which is attached to the manuscript.
- No animal studies are present in the manuscript.
- No human studies are present in the manuscript.
- Ethical Clearance: The project was approved by the local ethical committee at University of Babylon.

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تجزئة ورم الدماغ على أساس الشبكة العصبية التلافيفية وتكامل السمات العميقة والضحلة

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الملخص

يشير تقسيم أورام المخ إلى واحدة من أكثر المشاكل تحديًا في تحليل الصور الطبية. لإنشاء تحديد دقيق لمنطقة ورم المخ، يتم استخدام تقسيم ورم المخ. يشير استخراج السمات إلى إحدى الخطوات الأساسية في معالجة الصورة التي تساعد في التصنيف. يتم استخراج أنواع مختلفة من السمات من صور التصوير بالرنين المغناطيسي. تحتاج المصنفات التقليدية للتعلم الآلي إلى سمات مصنوعة يدويًا تستغرق وقتًا طويلاً وعرضة للأخطاء التي يرتكبها البشر. في مقابل ذلك، يعد التعلم العميق قويًا جدًا من حيث استخراج السمات وقد تم تطبيقه بالفعل على نطاق واسع لأغراض التصنيف. المقدمة بين استراتيجيات استخراج السمات المتعددة (دمج السمات العميقة والضحلة). وبالتالي، تستخرج الطرق الضحلة سمات الصورة يدويًا وبناءً على المعرفة السابقة من الصورة باستخدام طرق معالجة الصور. تستخدم الأساليب العميقة التعلم الآلي والشبكات العصبية لاستخراج معلومات الصورة تلقائيًا. تعتمد الطريقة المقترحة في هذه الورقة لتجزئة الصور على الجمع بين خوارزمية PSO التطورية وخوارزمية التجميع K-means. لمعالجة الصور، تعمل خوارزمية K-means بشكل مثالي. في التقنية المقدمة، يتم تطبيق PSO لتحديد المراكز المثلى للمجموعة. تعتمد نتيجة خوارزمية K-means على الحل الأساسي ولديها تقارب جيد. في Google Colab، استخدم النموذج المقترح لغة برمجة Python لتشخيص الدقة والحساسية ومصفوفة الخطأ وخاصية تشغيل المستقبل (ROC). توضح النتائج أن النموذج المقدم يتمتع بأداء عالٍ في تشخيص أورام المخ. وهذا يحقق دقة بنسبة 87.94٪ ومتوسط دقة 88.35٪.

الكلمات المفتاحية: تصنيف ورم الدماغ، التعلم العميق، استخرج الصفة، تصنيف الصور، التعلم الآلي، التجزئة.