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ORIGINAL STUDY

Classification of Brain Tumor Using Hybrid Pre-Trained Networks and MRMR Algorithm

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ABSTRACT

Brain tumor classification is one of the crucial uses of medical image processing. A longer life is possible if the tumor is correctly and promptly diagnosed. Because manually segmenting brain tumors for cancer diagnosis is difficult and time-consuming, automatic classification of brain tumor images is necessary for this task. Pre-processing, feature extraction, feature selection, and classification are the four stages of the general framework for automatic tumor detection from MRI images. The method for automatic brain tumor classification described in this research combines machine learning and deep learning algorithms. We used three pre-trained deep networks to extract the most detailed information from MRI images. ResNet, AlexNet, and GoogleNet are the networks that were utilized for feature extraction for the diagnosis of brain tumors, the classification model has been a support vector machine (SVM). Additionally, in this research, the best feature vector was chosen using the MRMR algorithm to improve classification speed and accuracy. The BRATS database is used to provide the training dataset. The BRATS validation dataset showed promising results for the investigated method. This method's complete tumor classification accuracy on experimental data is 99.5% on average in this dataset.

Keywords: Medical data mining, Diabetes disease, Feature ranking, Whale optimization algorithm

1. Introduction

The role of clinical diagnosis in contemporary healthcare has grown. Medical imaging specialists have focused a lot of emphasis on brain cancer because it ranks third among tumors that affect teenagers and young adults [1]. A brain tumor is one of the uncommon cell growths in the brain. Malignant or cancerous cells cause very few tumors; most tumors are benign [2]. Brain tumors classified as primary originate from within the brain. Brain metastases, also known as secondary brain cancer, are cancer cells that have spread to the brain from another part of the body [3]. A brain tumor may cause issues with feeling, speaking, moving, mental changes, vomiting, vision, migraines, seizures, and vomiting [4]. Depending on the location of the tumor and the size of the tumor, these symptoms may differ. Brain tumors are difficult to diagnose since their clinical symptoms vary widely depending on the type, location, size, and pace of growth of the tumor.

To prevent the tumors from progressing to an unmanageable stage, they should be diagnosed as soon

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as feasible. Magnetic Resonance Imaging is the technique used to detect brain malignancies (MRI). MRI is regarded as an advanced technique that offers information on the soft tissue structure of humans. This information is increased to allow for the observation of the region's structure, which aids in producing the detailed images in all directions. When it comes to medical imaging, magnetic resonance imaging (MRI) is utilized to provide a multitude of differences in the body's soft tissues [5]. Brain tumor information can be found in the MRI image [6]. MRI produces a large number of pictures, each of which provides a variety of parameters depending on interior anatomical structures [7]. It is imperative to diagnose brain tumors as soon as possible to prevent potential risks. The magnetic resonance imaging (MRI) method is widely recognized for its exceptional image clarity. The MRI shows a great degree of precision and tumor appearance. Because MRI scanning yields good results, it is used for medical diagnostics [8]. Brain tumors must be segmented in order to further refine the MRI categorization, as an MRI by itself is insufficient for both tumor detection and diagnosis [9]. It takes more time and many human efforts to recognize patterns or texture for classification from highly varied photos, especially if the data is vast [10].

The medical assessment and prognosis for brain tumors can be enhanced by an accurate and timely diagnosis based on magnetic resonance imaging (MRI). Subsequently, the results of the biopsy test determine the tumor's severity and confirm the presence of the disease. Brain tumors are categorized on a scale from grade I to grade IV, according to a report published by the World Health Organization (WHO) and the American Brain Tumor Association (ABTA) [11]. Tumors that are benign and malignant are categorized using this divide. Gliomas are classified as grade IV tumors, while malignant tumors are classified as grade III [12]. Benign tumors are classified as grades I and II. Tumors of grades I and II are low-grade tumors, with sluggish growth. Malignant brain tumors are grade III and IV tumors that grow quickly [13]. Individuals with grade II tumors need to be continuously observed and monitored. Patients are required to undergo magnetic resonance imaging (MRI) scans every six to twelve months in order to track their health. To ascertain the tumor grade level, specialists analyze the radiographic pictures to distinguish between normal and cancerous tissues. The obtained MRI [14] is used to use different feature extraction and classifier techniques to study the tissues, including gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF). To determine the different problems, these tissues need to be segmented using certain processes [15]. Different MRI modalities, such as dead and edematous tumor tissues, necessitate a continual inspection [16]. Since the tumors are found early, appropriate therapy is started to lower risk factors such ionizing radiation exposure, age, gender, exposure to radiation at work and at home, and family history.

Thus, in order to explore picture modalities, the MRI segmentation procedure [16] is utilized in our work. To increase the tumor identification rate, segmentation computes image attributes like texture, color, borders, and contrast information. To detect disease-affected regions with the least amount of computational complexity, image segmentation employs multiple techniques. The active contour method [17] is used in this procedure to address the problems with intensity homogeneity. To identify the brain tumor, a variety of textural and statistical features are retrieved from the segmented regions. Brain cancers can be identified using a variety of classifiers [18], including fuzzy clustering means (FCM), artificial neural networks (ANN), support vector machines (SVM), expectation-maximization (EM), and knowledge-based approaches [19, 20]. Finding the precise tumor location and concealed edge features while minimizing computing complexity is challenging, though [21].

If radiologists are able to accurately identify, segment, and categorize brain tumors in medical pictures, they can reap the benefits of computer-aided diagnosis approaches. However, radiologists believe that the manual method of identifying brain tumors is error-prone and time-consuming. The intricacy of current techniques in pinpointing the precise boundaries and locations of tumors reduces the overall accuracy of recognition. Furthermore, the highest classification error rate is produced by the features' restricted availability. Strength training methods are therefore necessary to enhance feature matching during testing and training [22].

Moreover, MRI-based brain tumor identification suffers from scalability and reliability problems due to the categorization challenge. To solve these issues, we propose a new and efficient method based on hybrid deep neural networks. In this method, a combination of 3 pre-trained deep networks has been used to extract features from MRI images. Then the MRMR algorithm was used to select the feature and finally the SVM algorithm was used to classify the brain tumors from MRI images. This paper's remaining parts are organized as follows: Researchers' contributions to the field of diagnosis of diabetes are covered in Section 2; the proposed method is examined in Section 3; the results are discussed in Section 4; and the study is concluded in Section 5.

2. Related works

Preprocessing, segmentation, feature extraction, and classification are all included in [23, 24]'s work. The RGB image is first given a color makeover as part of pre-processing, and then thresholding and morphological procedures are performed. Highly accurate automatic segmentation is made possible by combining probabilistic fuzzy C-means with probabilistic fuzzy clustering (probabilistic FCM). Information-theoretic metrics, wavelet transform, local directional pattern (LDP), empirical mode decomposition (EMD), and descriptors are used to extract section features. A deep belief network based on whale-cat swarm optimization is used for the final classification. The test using photos from the BRATS database outperformed the currently employed methods with higher accuracy, sensitivity, and specificity of 0.923, 0.95, and 0.96, respectively.

In [25] developed hybrid ensemble classifiers (HEC) to recognize brain cancers from MRIs. Offering answers for the problems related to size, form, volume, and border detection is the aim of this endeavor. To isolate the affected region, the collected MRIs are first subjected to the Otsu threshold. Then, a number of methods are used to extract the features, such as gray level co-occurrence matrix, stationary wavelet transform, and principal component analysis (PCA). The acquired data is subjected to hybrid ensemble techniques (decision tree, k-nearest neighbors, and random forest) in order to determine the tumor region using the majority vote methodology. The hybrid classification strategy requires less computation time than earlier methods.

In [26–28], a comprehensively improved deep learning method for classifying multimodal brain tumors is showcased. The BRATS dataset is used in the analysis. The first steps in the contrast design process include ant colony optimization, histogram equalization of the combined division, and training a new nine-layer CNN model. The properties that are solely associated with the second layer are eliminated and enhanced by the employment of differential evolution and flame. Using the matrix length methodology, the combined output of both approaches is given to the inter support vector machine. The recommended method's accuracy during the trial procedure was 99.06, 98.76, 98.18, and 94.6% for BRATS 2013, BRATS 2015, BRATS 2017, and BRATS 2018, in that order. The superiority of the suggested strategy is demonstrated by comparing the findings with those of alternative methods.

In [29] segmented brain tumors with a 2D-UNET CNN. Reducing major structural deviations and barriers associated with geographic variability is the aim of this approach. The images come from the BraTS 2019 dataset, which is processed by CNNs with advanced knowledge of brain tumor identification. As a result, the newly implemented system achieves a Dice coefficient of 0.9694.

In [30] demonstrated a novel Convolutional Neural Network that accurately classifies brain tumors in MRI images as benign or malignant using transfer learning. The proposed model is evaluated against many industry-standard pre-trained networks, including Res-Net, Alex-Net, U-Net, and VGG-16. The outcomes showed a significant improvement in prediction accuracy, precision, recall, and F1-score, respectively, when compared to the earlier methods. The recommended approach achieved a classification accuracy of 99.30 and 98.40% for benign and malignant cases, respectively, using upgraded Res-Net 50. The proposed approach enhances image fusion quality and may facilitate more accurate diagnosis.

In [31] employed the hybrid weighted fuzzy approach to use an MRI to locate a brain tumor. The images are from the DICOM dataset, which uses a processed fuzzy clustering algorithm to partition the dataset into areas based on the fuzzy membership function. Fuzzification is a technique that groups together related pixels to reduce processing complexity. To classify the affected region, an SVM with 97% accuracy in tumor classification is employed.

In [32] of diagnosing brain cancers using MRI imaging is less time-consuming. The suggested method enhances an image's visual quality by using a simple algorithm. Prior to segmentation, morphological analysis is carried out to eliminate non-tumor regions from the pictures. Segmentation and clustering methods are utilized to identify superior tumor regions. Based on their rankings, a number of deep neural networks extract features from these regions. A hybrid feature vector generated by an adaptive fusion network and multi-class support vector machines is used to classify tumors. By expanding the training set, overfitting is minimized. The method being described is trained and evaluated on a publicly available brain tumor dataset. Compared to previous approaches, the proposed technology enhances the automation and resilience of the entire diagnostic process, enabling the healthcare industry to achieve an approximate 98.98% accuracy rate overall.

Studies by a number of academics claim that different image processing and machine learning methods can identify brain tumors. The current techniques are applied to address computational challenges during MRI pixel investigation. Unfortunately, edge interior features are typically hard to discern, making precise tumor location segmentation more challenging. The misclassification error rate and classification problem are made worse by this issue. In this work, meta-heuristic optimized convolution neural networks are

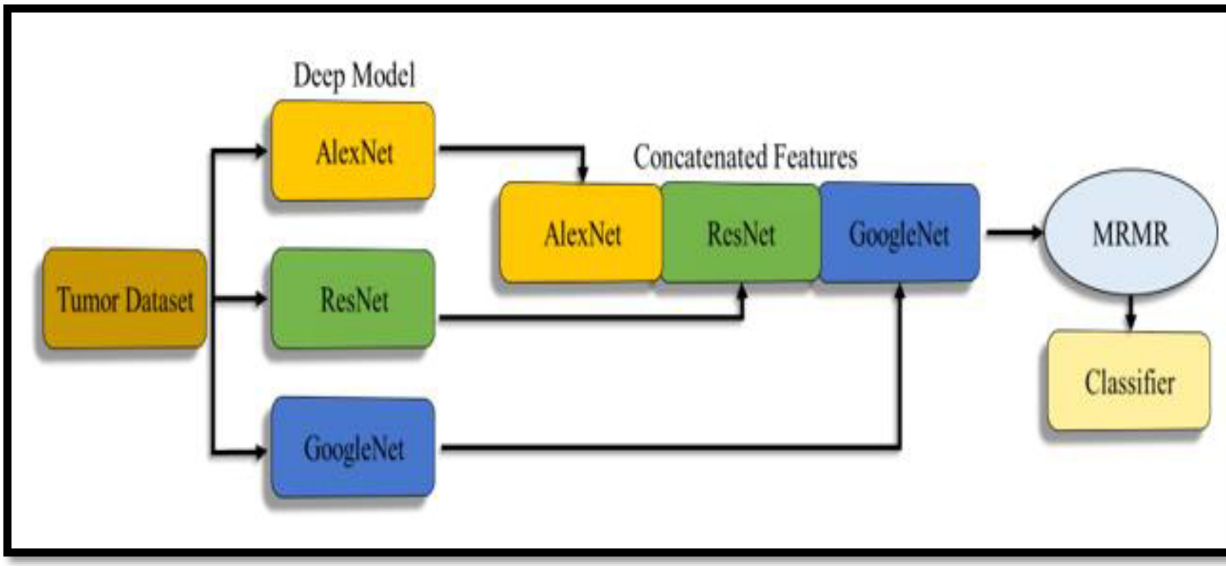

Fig. 1. General diagram of proposed method.

used to address these problems and lessen the challenges associated with brain tumor segmentation.

3. Proposed method

In this section, we will examine the method proposed in this research for the brain tumor classification. In this research, we used the REsNET50, AlexNet, and GoogleNet deep neural networks to classify the brain tumors. Deep neural networks are the best tools for extracting features from MRI images. Then the features extracted from each deep neural network are combined and sent to a classification model. However, due to the improvement of the classification accuracy, the entropy-based MRMR feature selection method has been used to remove the redundant features and thus increase the classification accuracy. Diagram of proposed method is shown in Fig. 1.

3.1. Preprocessing

The first step to brain tumors classification from MRI images is image preprocessing. In fact, this step is to prepare the data for the main steps of a supervised learning method. In this step, training images are first increased with data augmentation techniques and then their quality is improved by image processing methods.

3.2. Feature extraction with pre-trained models

To extract features, we start with pre-trained models and only change the weights of the last layer in these models. Pre-trained models are based on convolutional layers. There are millions of parameters in general convolutional neural networks, and training them requires many labeled training data and a lot of processing resources. But by using a model previously trained on a related task and reusing it in a new application, the transfer learning technique solves many of the challenges of general convolutional networks.

To extract valuable features from new samples, a pre-trained model can be used. To reuse the feature maps already learned for the dataset, a new classifier can simply be placed on top of the pre-trained model and trained completely from scratch.

In this research, we have used three different pre-trained networks named ResNet, AlexNet and GoogleNet for feature extraction. The working method is that we combine the feature vectors extracted from each network and obtain a general and comprehensive feature vector. These three networks are explained in the follow.

3.2.1. ResNet model

For computer vision applications, the Residual Network (ResNet) deep learning model is used. It is a design for a convolutional neural network (CNN) that can support a large number of convolutional layers—possibly thousands. Performance was negatively impacted by the limited number of layers that earlier CNN designs could support. But, when additional layers were added, researchers ran into the “vanishing gradient” problem [33].

The backpropagation approach used to train neural networks reduces the loss function and determines the weights that minimize it by using gradient

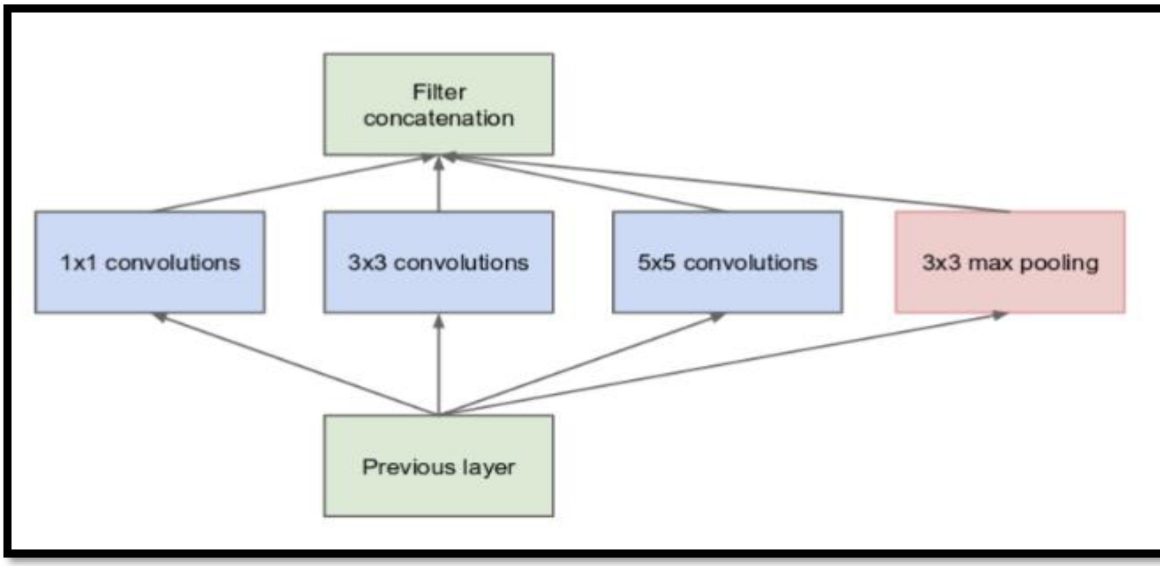

Fig. 2. Simple diagram from GoogleNet.

descent. A gradient will ultimately "disappear" if there are too many levels since performance will plateau or start to degrade with each extra layer.

The ResNet "skip connections" function presents a fresh approach to the vanishing gradient problem. Convolutional layers that are initially inactive (many identity mappings; ResNet) are stacked, skipped, and the activations from the previous layer are recycled. Skipping speeds up the initial training process by reducing the number of layers in the network [33].

When the network has been retrained, with all layers expanded, the leftover parts—referred to as the residual parts—are then free to explore more of the feature space of the input picture. The majority of ResNet models skip two or three layers at once, with batch normalization and nonlinearity in between. HighwayNets, a type of more sophisticated ResNet architecture, can learn "skip weights," which dynamically decide how many layers to skip [33].

3.2.2. AlexNet model

In the AlexNet network, due to the use of two GPUs for processing, all layers are double-layered. In this network, 96 11*11 convolutional filters with 4 steps and padding=0 are applied at first. Its array output is 55*55*96. The number of parameters of each convolutional layer is equal to: layer length * layer width * input depth * number of filters. In the next step, the images are passed through a Maxpool layer with dimensions of 3×3 and step size of 2, and the output is $27 \times 27 \times 96$. The number of learnable parameters in maxpool is zero. In the next step, the images are passed through 256 convolutional filters of 5*5 with step one and padding=2, the output of which is 256*27*27. In the next step, the images are again passed through the Maxpool filter with dimensions of 3×3 and step 2, the output is 96*13*13. In the next three steps, we use convolutional filters with one step and padding. Finally, there are three fully connected layers [34].

3.2.3. GoogleNet model

A deep neural network may experience the issue of overfitting if it is constructed with very deep layers. The GoogleNet architecture, which has filters of various sizes that can function at the same level, was presented as a solution to this issue. The network actually gets bigger with this concept rather than deeper. An illustration of a simple GoogleNet Module is shown in Fig. 2.

The convolution process is carried out on inputs with three different filter sizes: (1×1), (3×3), and (5×5), as can be seen in the diagram above. Convolutions are also subjected to a max-pooling procedure before being transferred to the following inception module [35].

The authors limit the number of input channels by inserting an additional (1×1) convolution before the (3×3) and (5×5) convolutions to lower the dimensionality of the network and speed up computations because neural networks take a long time and money to train [35].

There are a total of 22 levels in the GoogleNet Architecture, including 27 pooling layers. There are nine linearly stacked inception components altogether. The endpoints of the inception modules are linked to the global average pooling layer [35].

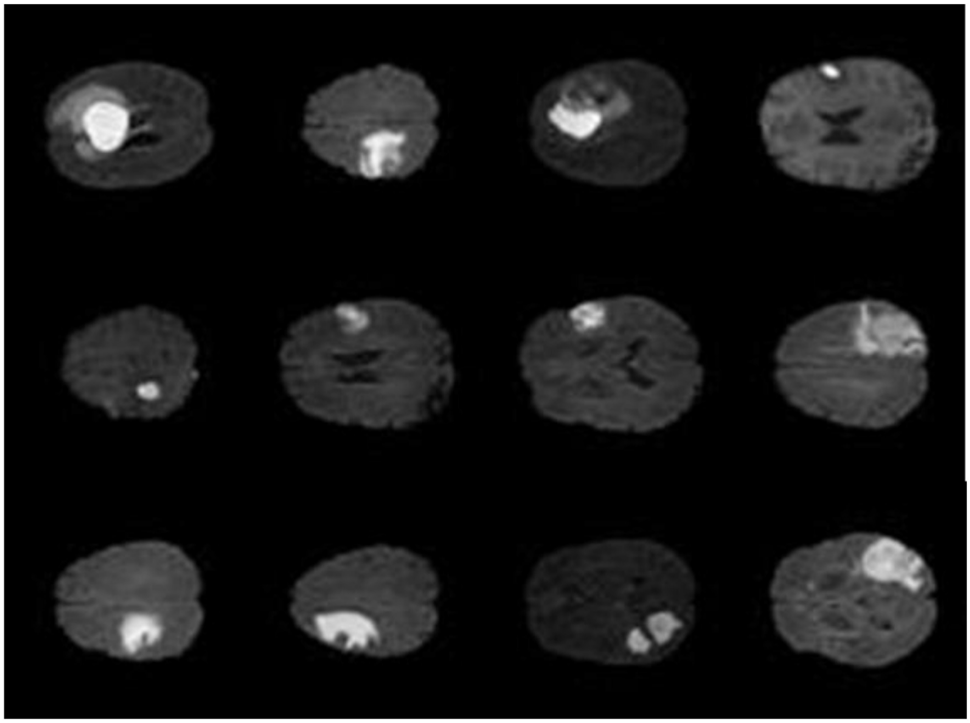

Fig. 3. Example of BRATS database.

3.3. Feature selection with MRMR algorithm

The second basic step in supervised learning methods is the feature selection step. In this step, a vector of the best features extracted in the previous step is selected and sent to the classifier algorithm for classification. The reason for selecting the feature is that it prevents additional computational load in the classifier and increases the accuracy and speed of classification. we adopted a feature selection method based on information theory. The mutual information between features with labels as well as the mutual information between features individually determine how the mRMR algorithm functions [36].

The mRMR takes into account both feature redundancy among the chosen features as well as feature relevance with class label. The following is its formula:

$$J(x_k) = I(x_k; y) - \frac{1}{|S|} \sum_{x_j \in S} I(x_j; x_k) \quad (1)$$

where S is a subset of the chosen features, x_k is the candidate feature, and $J(x_k)$ is the evaluation index. The MIM technique is used to select the initial feature. The greatest $J(x_k)$ feature will then be added to the subset of chosen features in each update [36].

3.4. Classification with SVM algorithm

The last step in supervised learning methods is classification. In this step, a classification algorithm (such as SVM or Naïve Bayesian) is trained based on the input features as well as the labels corresponding to each feature vector. In this work, we have used Support Vector Machine (SVM) algorithm [37] for classification.

Vapnik developed the SVM approach in 1992 as a productive classification method for nonlinear issues [37]. SVM seeks hyperplanes by maximizing the separation between classes.

It can resolve both linear and non-linear problems and is effective for a variety of real-world challenges. The fundamental idea behind the SVM algorithm is to divide the data into classes by drawing a line or a hyperplane.

For both classification and regression, Support Vector Machine (SVM), a supervised machine learning technique, is used. The most appropriate term is categorization, even though we also mention concerns about regression. The SVM method aims to find a hyperplane in an N-dimensional space that clearly classifies the data points.

When there is a measurable margin of class dissociation, support vector machines perform similarly well. Rooms with high dimensions are more effective.

It functions well when the number of dimensions is greater than the number of examples.

4. Results and discussion

The proposed method for classifying brain tumors will be explained, along with the simulation results, in this part. With MATLAB 2022, the suggested methodology in this study was simulated. The database of MRI pictures and the evaluation criteria are completely introduced in the next section. Subsequently, the outcomes of the suggested technique for categorizing brain cancers are showcased based on the assessment standards, and ultimately, the effectiveness of the suggested method in brain tumor classification is assessed in comparison to other methodologies.

4.1. Database

In this research, the BRATS database will be used [38]. 65 MRI pictures from four different modalities are included in the BRATS database. The database's image content is either of high quality or of low quality. 51 high-grade glioma patient photos are produced from 65 total photographs. Four different modalities, including T1, Tlc, T2, and Flair, were used to collect the photos from three separate colleges. For the categorization process in this method, a total of 30 photos of the Flair modality are obtained.

4.2. Evaluation criteria

To evaluate the performance of the proposed method, four criteria of accuracy, precision, recall and F-score have been used. The mathematical relationships of these criteria are presented below.

$$Accuracy = \frac{No.\ of\ recognized\ tumors}{Total\ No.\ of\ tumors} \times 100 \tag{2}$$

$$precision = \frac{TP}{TP + FP} \tag{3}$$

$$recall = \frac{TP}{TP + FP} \tag{4}$$

$$F1score = 2 * \frac{recall * precision}{recall + precision} \tag{5}$$

The aforementioned relationships denote the quantity of true positive diagnoses (TP), false positive diagnosis (FP), true negative diagnoses (TN), and false negative diagnoses (FN) in this context.

4.3. Setting of simulation

As mentioned earlier, in this research, three networks A, B and P have been used to extract features related to brain tumors from MRI images.

These pre-trained networks use Stochastic Gradient Descent as their optimizer and learning rate and momentum parameters are applied to the SGD optimizer. In addition, the loss function in these networks is also AM-Softmax. In the simulations, the scaling parameters of the coefficient (s) are 30 and the margin (m) is 0.4, and the training process is done in 500 rounds.

Also, in this study, we have increased the number of database images to 1340 images by using data augmentation techniques and then 70% of the data (938 images) is considered for training the proposed approach and the remaining 30% (402 images) for testing the proposed method.

4.4. Evaluation of results

In this section, the simulation results of the proposed method are presented in most of the evaluation criteria. The evaluation has been done on the test data and the aim was to distinguish images with tumors from images without tumors. As a result, we are faced with a two-class problem.

The confusion matrix for brain tumor diagnosis is shown in Fig. 4. This matrix, as can be seen, is for a two-class problem where the first class (0) contains MRI images of healthy subjects and the second class (1) contains MRI images of subjects with brain tumors. These results were obtained with experimental data, and the number of images belonging to the first class is 200 and the number of images belonging to the second class is 202. This matrix states that the accuracy in diagnosing healthy people is 99% and the accuracy in diagnosing patients with tumors is 100%. In addition, the last row and column in this matrix shows the overall accuracy of the proposed system, which is equal to 99.5%. It should be noted that this matrix is only for one simulation run.

Fig. 5 shows the simulation results according to all evaluation criteria for the proposed method. The numerical value of each evaluation criterion for classifying people with brain tumor from healthy people is shown in Fig. 5. As it is known, the criterion value of accuracy, precision, recall and F-score is equal to 99.5025, 99.5074, 99.5025, 99.5025 respectively.

Finally, the real and predicted labels for 81 images are shown in Fig. 6. As can be seen, only the label of sample 81 is not recognized correctly by the proposed method.

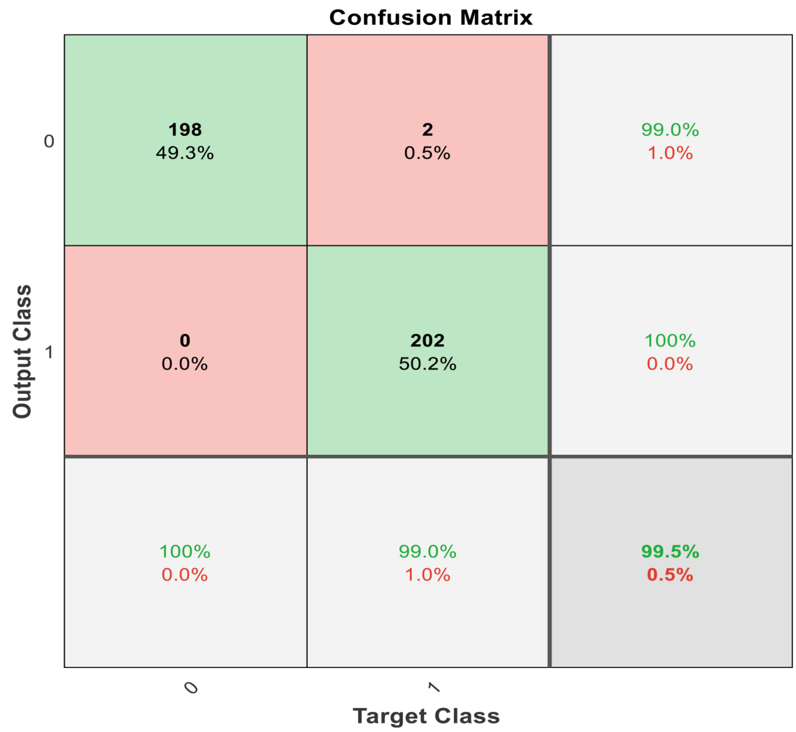

Fig. 4. Confusion matrix of proposed method.

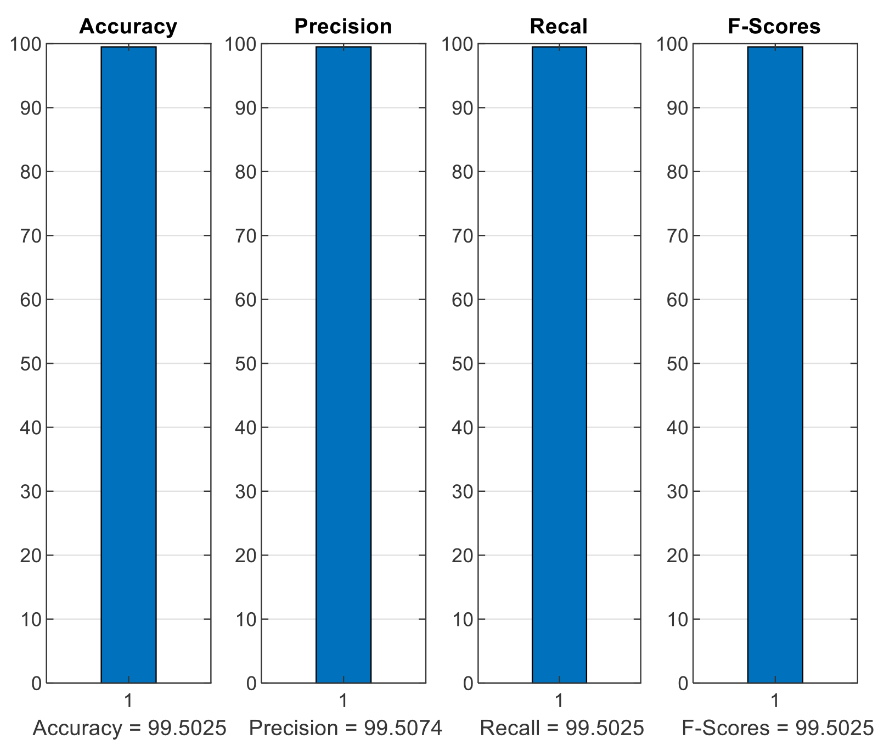

Fig. 5. Numeric results of evaluation criteria for proposed method.

5. Comparison results

Table 1 presents a comparison between the proposed approach and other methods based on the categorization accuracy values. Compared to other approaches reported in other studies, the suggested method is more accurate in diagnosing brain tumors. It should be mentioned that the suggested method's accuracy value was determined by averaging the outcomes of 20 simulation experiments.

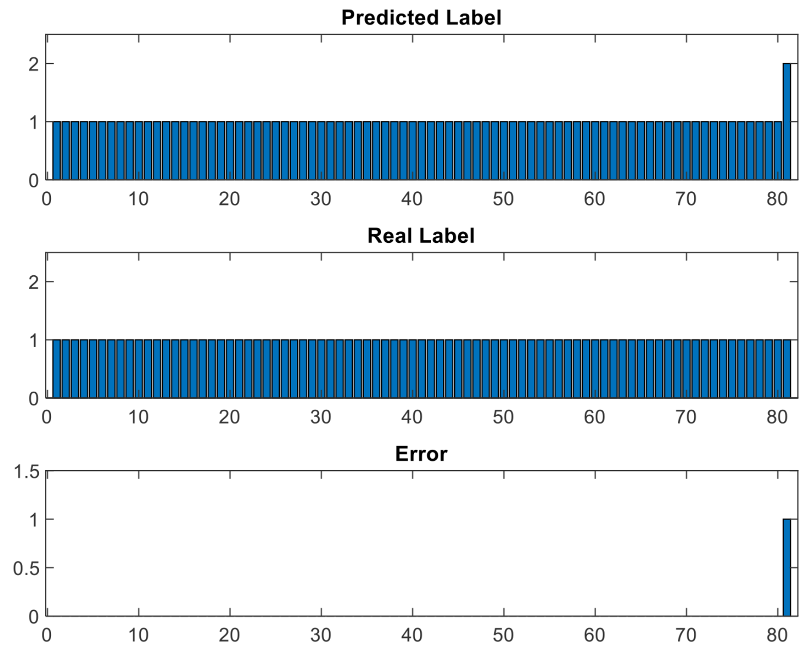

Fig. 6. Comparison of real and detected labels for 80 samples.

Table 1. Comparison of the proposed method with other methods in brain tumor diagnosis.

Method	Accuracy (%)
Fuzzy clustering [31]	97
Optimized CNN [26]	98.70
New CNN model + ACO [28]	98.18
ResNet model [30]	99.3
Proposed method (Pre-train networks + MRMR+ SVM)	99.5

The reason for the superiority of our proposed method in this research for detecting brain tumors is the extraction and selection of the best features and the use of the SVM classifier separately. In the methods of the most other research, convolutional neural networks perform both feature extraction and feature classification by several fully connected layers. But in this work, we finally give the best features to the SVM algorithm for classification, which is one of the best classification algorithms and can classify features with high accuracy.

6. Conclusion

This study's approach, which combines machine learning and deep learning algorithms, offers an automated way to diagnose brain cancers. Three deep networks that have been trained beforehand have been utilized to extract the most comprehensive information from MRI pictures. The deep networks utilized for feature extraction are ResNet, AlexNet, and GoogleNet. Then, to increase the classification accuracy and speed, the optimal feature vector is chosen by the MRMR technique. Lastly, the best features have been classified and brain cancers have been diagnosed using the support vector machine method. The performance of the suggested strategy was assessed in this study using the BRATS database, whose image count was augmented by data augmentation techniques. The entire tumor classification using this method in the provided dataset has an average accuracy of 99.5%, according to the simulation results.

Data and code availability statement

Not applicable.

Conflict of interest

The authors declare no conflict of interest.

Supplementary information

The datasets used and/or analyzed during the current study available from the corresponding author on reasonable request.

Ethical approval

Not Applicable.

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