

## PAPER

# A Novel Technique for Brain Tumor Detection and Classification Using T1-Weighted MR Image

Hanumanthappa S. (✉),  
Guruprakash C. D.

Sri Siddhartha Academy of  
Higher Education, Tumkur,  
Karnataka, India

[hanukit@gmail.com](mailto:hanukit@gmail.com)

## ABSTRACT

Brain tumors are particularly perilous because they form when cells in the brain multiply uncontrollably within the skull. Therefore, a fast and accurate method of diagnosing tumors is crucial for the patient's health. This study proposes a method for evaluating brain cancer images. The phases of implementation for the proposed work are as follows: In the first phase, we compiled a set of specialized feature vector descriptions for advanced classification tasks by employing both deep learning (DL) and conventional feature extraction techniques. In the second phase, we employ a proposed convolutional neural network (CNN) approach and a traditional subset of features from a genetic algorithm (GA) to select our deep features. The third phase involves using the fusion method to merge the prioritized features. Finally, determine whether the brain image is normal or abnormal. The results showed that the proposed method successfully classified objects accurately and revealed their robustness across different ages and acquisition protocols. According to the results, the classification accuracy of the support vector machines (SVM) classifier has significantly improved by combining conventional features and deep learning features (DLF), achieving an accuracy of up to 86.50% using the T1 weighted brain MR image.

## KEYWORDS

classification, conventional features, deep features, fusion features, genetic algorithm (GA)

## 1 INTRODUCTION

The brain is a vital organ that regulates all body processes and is an integral component of the neurological system. A brain tumor is one of the most dangerous diseases that can affect the brain and is caused by an unexpected increase in cell proliferation within the brain. In the event of prolonged neglect, treatment may become necessary. These tumors can result in severe brain malfunction and damage, which can be fatal. The World Health Organization (WHO) has predicted a five percent annual increase in the occurrence of brain tumors. Brain tumors are the tenth leading cause of death worldwide. Therefore, early and accurate tumor diagnosis

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can improve the patient's prognosis. A quick and accurate identification of brain cancer is crucial for the patient's health, as the stage and type of tumor determine the course of treatment. Tumors can be difficult to diagnose due to their wide range of sizes, locations, and shapes. The percentage of people who will recover from a brain tumor may decrease due to an incorrect or delayed diagnosis. Brain tumor diagnosis has always relied on precise tracing of tumor location and visual assessment of medical imaging. Magnetic resonance imaging (MRI), computed tomography (CT), and positron emission tomography (PET) scans were used to obtain these images. MRI scans are preferred by radiologists and medical professionals to detect brain tumors because they produce high-quality images of soft tissues [2]. When manually diagnosing tumors through ocular inspection, the surrounding healthy tissues often result in blurred tumor edges. This leads to manual tumor identification being time-consuming and often resulting in inaccurate tumor diagnoses. Images that are noisy for various reasons contribute to inaccurate cancer detection. This text includes techniques for acquiring medical images and discusses variations in imaging machinery. Biopsies are typically used to identify malignant or non-cancerous tissue. The process of diagnosing cancer is often lengthy and painful. The complexity of modern processes necessitates the adoption of automated technology [1].

There is potential for improving performance, even if multiple efforts have been made to accurately recognize brain tumors. The supervised approach to categorizing a brain tumor has considerable potential, but it requires specialized knowledge to identify the optimal characteristics and selection techniques. Using only deep learning algorithms requires a vast amount of labeled data. To address this gap, we propose a novel technique for the detection and classification of brain tumors using a T1-weighted MR image that integrates deep and conventional features.

The contributions of this manuscript are as follows:

- The proposed framework aims to create a set of specialized feature vector descriptions for high-level classification problems using conventional and deep learning (DL) feature extraction methods.
- The proposed CNN technique selects the combination of significant conventional features derived from deep features and the genetic algorithm (GA).
- The suggested model has been adjusted to utilize the fusion technique, which combines prominent conventional and deep feature vectors to generate a distinct set of fusion features.
- Our recommended model technique can accurately classify if MRI brain images as either diseased or normal with a high degree of accuracy.

## 2 RELATED WORK

Over the past 10 years, the detection of brain tumors has been the subject of extensive research. In this research work, the methods for cancer detection will be discussed. For distinguishing between brain images, there are generative and discriminative approaches for detecting brain tumors [7]. The domain-specific relationships between normal and diseased brain tissues are what drive generative approaches. Finding the precise location of a tumor might be difficult because they can manifest in various regions of the brain and vary in size and shape [6].

S. J. Prashantha and H. N. Prakash [11] proposed a hybrid technique for extracting features from both traditional and deep features and classifying brain images using support vector machine (SVM). [8] proposes a mixed approach for categorizing

brain structures. The classification is based on SVMs and GAs. The extracted feature is a texture feature based on wavelets. The spatial gray level dependence technique (SGLDM) is used to extract the feature. The retrieved feature is used as input in a SVM classifier. When it comes to feature selection for categorization, GA is the solution, a state-of-the-art approach to feature selection.

Jalab et al.'s approach [19] combines features of the gray level co-occurrence matrix (GLCM) with deep learning techniques (DLT) to improve the identification rate of brain scans obtained through MRI. A trial-and-error procedure was utilized to determine the design of the CNN architecture and the optimal number of hyper-parameters. The outcome is that the proposed model serves as an advanced feature extraction technique based on the brain MRI image that was collected.

Wang et al. [20] proposed a new technique for classifying lung nodule images, which involves a novel feature representation approach. It combines both international and regional elements. A lung nodule image is first divided into regional patches by Superpixels. These patches are reconstructed using an unsupervised deep autoencoder (DAE) into fixed-length local feature vectors. The bag-of-visual-words model, which generates the visual vocabulary, serves as the overall feature representation. The classification of lung nodules is done using the Softmax algorithm. The experimental findings demonstrate the effectiveness of the feature representation strategy across different parameter values.

Zulpe and Pawar [10] introduced GLCM texture feature extraction, a statistical method that considers the spatial interactions between pixels. This method reveals certain aspects of how the gray levels of an image's textures are distributed spatially. To obtain data on the variation in intensity at a specific pixel, this measurement compares the gray intensities of two neighboring pixels in an image—the reference pixel (i) and the neighboring pixel (j)—at a specific time. The two characteristics used to construct the GLCM matrices are the relative spacing and the relative orientation (angular relationship) of the pixel pairs.

Alelaiwi et al. [24] developed an automated method to assist medical professionals in distinguishing between various types of brain tumors. The study's execution involved three stages: preprocessing of brain images, extraction of brain features, and classification of brain tumors. Brain images were converted into intensity brain images using a min-max normalization algorithm during the preprocessing stage. The normalization algorithm ensured that the intensity values of the brain images were scaled to arrange [0, 1]. The next stage involved using the PCA-NGIST technique, which combines principal component analysis (PCA) with a normalized GIST descriptor to extract features from MRI images. The final phase involved classifying the types of tumors using regularized extreme learning machine (RELM) classification. Tumor types were identified and classified using the reinforcement learning machine (RLM) classification method. The researchers utilized the T1 dataset in their study, and they employed a fivefold cross-validation procedure. However, the T1 study did not compare its results to those of other approaches, which can be viewed as a limitation of the study.

Abiwinanda et al. [25] utilized a CNN to identify the three most prevalent types of brain tumors. During the learning phase, the "Adam" optimizer, a stochastic optimization method based on the concept of stochastic gradient descent, was used. T1-weighted contrast-enhanced MRI scans of brain tumors were used in the study to train the CNN. ReLU was used as the activation function. All convolutional layers in the designs utilized 32 filters, and all fully connected layers used 64 neurons in this model. The maximum pool kernel size was 22. The softmax activation function was employed in the output layer, and the highest recorded accuracy rate was 84.19%.

Plassard et al. [26] employed deep learning techniques to categorize brain images associated with meningioma, glioma, and pituitary tumors. This study utilized T1-weighted, contrast-enhanced MRI brain images. CNNs and fully connected neural networks are two distinct neural network topologies that were created. Furthermore, a fourfold cross-validation strategy showed that the generic strategies were equally effective as the specific approaches.

Al-Awadi et al. [9] aim to utilize MRI brain images to detect the presence of a brain tumor. These images are first preprocessed to remove arbitrary boundary lines and regions. The gray-level co-occurrence matrix (GLCM) and local binary pattern (LBP) methods are combined to extract various local and global properties. The best traits are chosen using the ANOVA statistical method, which is based on the highest variance. The selected features are then used to train the extreme learning machine (ELM) neural network model as well as several state-of-the-art classifiers.

Additionally, unlike previous studies on brain image classification, a technique can be employed to categorize images of different ages. This illustrates that the proposed method can be applied to classification tasks based on T1-weighted brain MR training images. Hence, we propose a novel technique for the detection and classification of brain tumors using T1-weighted MR images.

### 3 METHODOLOGY

Implementing a framework for extracting scientific features from published image data is the main objective of this work. This is followed by analytics to enhance classification capability and improve detection accuracy. To enhance the comprehension of images in relation to anomaly detection, this study seeks to improve the selectivity and accuracy of feature extraction from image data. The suggested implementation technique was created using the published framework. This study encompasses several stages, including image extraction, management of image slices, three different noise reduction techniques, selection of the optimal noise removal technique, image enhancement, skull removal, feature extraction, feature selection, feature fusion, and classification. These stages are depicted in Figure 1.

The algorithm developed to implement the aforementioned diagram for feature extraction/selection in order to quantify brain anomalies is presented in the following section, and the results are also analyzed. To improve the accuracy of feature extraction and selection for the detection of brain illnesses, this study aimed to conduct tests until the brain image has been enhanced.

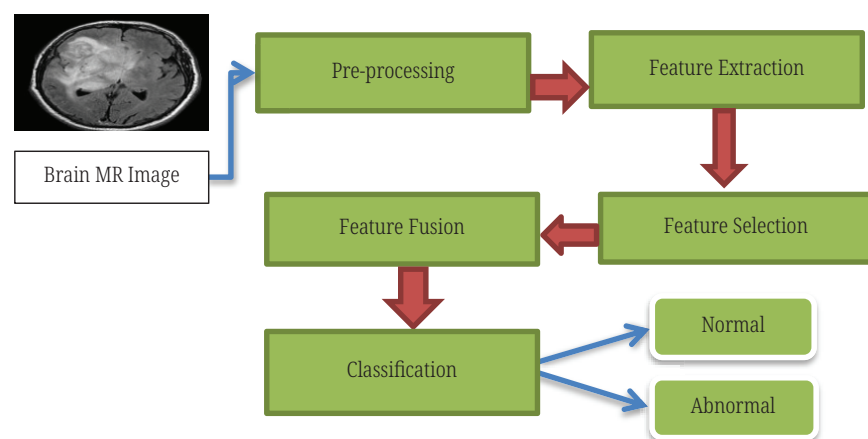


Fig. 1. Proposed framework

### 3.1 Preprocessing

The pre-processing stage of MR image processing is crucial. Preprocessed images are typically used in computer-assisted detection systems for the detailed analysis of human pathology. This work mainly consists of two pre-processing tasks. The first technique is called skull stripping, while the second technique is called contrast augmentation. Skull stripping is the process of removing all elements from the input images except for the brain tissues. The speed and accuracy of prognostic and diagnostic procedures in medical applications are enhanced by precise and automated skull-stripping techniques. The contrast enhancement of the input MR brain images is the second preprocessing stage. Contrast enhancement is a technique used to enhance the visual elements of an image, making it suitable for specific purposes. It contributes to improving the clarity of the image, which facilitates and accelerates further analysis. The hidden features in the images are also explored during the enhancement process. The methods used for both skull stripping and contrast amplification are based on mathematical morphology. In the proposed investigation, contrast-limited adaptive histogram equalization (CLAHE) is used to process MRI slice images in order to enhance contrast [11].

### 3.2 Feature extraction and selection

**Conventional feature extraction and selection.** The GLCM and Haralick texture patterns are generated in this proposed study based on the directions or orientations of an image. The expected texture elements are laid out in great detail in Table 1. The GLCM matrix sheds light on the spatial correlations of the gray levels present in the image and reveals certain properties of these connections. The Haralick features, which are used to characterize the textures of an image's textures, are calculated using the co-occurrence matrix. Within the region of interest (ROI), the pixels of the image are distributed in one of two orientations, taking into account the correlation between the discretized intensities of neighboring pixels.

**Table 1.** Features of GLCM and Haralick texture

Features of GLCM Texture			Features of Haralick Texture	
Average	Sum entropy	Sum variance	Energy	Sum average
Entropy	Sum variance	Autocorrelation	Entropy	Sum entropy
Variance	Sum average	Cluster shade	Contrast	Sum variance
Maximum probability	Angular second moment	Normalized-inverse difference	Sum of variance	Difference variance
Difference average	Inverse difference	Correlation & dissimilarity	Inverse difference moment	Difference entropy
Difference variance	Inverse difference moment	Normalized-inverse difference moment	correlation	Information measures of correlation
Cluster tendency	Inverse-variance correlation	Cluster prominence		

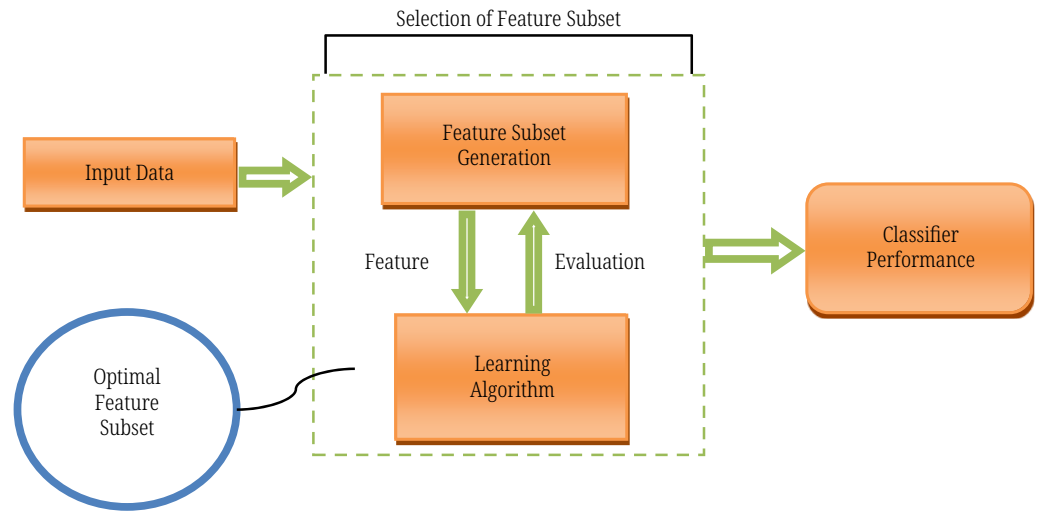


Fig. 2. Workflow of GAFSWM

We have adopted a wrapper model that is based on generalized additive fuzzy sets (GAFS) to focus on pertinent attributes. Figure 2 depicts the steps taken to select a feature subset for the GA in the wrapper model. There are three steps to this process. The identification of feature subsets is the initial step. Second, we want to assess the performance of the classifier using the narrowed-down features. Finally, repeat steps 1 and 2 as many times as needed to iterate. The identification of a subset of critical features by the GAFS module is one of the main objectives of this study.

**Deep learning feature extraction and selection.** To extract the entrenched features, we employ a feature extraction method using CNN. The suggested CNN architecture consists of an input layer (IL), a convolutional layer (CL), a sub-sampling layer (SSL), and a fully connected layer (FCL). The architecture of CNN is shown in Figure 3.

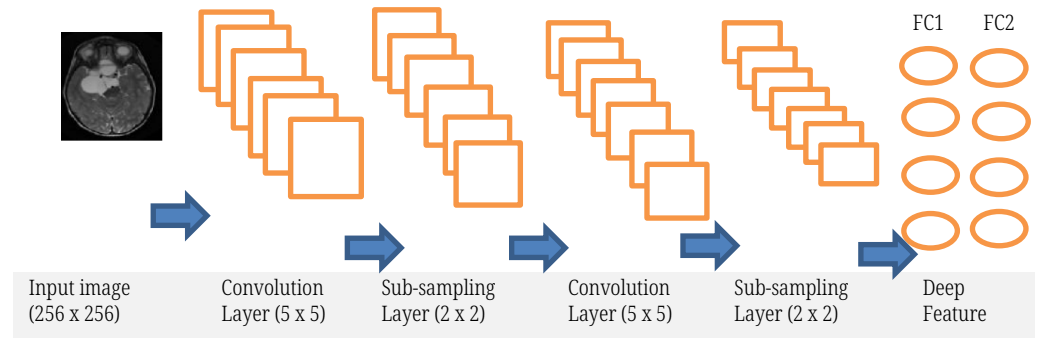


Fig. 3. Architecture of CNN

Table 2. Details of the CNN architecture

Layer	1	2	2	3	3	4	4
Layer Type	Input Layer	CL + Sigmoid	SSL	CL + Sigmoid	SSL	FCL1	FCL2
Size	256 × 256	5 × 5 × 9	2 × 2 × 9	5 × 5 × 135	2 × 2 × 15	1 × 3000	1 × 300
Feature Map	–	252 × 252 × 9	126 × 126 × 9	122 × 122 × 135	61 × 61 × 15	3000	300
Selected Feature Maps	65536	571536	142884	2009340	55815	3000	300

A convolutional layer receives an  $I \times I \times J$  image as its input, where  $I$  represents the height and width of the image and  $J$  represents the number of channels.  $N \times N \times M$



filters or kernels, where  $N$  is smaller than the image’s dimension and  $M$  can either be the same as the number of channels or smaller, will make up the convolutional layer.  $Q$  feature maps of size  $I - N + 1$  are produced when the image is convolved with the locally connected structure created by the filters’ size. The main objective of the proposed strategy for feature extraction and selection is to investigate the contributions of each input dimension and the input of the feature maps in each layer. In outline form, the CNN architecture used in this investigation is shown in Table 2.

**Feature fusion.** Feature fusion assists in learning an image’s features to effectively describe the abundant internal information of the image. Data fusion is essential. Feature fusion is crucial because it allows for the combination of these diverse feature vectors. This is important because different feature vectors from the same image capture different aspects of the image in varying ways. The effective discriminatory information is preserved, while the redundant information is mostly eliminated. Consequently, feature fusion can establish and obtain the most useful feature vector sets with the lowest dimension for the conclusion. The textural features extracted using GLCM and Haralick, along with the high-level features recovered using the CNN network, are combined to obtain a more comprehensive feature representation of the brain image. Edge and textural features are added to the low-level features recovered by the CNN’s convolution layer to enhance the feature representation [21]. For feature fusion, the features are concatenated. CNN captures spectral and spatial features at each stage to provide high-level features, while the local texture information in the image is represented by GLCM and Haralick features. The deep features of the two channels are designated as DF1 and DF2, respectively. The conventional feature vectors of the channels are also named Conv1 and Conv2. A single feature vector is created by concatenating the features in each branch as (Conv1, DF1, Conv2, DF2). We adopted a linear feature fusion strategy to combine the features after extracting the high-level deep features and conventional features. This strategy involves setting a fixed proportion ( $\beta$ ) for the feature fusion process. The fusion features for classification are computed as follows:

$$NFV = \beta \cdot Conv + (1 - \beta) \cdot DF \tag{1}$$

NFV stands for fusion feature vectors, Conv for conventional feature vectors, and DF for deep feature vectors. The  $\beta$  parameter represents the weight that indicates the relative importance of two different features. The fused features will then be passed to the classifier for the final classification task. Figure 4 shows a diagrammatic illustration of feature fusion.

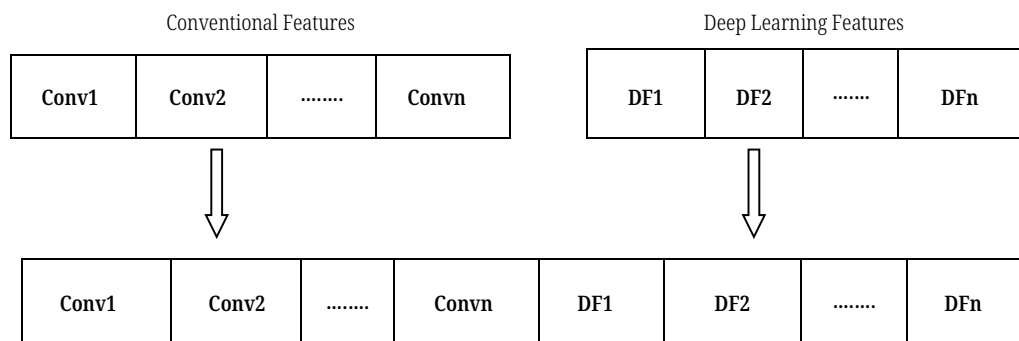


Fig. 4. Feature fusion

**Classification.** The SVM classifier was used in this study to classify the data. The SVM is a two-step process that involves training and testing for binary classification. A finite training set is created by supplying existing data and previously identified

decision values to the support vector machine during the training phase. In this training batch, SVM learns how to classify unlabeled data. After manually tagging the training images with a class label, the SVM algorithm is applied to the labeled data. The prediction model outputs and the testing phase also included a collection of observations used to evaluate the performance of the model. A test brain MR image is compared to every image from the trained set using an SVM classifier. Using the stated method, SVMs are employed to classify brain MR images as either normal or abnormal.

## 4 EXPERIMENTATION

### 4.1 Dataset

There are 22 different subjects and instances in the dataset. MRI images with a T1 weighting are obtained from the radiopaedia.org online database. Radiologists from all over the world have primarily gathered the resources for the dataset. The ages of the subjects ranged from 1.5 to 72 years. The image resolution ranges from  $256 \times 256$  to  $1024 \times 1024$  pixels, and we have captured 200 images. These images include 100 normal images and 100 abnormal images.

### 4.2 Experimental setup

In this study, the SVM classifier was used to investigate the radiopaedia.org internet database. This section describes the study and its findings. Figure 5 displays the preprocessing results of the T1 weighted modality. This dataset is divided into two categories.

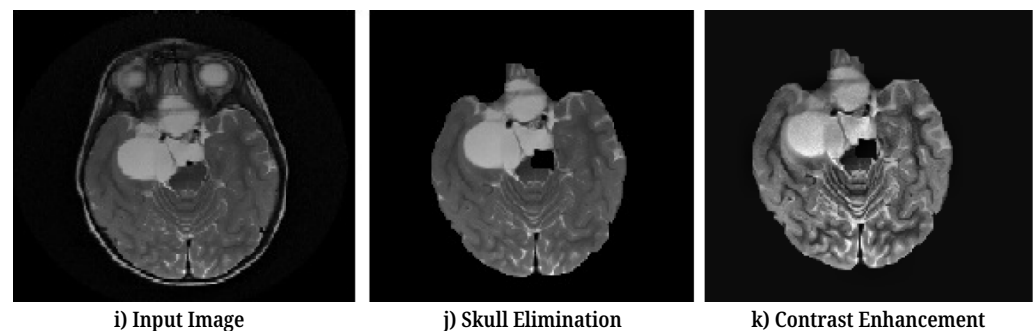


Fig. 5. T1-weighted modality examples of (i) Input image, (j) Skull elimination, (k) Contrast enhancement images

**Normal and aberrant.** During the feature extraction phase, the GLCM features, Haralick textures, and DLF are extracted. A genetic algorithm is used to select common features, while the proposed CNN approach is used to choose deep features. We have developed a technique for linear feature fusion that involves combining the extracted important conventional and deep features. This technique has been utilized for the purpose of classification. The experiment takes into account three distinct features: GLCM, Haralick, and DL FC-1 and FC-2. It also considers fusion features of GLCM + Haralick, which includes (GLCM + Haralick) and (GLCM + Haralick + DL FC-2). For the experiment, we collected a total of 148 features, including 96 GLCM features and 52 Haralick features. In Figure 6i, we can see the number of features selected using the GAFS wrapper method. In our proposed classification method, we evaluate the performance of the classifier using two sets of images. Both the



200 images accurately identified by our suggested system and a randomly selected subset of previously trained images make up the second set.

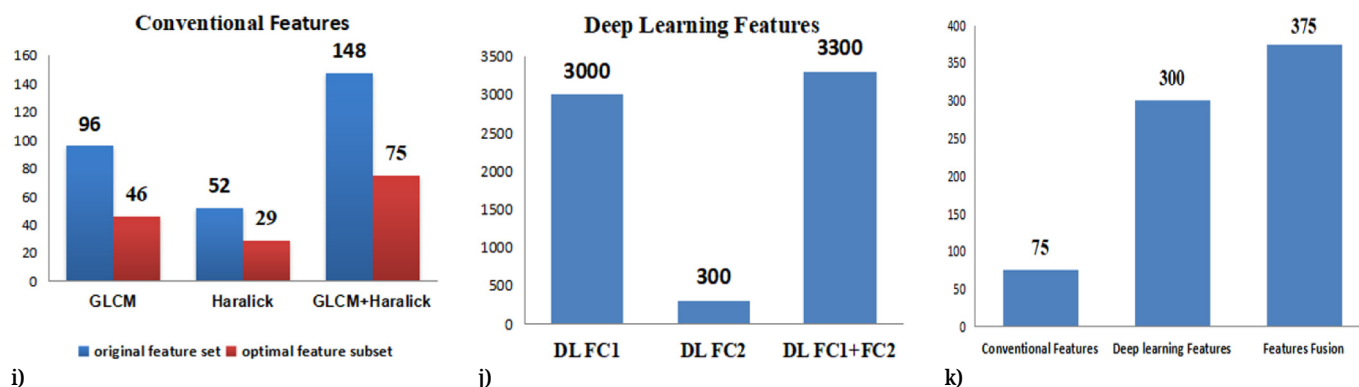


Fig. 6. (i-k) Features of the proposed method are described

## 5 RESULT AND DISCUSSION

In this research, we will examine the effectiveness of the suggested classifiers and present the results of our trials. The population size and selective pressure used in feature selection utilizing a genetic algorithm both significantly impact the experimental outcomes for the GAFS model. We have used the following parameters: maximum number of iterations = 10, population size = 72, number of offspring = 8, and parameter = value based on previous runs. Here, we present the outcomes of our experiments and analyze the effectiveness of the proposed classifiers. The experimental results of the GAFS model are highly sensitive to the population size and selective pressure applied during feature selection using a genetic algorithm. Parameters have been set based on the results of multiple iterations of the genetic algorithm. In this analysis, we employ a fitness-proportionate selection approach, and our selection probability,  $f_i$ , is calculated using equation (2).

$$f_i = \frac{m_i}{\sum_j^n m_j} \tag{2}$$

If the person “ $i$ ” in the population has fitness  $m_i$ , equation 1 will determine the likelihood of it being chosen, where “ $n$ ” equals the total number of people in the sample. An optimal collection of features is produced by the neural network built using the GAFS technique, which assesses an individual’s fitness.

Specifically, we evaluate the performance of a CNN architecture that consists of two fully connected (FC1 and FC2) layers, two subsampling layers ( $2 \times 2$ ), 15 convolution layers, and 9 convolution layers with a  $5 \times 5$  kernel size. The network is set up using the following hyperparameters: The parameters of this model are as follows: a learning rate of 0.001, 50 epochs, 20 batches, a sigmoid activation function, and random weight initialization. Several findings from previous experiments are used to inform the parameter settings.

We began with a complication of traditional features and then refined it to a selection of 75 optimal ones. In addition, the first fully connected layer (FC1) produces 3000 deep features, while the second fully connected layer (FC2) produces only 300 deep features. In Figure 6j, we can see the number of characteristics that were identified using deep learning. Linear feature fusion is utilized in the current study on feature fusion,

leading to the generation of novel feature vectors. As can be seen in Figure 6k, this phase involves generating 375-dimensional fused feature vectors from 75 conventional features and selecting 300 deep features from the second fully connected layer, FC2.

A total of seven experimental sets are used to determine whether the proposed strategy is effective. Inputs to this work can be any type of feature vector. The purpose of conducting these trials is to have a benchmark to compare against. We have computed a  $2 \times 2$  confusion matrix for the experimental setting, where 2 represents the number of expected classes. The classification confusion matrix used in the suggested method is displayed in Table 3. Both traditional texture analysis and deep learning feature analysis techniques are compared using a confusion matrix. True positive (TP), true negative (TN), false positive (FP), and false negative (FN) are all terminologies that can be used to describe this phenomenon. Images are deemed TP if the model accurately identifies them as belonging to the abnormal class, TN if they are correctly predicted as belonging to the normal class, FP if the model mistakenly predicts them as belonging to the abnormal class, and FN if the model mistakenly predicts them as belonging to the normal class.

**Table 3.** SVM classifier classification confusion matrices

Features Techniques Used	TP	TN	FP	FN
GLCM	88	42	12	58
Haralick	86	80	14	20
GLCM + Haralick	93	37	7	63
Fusion features (GLCM + Haralick)	86	81	14	19
DL FC1	92	78	16	14
DL FC2	85	75	15	25
Fusion features (GLCM + Haralick + DL FC2)	91	82	14	13

Results from a comprehensive examination of the performance of the suggested categorization model are presented in Table 4.

**SEN:** Sensitivity **SPE:** Specificity **PRE:** Precision **REC:** Recall **FM:** F-Measure **ACC:** Accuracy

**Table 4.** Performance of the suggested approach

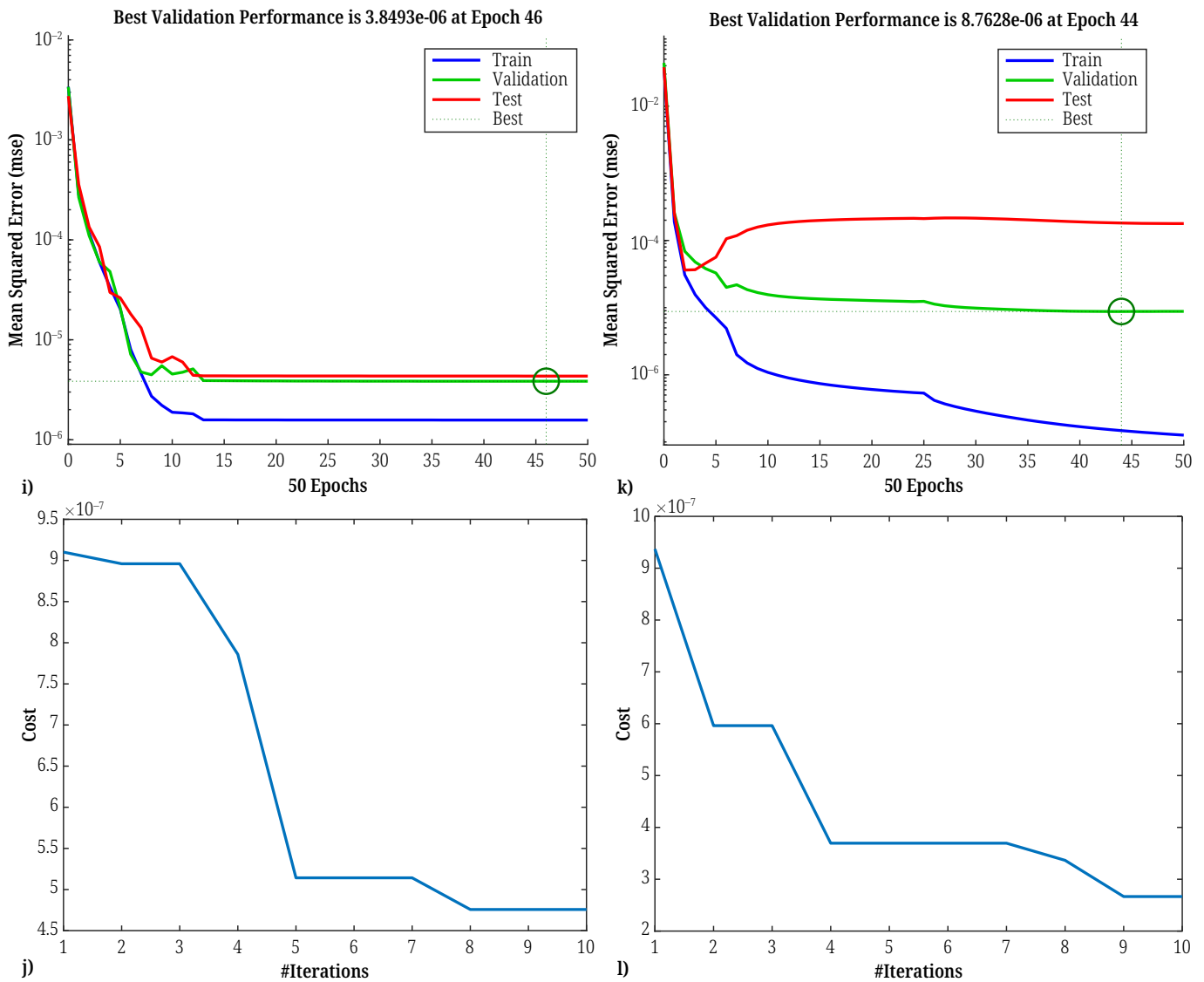
#Feature	#SEN	#SPE	#PRE	#REC	#FM	#ACC (%)
GLCM	0.6027	0.7778	0.8800	0.6027	0.7154	65.00%
Haralick	0.8113	0.8511	0.8600	0.8113	0.8350	83.00%
GLCM + Haralick	0.5982	0.8409	0.9300	0.5962	0.7266	65.00%
Fusion features (GLCM + Haralick )	0.8190	0.8526	0.8600	0.8190	0.8390	83.50%
DL FC1	0.8679	0.8518	0.8297	0.8679	0.8598	85.500%
DL FC2	0.7727	0.8333	0.8500	0.7727	0.8095	80.00%
Fusion features (GLCM + Haralick + DL FC2)	0.8750	0.85412	0.8666	0.8750	0.8708	86.50%

In this section, a performance comparison is presented between the categorization accuracy of the proposed study and that of other recently published studies, as shown in Table 5. The accuracy of the tumor classification approach used by the author [18], which is based on SVM, was 64.00%. The accuracy of the abnormal tumor classification methods developed by authors [16, 17], as well as SVM and CNN, was 75.00% and 84.19%, respectively. Table 5 compares the accuracy of the proposed

method for efficient classification with that of authors [18], [16], and [17]. The suggested method includes feature extraction, feature selection, feature fusion, and classification experiments. It was tested on the T1-weighted radiopaedia.org web database to validate the results in terms of accuracy. The proposed method achieved an accuracy of 86.50%, which is higher than the accuracy of existing brain tumor detection methods. Figure 7 displays the sample runs of GLCM and Haralick. Figure 8 displays the experimental results of the SVM classification. It performs structural risk minimization in order to achieve optimal generalization performance. The SVM classifier correctly identified normal and abnormal cases with an accuracy of 86.50%.

**Table 5.** Comparative analysis of existing methods with proposed method

Authors	Dataset	Accuracy (%)
[18]	200	64.00%
[16]	100	75.00
[17]	62	84.19
<b>Proposed Method</b>	<b>200</b>	<b>86.50%</b>



**Fig. 7.** Sample runs of GLCM (i–j) and Haralick (k–l)

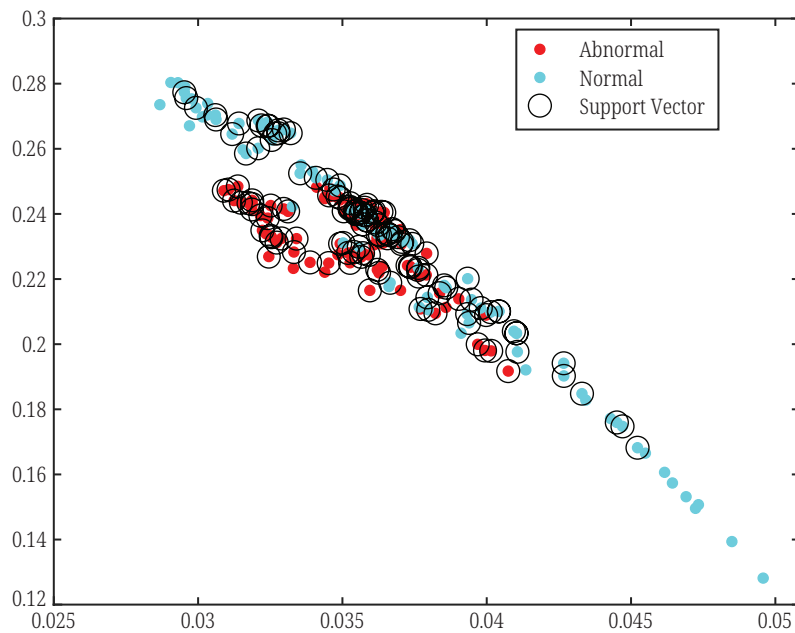


Fig. 8. Results of an experiment by SVM

## 6 CONCLUSION

In this paper, we have proposed an automated method for categorizing MR brain images. Additionally, we demonstrate the outcomes of categorizing images taken at various ages, ranging from 1.5 to 72 years. We utilized a CNN architecture and a GAFS wrapper model, which we had previously proposed, to complete the feature extraction and selection. Then, utilizing a fusion technique, we generated a compilation of complementary fusion features that surpass a set of independent characteristics in terms of recognition. For each MRI image, the suggested technique selects 375 subset features. These highly positive results are evident in the experimental data that was collected. A classification accuracy of 86.50% has been achieved using all available T1-weighted brain MR images.

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## 8 AUTHORS

**Hanumanthappa S.** received degree in Bachelor of Computer Science and Engineering from Visvesvaraya Technological University, Belagavi, Karnataka, India and Master of Technology in Computer Science and Engineering from Visvesvaraya Technological University, Belagavi, Karnataka, India. Currently he is pursuing Ph.D in Computer Science and Engineering at Sri Siddhartha Academy of Higher



Education, Tumkur, Karnataka, India. He is currently working as Associate Professor in Department of Information Science and Engineering at Kalpataru Institute of Technology, Tiptur, Karnataka, India. He has 18 years of teaching experience. His research interest includes image processing, Bio-Medical Image Analysis, Pattern recognition, Machine Learning and Deep Learning. He has published papers both in National and International conferences and Journals (E-mail: [hanukit@gmail.com](mailto:hanukit@gmail.com)).

**Dr. Guruprakash C. D.** received degree in Bachelor of Computer Science and Engineering from Bapuji Institute of Technology, Mysuru University, Karnataka, India. Master of Technology in Computer Science and Engineering from Mysuru University, Karnataka, India. He is Currently working as Professor in Department of Computer Science and Engineering at Siddhartha Institute of Technology, Tumkur, Katakana, India. He has 23 years of teaching experience. His research interest includes Computer Network and Image Processing. He has published many papers in National and International conference and Journals.