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RESEARCH ARTICLE

A Novel Hybrid System of Detecting Brain Tumors in MRI

RAGHAV AGARWAL[1], SAGAR DHANRAJ PANDE[1], SACHI NANDAN MOHANTY[1], (Senior Member, IEEE), AND SANDEEP KUMAR PANDA[2], (Member, IEEE)

[1]School of Computer Science and Engineering (SCOPE), VIT-AP University, Amaravati, Andhra Pradesh 522237, India
[2]Department of Artificial Intelligence and Data Science, Faculty of Science and Technology (IcfaiTech), ICFAI Foundation for Higher Education, Hyderabad, Telangana 501203, India

Corresponding author: Sandeep Kumar Panda (sandeeppanda@ifheindia.org)

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ABSTRACT The growth of irregular brain cells leads to a disease called brain tumor (BT). It is difficult to predict a patient's chance of survival due to the low rate and wide range of tumor shapes. Even though it is possible to manually detect cancer, doing so is difficult and time-consuming and runs the risk of producing false-positive results. This can be done via MRI, which is necessary for locating cancer. It is very difficult to reliably identify different illnesses from MRI images for successful therapy via a computer-aided diagnostic system. In the experiment, three openly accessible benchmark datasets were utilized. To perform feature extraction in our proposed method, a CNN model was employed, followed by the application of five machine learning classifiers: Decision tree (DT), Naive Bayes (NB), Adaptive Boosting (AdaBoost), K-nearest neighbor (KNN), and support vector machine (SVM). The outcomes show that the proposed CNN architecture with the KNN classifier performs better than previous CNN models by outperforming other cutting-edge DL models under various classification metrics. Finally, the achieved F1-Score, precision, recall, and accuracy values for the classification and detection of the proposed model were 99.58%, 99.59%, 99.58%, and 99.58%, respectively. For the comparison study, additional Transfer Learning models are utilized. Experimental findings support the strength of the proposed architecture, which has rapidly accelerated and improved the classifications of BTs. The designed method outperforms the body of existing knowledge, demonstrating that it is a quick and precise method for classifying BTs.

INDEX TERMS BTs classification, deep CNN (DCNN), image processing, feature extraction, hybrid models, comparative analysis, MRI images.

I. INTRODUCTION

Based on the information provided by the World Health Organization (WHO) [1], the National Brain Tumor Society [2], and the Indian Society of Neuro-Oncology (ISNO) [3], BTs are considered highly lethal due to their formation from the unregulated proliferation of malignant cells within the brain. For 30 years, there has been a sharp increment in the incidence of BTs, which has led to millions of deaths globally. A space-occupying lesion known as a "brain tumor" mostly affects the neurological system. Its most prevalent symptoms are headaches, excessive intracranial pressure, and locally centered sex issues. It may also be referred to as a BT or growth inside the skull. BTs make up around 1% to 3% of all cancers in the body. Tumors can lead to fatality by inflicting harm on the healthy regions of the brain, resulting in damage to brain tissue [4]. The majority of people are quite uneducated when it comes to BTs and hemorrhages, and many individuals die from a lack of early identification and care. Therefore, it is crucial to accurately and promptly detect brain illnesses.

Cell damage can be caused by several factors, including genetics and exposure to chemicals or radiation [5]. Brain tumors are ranked tenth on the list of the world's top ten

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TABLE 1. Hyperparameter results for training and test dataset splitting.

Split-ratio(Train-Test)	Training Accuracy(%)	Test Accuracy (%)
75-25	100	99.59
70-30	99.93	98.92
65-35	99.79	99.01
60-40	99.54	99.43

causes of death [6]. In 2020, there were 24103 fatalities [7]. Early detection is key to improving prognosis and survival rates [8]. Treatment options include surgery, radiation therapy, chemotherapy, and a combination of these methods [9]. MRI and CT scans are the most commonly used imaging techniques for identifying brain tumors [10]. MRI is preferred due to its higher contrast capabilities [11]. The quality of MRI images has improved, and the use of deep learning techniques is essential for detecting brain abnormalities. Researchers in various medical fields use traditional DL to improve outcomes [12].

This study being presented introduces a novel automated DL-based approach for the swift interpretation and diagnosis of brain MRI images. The main contributions of this manuscript can be outlined as follows:

1. A novel hybrid diagnostic system that classifies MRI images as normal, meningioma, pituitary, and glioma using DCNN.
2. To offer an in-depth review of the hybrid CNN that makes use of DT, NB, AdaBoost, KNN, and SVM.
3. The proposed architecture is systematically compared with established and renowned techniques such as VGG, ResNet, and MobileNet families.
4. By evaluating performance against state-of-the-art architectures, this study aims to demonstrate the effectiveness and superiority of the designed architecture.
5. ROC-curve, F1-score, accuracy, precision, recall, and other performance metrics have been used to assess how well the proposed system performs in comparison to competing models.

The rest part of the manuscript was divided into the sections as follows: The related work is described in Section II, the methodology utilized in this study is laid out in Section III, the result analysis of the experimental data is covered in Section IV, the discussion is presented in Section V, and the conclusion and future remarks are provided in Section VI.

II. RELATED WORK

The detection of BTs using MRI has been a matter of numerous studies and research projects in recent years. This section evaluates several credible works. To identify brain cancers on MRI scans, several DL-based methods have been developed recently. To address the issue of low performance in feature selection by traditional DL algorithms, numerous researchers have put forth new strategies aimed at enhancing their ability to classify data. These strategies are designed to improve the capacity of accurately categorizing data. By incorporating innovative techniques and approaches, this study aims to overcome the limitations of state-of-the-art (see Table 2) algorithms and achieve better results in feature selection and categorization tasks. Even though shared datasets are frequently used, different studies' findings have led to a variety of conclusions. This is mostly because various parameters are used even when the same procedure is used. In several tests, the categorization process and the current models were changed. This was done to increase accuracy rates. The bulk of them focus on the binary classification to identify brain cancers.

In [13], the most optimal CNN model for MRI-based BT identification is chosen by evaluating the performances of various transfer learning models. The DL framework is built using seven conventional feature extractors, and the five conventional classifiers are used to categorize the features that were extracted from each pre-trained model. Out of all the models used in this inquiry, the best performance model, the VGG19-SVM, had the highest accuracy at 99.39%. Feature Selection through VGG would be computationally expensive because of its deep and complex layers, and hence a simpler CNN model needs to be literate to maintain good performance. The model did not examine all types of tumors, including meningiomas, gliomas, and pituitary tumors, in the MRI dataset.

Reference [14] modifies the ResNet50 model by removing the initial five levels of its structure and appending ten additional levels at the end. This alteration results in an increased number of layers and higher system complexity, despite achieving a classification accuracy of 97.01%.

An ensemble classifier demonstration was suggested by [15]. In contrast to the DenseNet-169 model, the ResNeXt-101 model was able to attain an overall accuracy of 96.13% for a large dataset and 92.37% for a small dataset. For a knowledge-based, real-time healthcare detection system, the model capacity is inadequate. In some cases, a single classifier performs better than an ensemble configuration with average results.

Reference [16] introduced a hybrid architecture for the automatic identification of BTs in MRI, utilizing multiple eigenvalue selections. Their strategy achieved an accuracy of 91.02% and marked less performance for precision and recall of 86% and 87% respectively.

Reference [17] employed Inception V3 and DenseNet201 models to detect brain cancers. They utilized a method that incorporated precise predictions and integrated multistage tumor feature extraction. The DenseNet201 model showed an accuracy of 99.51%, while Inception V3 showed an accuracy of 99.34%.

Nine previously trained DL models and transfer learning (TL) were used by [18] to categorize BT. They experimented with MR images using improved TL-based models. The proposed approach led to an overall accuracy of 98.71% in MRI detection.

Reference [19] developed a CNN model for the classification of BTs. Their model employed two convolutional

TABLE 2. Comparative analysis of state-of-the-art models.

Reference	Strength	Threat	Accuracy(%)
[13]	Five types of traditional ML classifiers were hybrid with seven Transfer Learning models, VGG-SVM got the highest accuracy	The model was not tested against categorizing all types of tumors (Binary Classification)	99.39
[14]	ResNet50 was modified by pulling out the first 5 layers and increasing 10 layers at the end	The complexity of the system was expanded because of the addition of more layers	97.01
[15]	An ensemble classifier demonstration was put in and evaluated on binary as well as 4 classes of dataset	Not suitable for real-time medical diagnosis systems due to insufficient model size, in some cases, a single classifier outperformed	96.13
[16]	Utilized multiple eigenvalues selection technique	The value of precision and recall (86%, 87%) is comparatively less	91.02
[17]	Generated connected, multistage tumor feature extraction and accurate forecasts	A dataset having 3 classes of tumors was used and the model was not tested for the no-tumors	99.51
[18]	Nine pre-trained DL Transfer Learning models were used	No new unique work was seen and the model was not tested for the no-tumors	98.71
[19]	CNN model with 2 convolutional layers and 2 completely connected layers	A dataset having 3 classes of tumors was used and the model was not tested for the no-tumors	97.39
[20]	Proposed a multi-scale deep CNN	A dataset having 3 classes of tumors was used and the model was not tested for the no-tumors	97.3
[21]	Used transfer learning with three separate pre-trained CNN models, best accuracy by VGG16	No new unique work was seen and the model is not tested for the no-tumors	98.67
[22]	Used three transfer learning techniques, got the highest accuracy with ResNet50	No new unique work was seen, Binary classification	95
[23]	The final layer of the transfer learning model ResNet50 has been exchanged with global average-pooling and softmax layers	A dataset having 3 classes of tumors was used and the model was not tested for the no-tumors	97.48
[24]	Modified AlexNet CNN model	Binary classification (i.e., Normal or abnormal)	91
[25]	Used 5 pre-trained and a sequential CNN model	Very low accuracy and the model is not tested for the no-tumors	84.19
[26]	Used Random Forest classifier	Low accuracy	86
[27]	Developed an AlexNet model	No new unique work was seen, Binary classification	99.04
[28]	Investigated the Berkeley wavelet transform, extracted features were transmitted into SVM	----	96.51
[29]	Used two ML algorithms separately, highest accuracy got with KNN overperforming SVM	Low accuracy	88
[25]	A customized CNN was used	Very low accuracy	84.19
[30]	CNN features were used by the classifier	Very low accuracy	81
[31]	Tested the model on radiological scans	A radiological scan is more harmful than MRI and the model is not tested for the no-tumors	97.14
[32]	Features extracted from CNN were fed into different ML classifiers. The highest accuracy got from the SVM classifier	----	96.19
[33]	CNN and SVM got hybrid	Used a few pieces of data for training purposes	98.49
[34]	Used K-means clustering and the VGG19 CNN architecture	Binary Classification (i.e., Malignant and Benign)	94
[35]	created a customized CNN architecture and VGGNet model	Proposed CNN got low accuracy (86%) as compared to VGGNet (97%)	97
[36]	proposed several CNN-based categorization techniques. ResNet-50 has the highest accuracy score	----	96.5
[37]	presented a refined EfficientNet-B0 network	Binary Classification	98.87
[38]	Proposed a custom CNN	----	97.72

layers and two Dense layers to gather and classify tumor features, achieving an accuracy of 97.39% in BT classification.

Reference [20] put a multi-scale DCNN specifically designed for evaluating cancer MRI images. By assessing the effectiveness of their model on an MRI dataset, they achieved an accuracy of 97.3%, however, the model is only used to classify the type of tumors and does not talk about the cancer-free patient.

In [21], BTs were classified using transfer learning models with three pre-trained CNN models. Among them, VGG16 got the highest accuracy rate of 98.67%. Though the Transfer Learning approach requires a large dataset for its effective working and is computationally expensive, a novel hybrid system is required.

Similarly, in [22], transfer learning methods were operated to classify BT images into two classes using the VGG16, ResNet50, and InceptionV3 models. The proposed model

achieved a maximum accuracy of 95%. By utilizing ResNet-50 and an MRI of the brain, [23] suggested the DCNN network and trained it with the data augmentation strategy, the proposed model's accuracy was 97.48%. To distinguish between normal and disordered brain MRI, [24] proposed a CNN model. The accuracy rate of their modified AlexNet CNN model was 91%.

Using a sequential CNN model and five separate pre-trained models, [25] classified BT MRI, with the best overall classification accuracy is 84.19%. The strategy showed a low-performance accuracy and is not reliable for real-time scenarios. Reference [26] used the brain MRI dataset and the random forest classifier to obtain 86% accuracy which does not seem effective. Reference [27] created an AlexNet model, trained the network on the dataset, and achieved a 99.04% accuracy rate.

The SVM was used by [28] for the categorization step. They also researched the Berkeley wavelet transform to look for BTs. They communicated relevant features into the SVM after extracting them. The accuracy of the experimental results was 96.51%.

Reference [29] has developed a brain cancer diagnosis system that utilizes machine learning models, specifically SVM and KNN, for the categorization of different stages of glioma. The system got an accuracy rate of 85% and 88% for SVM and KNN, respectively, and hence doesn't demonstrate its effectiveness in accurately categorizing brain cancers.

A different experiment [25] was successful in achieving a total accuracy of 84.19% with CNN and the Figshare dataset. On the Figshare dataset, [30] constructed a CNN architecture and diagnosed three various forms of BTs with an accuracy of 81%. However, using CNN features should improve the classification model's performance accuracy.

Reference [31] shows how researchers achieved a 97.14% accuracy rate when classifying BT's radiological scans into three categories: pituitary tumors, gliomas, and meningiomas. A different study's authors [32] suggested extracting the MR image characteristics using a deep-learning neural model before feeding them to more conventional ML-based classifiers like NB, SVM, and Multilayer Perceptrons (MLP), and they achieved an overall SVM classification accuracy of 96.19%.

CNN and SVM were combined in a hybrid model [33] to identify brain cancers in MRI images. Additionally, they pre-processed the MRI images, which significantly raised their accuracy score. Only 100 images were used for training and 220 images were used for testing, making their evaluation method insufficient. The hybrid CNN-SVM model's total accuracy is 98.4959%.

In [34], BTs in MRI images were identified and segmented using a combination of K-means clustering and the proposed VGG19 CNN architecture. The method involves dividing the input MR images and preprocessing their intensities with normalization. The shown architecture got an accuracy of 94% in identifying and segmenting BTs.

In [35], a customized CNN architecture and VGGNet were employed to categorize 253 brain cancer images. Among these images, 98 were identified as false tumors, while 155 were confirmed as actual tumors. To address overfitting and enhance the diversity of data samples, the researchers applied data preparation and augmentation techniques. While VGGNet achieved a validation accuracy of 97% on a specific dataset, the personalized CNN model exhibited a lower validation accuracy of 86%.

The researchers in [36] presented numerous CNN-based categorization methods, each with many repetitions, including VGGNets, GoogleNets, and ResNets. GoogleNet and VGGNets have lower accuracy ratings (93.45% and 89.33%, respectively) than ResNet-50 (96.50%).

In [37], a study concentrated on exploring five additional convolutional models and transfer learning models for BTs in medical imaging. They introduced an improved EfficientNet-B0 network, which achieved an impressive accuracy of 98.87% on the validation dataset of binary class.

Reference [38] proposed a model comprising a convolutional component and a classifier component. 10 convolutional layers, 5 batch normalization layers, and 4 max-pooling layers were constituted in the convolutional component. The classifier component achieved an overall accuracy of 97.72% and relied on 3 dense layers and 2 dropout layers.

III. METHODOLOGY

A. DATASET DESCRIPTION

The developed framework is analyzed and evaluated using combined three publicly available MRI datasets ([39], [40], [41]). The dataset comprises a total of 4850 MRI images and is divided into two folders i.e., Train and Test. The dataset split consists of 75% training images (3637) and 25% test images (1213) to ensure class balance and appropriate representation of each class in both subsets. Each folder consists of four classes, namely GLIOMA, MENINGIOMA, PITUITARY, and NO-TUMOR.

The dataset is split into a 75-25 ratio for training and testing based on the results of the highest accuracy gained from the best hybrid classifier (refer to Table 1) as per the optimal split ratio to ensure that our model is not overfitting on training data.

B. IMAGE PRE-PROCESSING

The most crucial stage of the image analysis process is data preparation. Images of varying sizes can be found in the mentioned datasets. Each image has a unique size. For the MRI image problem of BT detection to be properly classified, the right pattern must be found, which may involve proper edge detection, analysis of intensity histograms and textures, and examination of morphological characteristics that indicate abnormalities such as mass, irregular growth, and changes in tissue density within the images. Several difficulties must be

overcome by the MRI image classification models, including the possibility of mislearning, which can lower classification accuracy. So, before the model receives the dataset, it needs to be cleaned up and standardized.

The data will be transformed into a typical categorized format during image preparation. Images were resampled and scaled into a typical size as the initial step in the data cleaning and data pre-processing procedure to make sure they all had identical widths and heights. Additionally, the input image is converted into a collection of pixels with the range [0, 1] known as data normalization. To normalize the pixel range of each image, the range of pixel values (0 to 255) is transformed by dividing each pixel by 255. This normalization process results in a new range of pixel values spanning from 0 to 1 for each dataset image.

The intensity levels, which range from 0 to 1, were left in their original float32 format; the photos were only scaled and normalized. Since DL algorithms are often developed to operate on the raw data, the photographs weren't further pre-processed. The parameters X_train, X_test, and y_train, y_test were also constructed along with scaling the MR images. This work uses the image form (224,224,3). Each of the input images was automatically extended to 224 by 224 dimensions by a Keras script that also helped to normalize and resize all of the image samples.

C. ARCHITECTURE OF THE PROPOSED MODEL

CNN networks are frequently utilized down to the pooling layer. The features are found in the final pooling layer. The networks are combined with several traditional classifiers after the final pooling layer, which is followed by another flattened layer. The flattened layer serves as a dimensionality reduction function by removing too many factors. Furthermore, the feature map generated by the initial pooling layer is flattened into a 1D array before being passed to the classifiers in the subsequent phase. In this study, five classifiers are employed to classify the MR brain images into four classes: GLIOMA, MENINGIOMA, PITUITARY, or NO-TUMOR. The performance of each extractor-classifier pair is validated using metrics such as F1-Score, precision, recall, Accuracy, and AUC-ROC curve. These performance measures provide an assessment of extraction effectiveness and the process of classification of different BT categories.

In this study, the proposed model is trained using a set of training images. The model's weighted values in various layers are automatically adjusted to optimize classification outcomes. Extracted features from the final average pooling layer of the proposed model, both from the training and test images. These extracted features are utilized by the classifiers to categorize tumors into four types. The results obtained from this stage are further improved by employing DT, NB, AdaBoost, SVM, and KNN classifiers. The validation of the designed model (as shown in Figure 1) is compared with other state-of-the-art DL models at each step of the process.

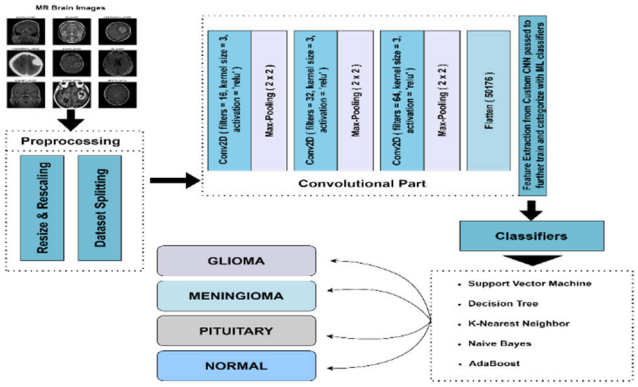

FIGURE 1. CNN architecture of proposed model.

In Section IV-B of the study, the designed DL architecture is evaluated using various evaluation metrics. The results of this evaluation are presented in Table 5. Each combination of DL-based feature extractor and classifier is assessed using various evaluation metrics. These metrics provide a comprehensive evaluation of the performance of each combination and help assess the effectiveness of the designed DL-based architecture in classifying BTs.

ALGORITHM

INPUT: The input data is denoted as X, whereas the corresponding label dataset is denoted as K.

- Input data and label sets are further divided into training data (X_{train}, K_{train}) and testing data (X_{valid}, K_{valid}) these can be represented as follows.

Set X_{train} <- $X_{75\%}$, K_{train} <- $K_{75\%}$

Set X_{test} <- $X_{25\%}$, K_{test} <-$K_{25\%}$

OUTPUT: Classification of labels (Y_{valid})with the ais of the testing dataset (X_{valid}) based on the trained framework.

STEP-1: Define and Train the CNN model having:

- 3 convolutional 2D-layers along with max-pooling
- Extract the feature set, F with a dense layer
- Adam optimizer and cross-entropy optimizer

STEP-2: Create a custom model taking extracted features from the dense layer of the CNN

- Extract the features of the Input data with our custom model
- Train_feature <- X_{train}
- Test_feature <- X_{test}

STEP-3: Hybrid the extracted features with the different classifiers

- Classifier.fit(Train_feature, K_{train})

STEP-4: Test and predict the models with the Test dataset

- Classifier.score(Test_feature, K_{test})
- Y_{test} <- classifier.predict(X_{test})

STEP-5: Calculate the evaluation metrics with the aid of Y_{test} and K_{test}

- Compare labels of Y_{test} and K_{test}
- Compare the evaluation metrics of different classifiers.

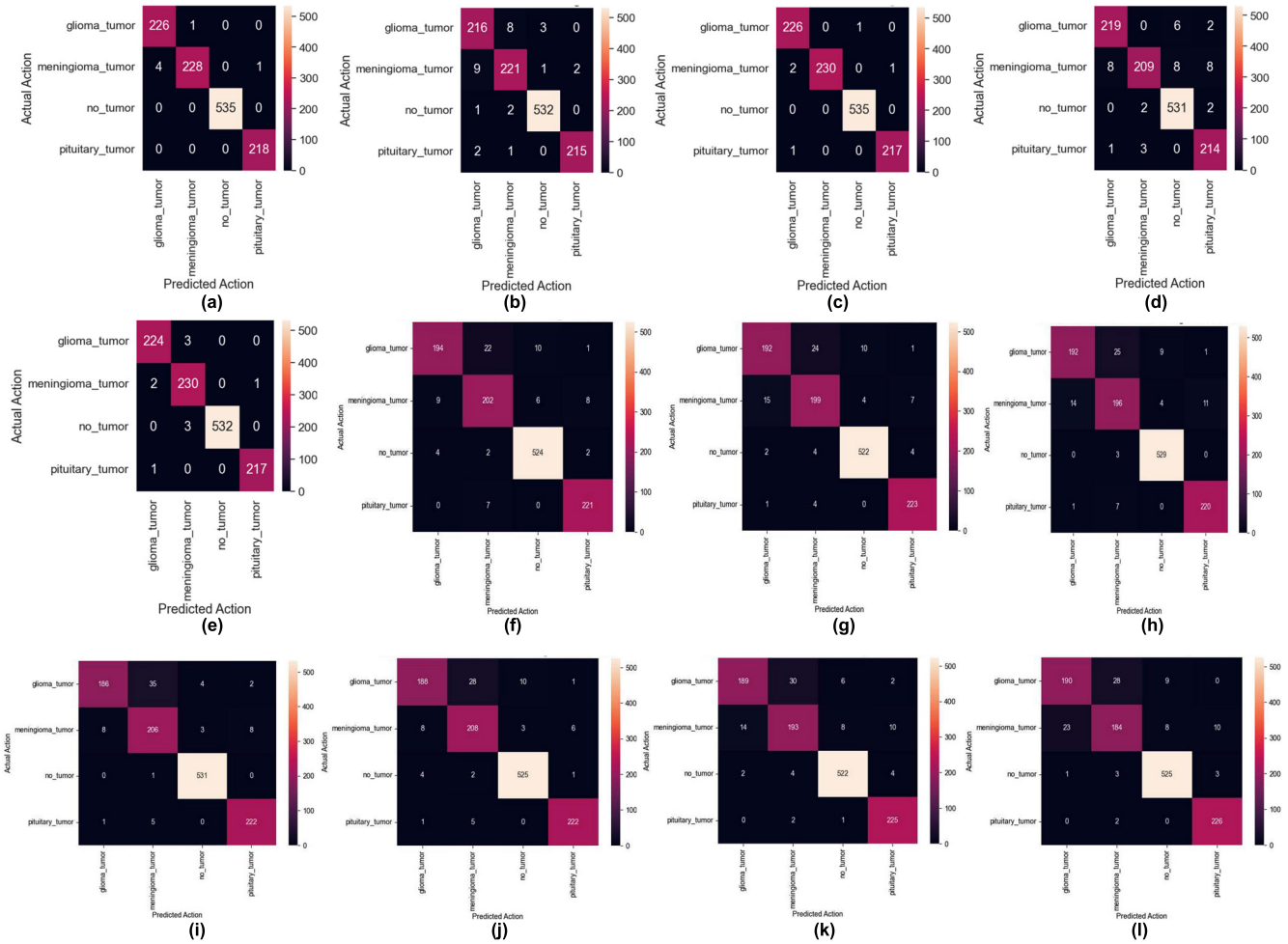

FIGURE 2. Confusion Matrix: (a). CNN-SVM (b). CNN-DT (c). CNN-KNN (d). CNN-NB (e). CNN-AdaBoost (f). VGG19 (g). VGG19 (h). Resnet50 (i). ResNet101 (j). ResNet152 (k). MobileNet (l). MobileNetV2.

1) CONVOLUTIONAL NEURAL NETWORK (CNN)

Among the various deep-learning neural networks available, this method is particularly appealing due to its increased depth. The deeper the network, the better it becomes at handling complex and challenging tasks. The additional layers in the network enable it to capture more intricate features and patterns, making it well-suited for tackling difficult tasks in various domains.

CNNs, which are highly developed feedforward neural networks, utilize the unique convolution characteristic. The fact that the placements of the filters are not fixed allows convolutions to search for translation invariance. The convolution operation significantly decreased the number of parameters. A CNN model generally has three layers. The pooling layer compiles a representation of specific input elements, the dense layer does the same, and the convolutional layer employs kernels to reduce parameter sizes. These layers carry out several functions, including dimensionality reduction, feature extraction, and feature classification. In the convolution stage, filters are used to compress the input data and produce the associated activation map. The dot product is utilized to speed up deployment since the sliding movement is linear. With p and q serving as the input vectors and weight functions, respectively, we can properly characterize the convolution (g∗h) (k) on each time t in all dimensions, as shown in (1).

$$(g * h)(k) = \int g(t)\, h(k - t)\, dk \tag{1}$$

where t is a discrete parameter and r is in Rn for some n>=1. The discrete convolution is expressed here as indicated by (2):

$$(g * h)(k) = \sum\nolimits_k g(t)\, h(t - k) \tag{2}$$

CNN models often employ two- or three-dimensional convolutions. As a consequence, we may mathematically define the convolution process as illustrated by the following equation, using the 2-D input picture X as our model and assuming that Y represents a 2-D kernel.

$$(X * Y)(p, q) = \sum\nolimits_m \sum\nolimits_k X(m, k)\, Y \times (p - m, q - k) \tag{3}$$

Mathematically, the convolution process for 3-D image data can be described in (4):

$$(X * Y)(p, q, r) = \sum_m \sum_k \sum_o X(m, k, o) \times Y(p - m, q - k, r - o) \quad (4)$$

ReLU, Sigmoid, and activation functions can all be utilized to add nonlinearity to the model. The formalization of the sigmoid activation is seen in (5):

$$O(\mathrm{p}) = 1/1 + \exp(-p)\, p \epsilon R. \quad (5)$$

The sigmoid activation function is indeed a suitable option for describing predictions within the [0, 1] range. This activation function maps the input values to a probability-like output, where values closer to 0 represent low probabilities and values closer to 1 represent high probabilities. It is commonly used in tasks such as binary classification, where the output needs to be interpreted as a probability or a confidence score between 0 and 1. Since the sigmoid function is monotonically expanding, it could contribute to the problem of vanishing gradients. In other words, because the input p is so far from zero, the gradient of p approaches 0 when neurons expand to such vast proportions. Later optimization is quite challenging to perform.

Equation (6) provides the mathematical definition of the activation function ReLu as follows:

$$ReLU(p) = \max(0, p) \quad p \in R \quad (6)$$

ReLU(p)=1 when p > 0 and ReLU(p)=0 when p<=0 are produced as a result. ReLU can converge more quickly than sigmoid.

In a CNN model, the pooling layer is employed to decrease the dimensionality without losing significant data and to generate the statistical breakdown of the inputs. There are many different ways to pool. A 2-D or 3-D point (i, j, k) is used to represent each input feature. Using the max pooling technique, the layer calculates the maximum values while taking into consideration each rectangle point around the data. The mean of the local data is determined via average pooling.

The following parameters determine the output of a fully linked layer with n inputs and m outputs: The weight matrix is represented by W ϵ Ma,b, where a denotes the rows, n denotes the columns, and z ϵ Ra the bias vector. Formally, equation 7 may be used to represent the result of applying an activation function to the fully connected FC layer for a vector of input, p ϵ Rb:

$$FC(p) = f(W * p + z) \in \boxed{R^a} \quad (7)$$

W∗p is the matrix product from (7). F is employed component-wise. Fully connected layers are typically stacked as the final levels of a preceding CNN when creating classification models. The CNN flattens the extracted features into a single vector shape.

2) FEATURE EXTRACTION USING DEEP-CNN

Since the extraction of important characteristics from images is a fundamental part of image categorization, the idea of DL enables the models to be appropriately trained to discriminate different levels of visual representation. Along with their properties, the form and structure of brain MR images are also obtained.

This study proposed a DCNN model, which combines a feature extractor with a classifier. The DCNN model is a type of CNN specifically designed for DL tasks. It leverages multiple layers of convolutional operations to extract meaningful features from input data, followed by fully connected layers for classification or regression tasks. The DCNN architecture is well-suited for image processing and pattern recognition tasks, including the analysis of medical images such as MRI scans for BT detection. Reduced overfitting, low learning rates, and a lack of training precision are just a few of the shortcomings that the proposed model attempts to address. A convolutional component and a classifier component make up the proposed model.

Our training method can be referred to as problem-based because we built our model from scratch. The training approach uses a batch size of 32 and 50 epochs with 114 stepper epochs. When the batch size is set to 32, it means that during training, the trained model receives 32 samples at a time until all of the training data has been processed, completing one single epoch. The batch size determines the number of samples that are processed together before updating the model's weights based on the accumulated gradients. Using a batch size of 32 allows for more efficient computation and memory usage, as well as smoother convergence during training.

Choosing the correct characteristics for categorization is challenging. As a result, a hybrid approach with several components is adopted. The classification of data is done using ML and DL methods. To ensure the validity of our experiment, the proposed models are compared and evaluated against several transfer learning and other state-of-the-art models. The results of each model are put in the following section, highlighting the varying degrees of accuracy achieved in detecting BTs using MRI. This comparative analysis provides valuable insights into the effectiveness of the designed models and their potential advantages over existing approaches in the field.

3) CLASSIFIERS

This section discusses the last processing step for the proposed model creation. Dataset classification is the final step in the model. Classification is the action of classifying and labeling input patterns. Numerous aspects, including classification accuracy, algorithmic performance, available processing power, and others, must be taken into account while selecting the best classifier. The process of learning

TABLE 3. ML classifiers parameter set.

ML classifier	Parameter taken
SVM	Kernel = "linear" C = 1 (Default)
Decision Tree	Random State = 0 Min_samples split = 2 (Default)
KNN	n_neighbors = 1
Naïve Bayes	Naïve Bayes Type = "Gaussian"
AdaBoost	base_estimator ="DecisionTreeClassifier" base_estimator max_depth = 5 n_estimators = 100 random state = 42

from and predicting the dataset using the model is known as machine learning and testing. The two key domains for any classification model are training and testing.

The effectiveness of training the classification network has a significant impact on classification accuracy. A better-trained classifier model will always create class labels without over-fitting or under-fitting and predict outputs. Data is classified by classifiers. It is a technique for classifying input data using an algorithm. For intelligent disease diagnosis, supervised machine learning algorithms are typically used. In this work, various machine learning-based classification techniques were employed, including DT, NB, AdaBoost, SVM, and KNN, and the set of parameters of each classifier is given in Table 3. These techniques were utilized as a part of the classification process to effectively categorize BTs based on the extracted features. By leveraging these diverse classification algorithms, the study aims to explore the strengths and limitations of each technique and identify the most suitable approach for accurate tumor classification.

In this paper, the classification accuracy of the supplied attributes is determined using five popular and extensively used ML models. The SVM, the first classifier, transfers data from the input space to a high-dimensional space using a kernel function. The DT algorithm for supervised learning is the second algorithm. A tree structure is used to illustrate the classification of occurrences based on features. Then comes KNN because KNN is easy to use, has great classification accuracy, and computes quickly, it is frequently used as a feature selection classification method. The NB model, a probabilistic method, is the fourth model. Based on the probability of its attributes given that class, Bayes calculates the likelihood that a new data point belongs to that class. From the training data, it first learns the probability of each feature given to each class. It uses the Bayes theorem to determine the likelihood of each class given the characteristics of a new data point. In the end, it chooses the class that will be predicted for the new data point with the highest probability. The last place goes to AdaBoost, an ensemble classifier that assembles groups of base learners using supervised learning. The weak classifier is a learner who receives a boost to help them develop into the strong classifier. It should be noted that the classifier is not specific to our research; rather, we just use the classification results as a benchmark.

4) TRANSFER LEARNING

Transfer learning is a technique that takes knowledge that has already been acquired and applies it to a new task. Machine learning algorithms are used [42] Transfer learning enables the improvement of models with limited data by leveraging existing knowledge. By utilizing pre-trained models that were trained on large datasets, new classification algorithms can benefit from the learned features. This approach is particularly useful when the new task is related to the original task. It allows for better performance without the need for extensive data or computational resources. However, both the method used to gather the data and the method used to categorize it must be equivalent. Classifying unrelated data is not possible using the transfer learning technique [43].

For instance, data from a DL-based computer vision model that can detect lung cancer can be used to detect other cancers. Given that it was able to learn particulars about the characteristics and composition of cancerous tissues from a model. It could include in the newest classification framework. Despite this, the model is unable to diagnose a separate illness using these data. However, BTs can be identified using the same method. The ImageNet competition is widely recognized as a prominent application of transfer learning technology. In this competition, researchers face the challenging task of classifying hundreds of photos, which can be exceedingly difficult to accomplish using conventional computer methods alone. Therefore, it may not always be possible for researchers to get such sophisticated equipment. By facilitating the reuse of the data in the earlier employed models, the transfer learning approach substantially aids research in this situation. Transfer learning models built on ImageNet are used in this investigation.

D. HYPERPARAMETERS AND LOSS FUNCTION

This section implements the selection of the loss function and hyperparameters for the challenge to obtain meaningful results. The performance of the DL model is evaluated based on accuracy and loss [44]. The major goal of a DL model is to minimize the error rate, as a model with a lower calculated loss is considered more efficient. In this study, cross-entropy (CE) was utilized to measure the average deviation between the actual and predicted values. Equation 7 provides the loss measurement for two-class classification, where x denotes binary values of 0 or 1, and m represents probability [45].

$$Cross\ Entropy = -(x \log(m) + (1 - x) \log(1 - m)) \quad (8)$$

To achieve the maximum reduction in loss during the training phase, we utilized the Adam optimizer [46]. This optimization method utilizes an adaptive gradient descent algorithm to expedite the convergence of weights toward local minima. Adam was chosen over other optimization techniques like SGD and RMSProp due to its simplicity, efficient memory usage, and shorter learning curve. Furthermore, Adam has proven to be an excellent tool for analyzing trained models on medical images. Table 4 provides the hyperparameter values, including a low learning

TABLE 4. Hyperparameter for models.

Hyper-parameter	Value
Image size	224 x 224
Weight	ImageNet
Epochs	50
Batch size	32
Optimizer	Adam
Learning rate	0.001
Loss	Categorical cross-entropy

rate (LR) that has been adjusted to work in conjunction with the other hyperparameters. With a batch size of 32, Adam successfully facilitated the efficient transmission of data across the network without exhausting the computer's memory. Each model was trained for a specified duration to observe its performance after 50 epochs.

IV. RESULTS ANALYSIS

The main goal of this part is to effectively assess proposed models for feature extraction from brain MRI. After that, a variety of classifiers are used to categorize the collected characteristics. The results demonstrate that the designed model outperforms other models in accurately identifying BTs in MR images, specifically classifying them into glioma, meningioma, pituitary, and no tumor categories.

A. EXPERIMENTAL SETUP

This whole work was trained using a system that complied with the following criteria: AMD Ryzen 7 5800H with a 3.20 GHz Radeon graphics processor. Our experimental setup consisted of a 512 GB SSD, a 64-bit operating system, and 32 GB of RAM. The research utilized an NVIDIA RTX 3050 GPU for the computational tasks. Python 3.8, along with libraries such as Scikit-learn, OpenCV, and Matplotlib, was employed to conduct the studies.

B. EVALUATION MATRICES

The confusion matrix (CM) is a commonly used method to evaluate the performance of a trained model in predicting a specific test dataset. It provides a detailed summary of the model's predictions and their alignment with the actual labels in the dataset. Some examples of ground truth labels that are equally presented in rows and columns on the CM include glioma, meningioma, pituitary, and normal. Each validation sample's percentage of accurate predictions or classifications that match the expected findings is displayed. In the evaluation of DL models, True Positives (TPs) represent correctly classified positive samples, while True Negatives (TNs) indicate correctly classified negative samples [47]. False Positives (FPs) are predictions labeled as positive but were actually negative, whereas False Negatives (FNs) are negative samples that were classified as positive [28]. The effectiveness of the DL models was assessed using several performance metrics, including accuracy, precision, recall, F1 score, and the AUC-ROC curve. Equations (9)-(14) were employed to calculate the overall accuracy, precision, sensitivity, and F1 score for each model.

1) ACCURACY

The ability of a neural network to accurately differentiate between several classifications, such as normal, glioma, meningioma, and pituitary cancers.

The total amount of accurate classifier estimations divided by the overall number of estimations yields the outcome.

$$\text{Acc} = TP + TN/T\text{P} + \text{TN} + \text{FP} + \text{FN} \tag{9}$$

2) PRECISION

The ratio of precise positive forecasts to all forecasts that are positive can be calculated using the following equation:

$$\text{Pre} = \text{TP}/(\text{TP} + \text{FP}) \tag{10}$$

3) RECALL OR SENSITIVITY

It is essential for accurately identifying patients with a specific illness. It can be summed up as the proportion of precise positive estimations to genuine positive samples. To calculate it, use the following formula:

$$\text{Rec} = \text{TP/TP+FN} \tag{11}$$

4) F1 SCORE

The capacity to accurately split classes into suitable data given the variety of classifications. The F1 score is a metric that represents the harmonic mean of precision and recall. It quantifies the balance between the FP and FN classes and is calculated using the following equation:

$$\text{F1 Score} = (2 * (\text{Pre} + \text{Rec}))/(\text{Pre} + \text{Rec}) \tag{12}$$

Or

$$\text{F1 Score} = (2 * (\text{TP}))/(2\text{TP} + \text{FP} + \text{FN}) \tag{13}$$

5) AUC-ROC

ROC is a method for visualizing data and choosing the best classifier for each classification criterion. The true-positive rates and false-positive rates are listed next to them.

The AUC (Area Under the Curve) is a measure that summarizes the ROC curve. The ROC curve contrasts the TP rate (TPR) and FP rate (FPR) at various threshold levels. It effectively separates the signal and noise, and the AUC quantifies the classifier's ability to differentiate between classes. The AUC is computed as follows:

$$\int_{-\infty}^{\infty} TPR\,(T)\,FPR'\,(T)dT \tag{14}$$

here, FPR' (T) = FPR is the first derivative of concerning T, where T stands for sample data.

We evaluated the effectiveness of our proposed model using a CM to analyze the classification results. The CM counted the number of correctly and incorrectly classified data and performance metrics were calculated based on

TABLE 5. Accuracy values of the proposed hybrid method combination.

Model Combination	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
CNN-SVM	**99.51**	**99.50**	**99.50**	**99.50**
CNN-DT	97.61	97.60	97.60	97.60
CNN-KNN	**99.59**	**99.59**	**99.58**	**99.58**
CNN-NB	96.70	96.72	96.70	96.71
CNN-AdaBoost	99.18	99.18	99.17	99.17

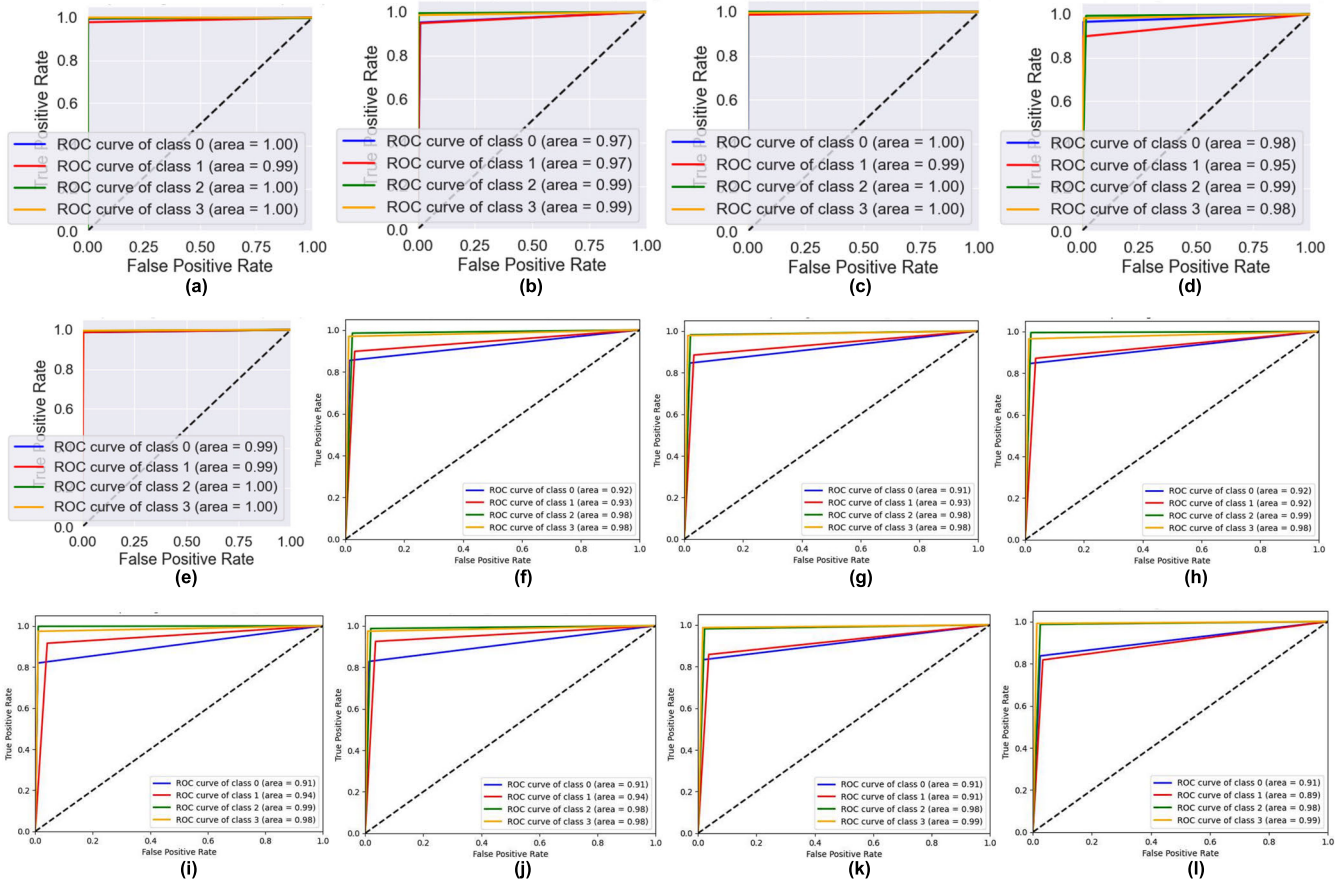

FIGURE 3. Area Under the ROC curve: (a). CNN-SVM (b). CNN-DT (c). CNN-KNN (d). CNN-NB (e). CNN-AdaBoost (f). VGG19 (g). VGG19 (h). Resnet50 (i). ResNet101 (j). ResNet152 (k). MobileNet (l). MobileNetV2.

TABLE 6. Accuracy values of other CNN models.

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
ResNet101	94.47	94.67	94.47	94.56
ResNet152	94.31	94.39	94.30	94.34
VGG16	94.14	94.16	94.14	94.14
ResNet50	93.81	93.80	93.81	93.80
VGG19	93.73	93.71	93.72	93.71
MobileNet	93.15	93.14	93.15	93.14
MobileNetV2	92.82	92.67	92.82	92.74

the evaluation criteria mentioned earlier. Our proposed model showed improved performance in accurately identifying contrasting images compared to other CNN models, as illustrated in Figure 2. Figure 3 displays the ROC curve, where our proposed model outperforms existing CNN models in detecting BTs. The AUC, an important evaluation metric for classifiers, indicates the degree of separation between different groups. A higher AUC signifies a more effective distinction between individuals with tumors and those without [48]. A model with an AUC close to 1 is considered highly proficient. Figure 4 presents the evaluation metrics and AUC-ROC curve results for our proposed model.

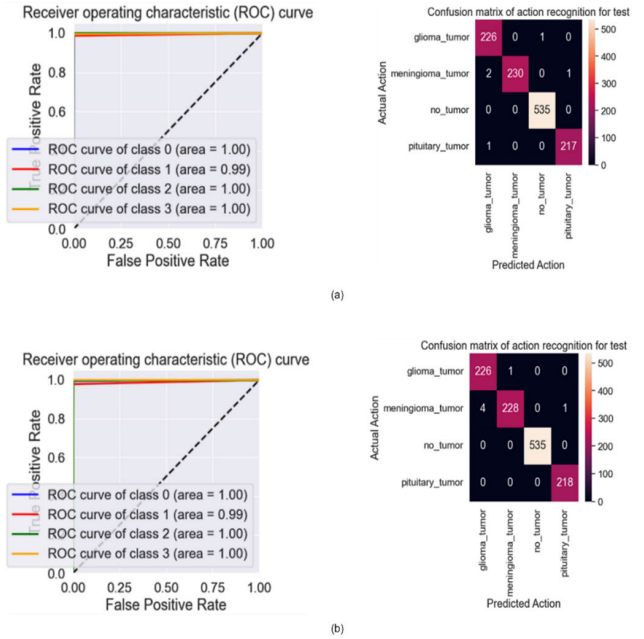

FIGURE 4. AUC-ROC curve and CM of the best-proposed model i.e., (a) CNN-KNN (b) CNN-SVM.

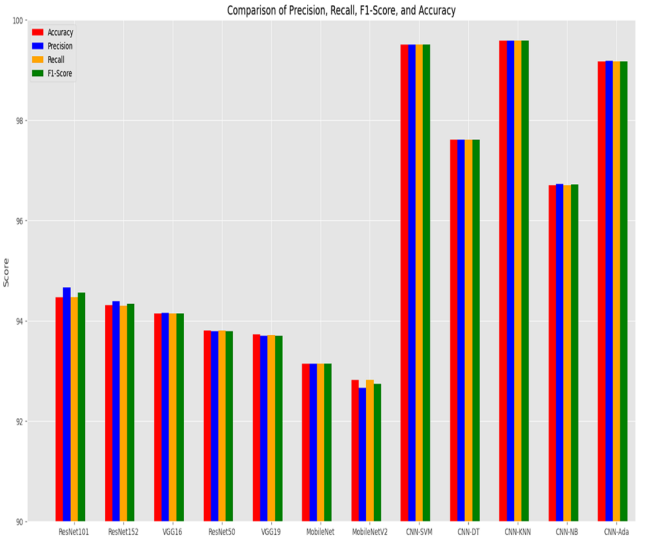

FIGURE 5. Bar chart representation for comparison between the proposed model with other CNN transfer learning models.

C. COMPARATIVE ANALYSIS OF THE PROPOSED MODEL WITH TRANSFER LEARNING MODELS AND STATE-OT-ART METHODS

This section describes the productivity of seven different pre-trained transfer learning models—VGG16, VGG19, ResNest50, ResNet101, ResNet152, MobileNet, and MobileNetV2—, as well as five classifiers i.e., DT, NB, AdaBoost, SVM, and KNN is highlighted. Table 5 highlights the highest accuracy scores achieved by each combination of model and classifier, with the highest scores indicated in bold. The CNN-KNN classifier beats all other classifiers' accuracy.

TABLE 7. Comparison of the Proposed model with other state-of-art.

Reference	Method	Accuracy (%)
[38]	Deep-CNN	98.22
[21]	VGG16	98.67
[37]	Refined EfficientNet-B0	98.87
[27]	Modified AlexNet	99.04
[13]	VGG19-SVM hybrid	99.39
[52]	PCA-CNN	99.27
Proposed Model	CNN-KNN	99.59
	CNN-SVM	99.51

A variety of standards were used to evaluate the models in this step. Tab. 6 displays the transfer learning strategy's complete performance limitation over our proposed model. With a 99.59% accuracy rate, the proposed hybrid model performed better than other models at correctly identifying all instances of BTs. ResNet101, ResNet152, and VGG16 models, on the other hand, had accuracy rates of 94.47%, 94.31, and 94.14%, respectively. ResNet50, VGG19, and MobileNet were the next three networks to achieve the highest accuracy value, with accuracy values of 93.81%, 93.73%, and 93.15, respectively. Finally, the MobileNetV2 model's accuracy reached 92.82%. Afterward, the proposed model is also compared with the highly accurate state-of-the-art algorithms (refer to Table 7). The proposed model outperformance all the popular transfer learning models and other state-of-the-art models.

V. DISCUSSION

Medical professionals have benefited from the latest developments in imaging technology. With the rapidly growing volumes of data, researchers in medical informatics have been able to reveal the best uses for this information. Early diagnosis of BTs is crucial for successful treatment, and this is where analytical comparisons between the suggested model and several previously investigated models come in handy. The classifier and convolutional sections are the two main components of the models used in research. These models are designed to extract features from images using a custom CNN and then classify the tumor type based on the extracted feature set using the classifier. The features can include edge detection, texture analysis, intensity histograms, and morphological features, which indicate abnormalities such as mass, irregular growth, and changes in tissue density. Once the convolutional component extracts the features from the input images, the classifier component assigns these characteristics to one of the targeted classes. Several well-known transfer learning models [49] and state-of-the-art have been put to the test. With just a few parameters that need to be taught, these analyzed deep models need a significant amount of computation and memory. Since four classes make up the "Brain Tumour" instance, the classifier component of these models needs to be altered. To implement the transfer learning technique [50], we added a dense layer with four classes and a "Softmax" activation function [51] to every

model that was evaluated. The proposed strategy outperforms all the popular transfer learning models, reducing complexity, and improving feature selection, and categorization. The Study obtained two hybrid classifiers, CNN-KNN and CNN-SVM, showing better results than many state-of-the-art models. Although the CNN-KNN hybrid showed slightly higher accuracy than the CNN-SVM, the CNN-SVM classifier model made no wrong estimations where a person was predicted to have a normal tumor, while the CNN-KNN misclassified for only one case. Therefore, both CNN-KNN and CNN-SVM can be taken as the best-proposed model. This study shows an effective approach to reducing the risk of getting false predictions of BT through MRI, which can cause patient death and the implications of the suggested model for public health and disease growth prevention.

VI. CONCLUSION AND FUTURE REMARK

Based on the findings of the study, it is recommended to use a combination of CNN and ML classifiers to diagnose glioma, meningioma, pituitary, and no-tumor brain diseases with high accuracy. To ensure the accuracy of the results, a sufficient amount of data is required for training and testing the model. Pre-processing techniques were also applied to enhance image scaling and data cleansing, which positively impacted all the models under study. After exposing the CNN model to the ML traditional classifiers, the model was able to quickly and accurately classify MRI image attributes. The suggested model was tested with a dataset of 1213 MRI images and achieved an impressive overall accuracy of 99.59% in identifying BTs. The study also found that the recommended categorization techniques performed better than several conventional procedures [53]. Although it is challenging to identify different illnesses from MRI images for successful therapy via a computer-aided diagnostic (CAD) system, the designed model can be used as a computer-assisted automated classification tool to accurately discover brain abnormalities in MRI in practical applications. However, to ensure the networks function at an advanced level and are exceptionally generalizable, a huge amount of data is required.

To improve the accuracy of our model in future iterations, we plan to incorporate more MRI images into the dataset. This will involve exploring additional medical image types such as computed tomography (CT), ultrasound, and X-ray, as detailed in the technique we have described. To further optimize the system's performance, we will also investigate other DL methods like data augmentation and GAN. To make our work more applicable to a wider range of brain conditions, we hope to expand the categories within the model to include additional disorders such as secondary tumors, Alzheimer's disease, and other relevant conditions. This will allow for a more comprehensive and versatile system capable of diagnosing a broader range of brain conditions.

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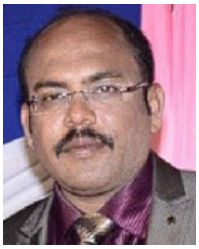
RAGHAV AGARWAL received the B.Tech. degree in computer science from the Vellore Institute of Technology, Andhra Pradesh. He worked on different technical and research-focused projects. He has published two patents on healthcare along with many journals and conferences during his graduation. Beyond the classroom, he regularly engages in research programs across the world that are relevant to his area of interests include AI/ML and data analytics.

SAGAR DHANRAJ PANDE received the Ph.D. degree in computer science and engineering from Lovely Professional University, Phagwara, Punjab, India, in 2021. He is currently an Assistant Professor (Senior Grade) with VIT-AP University, Amaravati, Andhra Pradesh, India. He has published and presented more than 60 papers in Springer, Elsevier, CRC, Taylor & Francis, and other reputable journals which are Scopus indexed and peer-reviewed journals. Also, he has published papers at international conferences springer on the topics of data mining, network security, and the IoT and its applications. He has supervised several postgraduate students in cybersecurity, computer networks, communication, and the IoT. He is responsible for teaching artificial intelligence, deep learning, machine learning, cyber crime and security, and python programming courses to undergraduate and postgraduate students. His research interests include deep learning, machine learning, network attacks, cyber security, and the Internet of Medical Things (IoMT). He received the ''Young Researcher Award'' and ''Best Ph.D. Thesis Award,'' in 2022, from Universal Innovators. Also, he received the ''Emerging Scientist Award,'' in 2021, from VDGOOD Professional Association.

SACHI NANDAN MOHANTY (Senior Member, IEEE) received the Ph.D. degree from IIT Kharagpur, India, in 2015, with MHRD Scholarship from the Government of India, and the Ph.D. degree from IIT Kanpur, in 2019. He has guided six Ph.D. scholar. He has published 60 international journals of international repute. He has edited 24 books in association with Springer and Wiley. His research interests include data mining, big data analysis, cognitive science, fuzzy decision-making, brain–computer interface, cognition, and computational intelligence. He was elected as a fellow of the Institute of Engineers and a Senior Member of the IEEE Computer Society Hyderabad Chapter. He received three best paper awards during the Ph.D. degree with IIT Kharagpur from the International Conference in Beijing, China, and the others from the International Conference on Soft Computing Applications organized by IIT Roorkee, in 2013. He was a recipient of the Best Thesis Award First Prize Award from the Computer Society of India, in 2015. He is also a Reviewer of *Robotics and Autonomous Systems* (Elsevier), *Computational and Structural Biotechnology Journal* (Elsevier), *Artificial Intelligence Review* (Springer), and *Spatial Information Research* (Springer). Top 2% world scientists ranking by Stanford University and Elsevier BV, in 2023. He is also the Editor-in-Chief of *EAI Endorsed Transactions on Intelligent Systems and Machine Learning Applications*.



SANDEEP KUMAR PANDA (Member, IEEE) is currently a Professor and the Head of the Department of Artificial Intelligence and Data Science, Faculty of Science and Technology (IcfaiTech), ICFAI Foundation for Higher Education (Deemed to be University), Hyderabad, Telangana, India. He has published 60 papers in international journals and international conferences and book chapters in repute. He has 17 Indian patents on his credit. He has four edited books named *Bitcoin and Blockchain: History and Current Applications* (USA: CRC Press), *Blockchain Technology: Applications and Challenges* (Springer ISRL), *AI and ML in Business Management: Concepts, Challenges, and Case Studies* (USA: CRC Press), and *The New Advanced Society: Artificial Intelligence and Industrial Internet of Things Paradigm* (USA: Wiley Press), in his credit. He has ten lakh seed money projects from IFHE. His research interests include blockchain technology, the Internet of Things, AI, and cloud computing. He is a member of ACM and a Life Member of IAENG. He was a recipient of the Research and Innovation of the Year Award 2020 from MSME, Government of India, and DST, Government of India at New Delhi, in 2020. He was also received the ''Best Teacher Award'' from ICFAI Foundation for Higher Education, Hyderabad, Telangana, INDIA on 13th Convocation 2023.