DOI: https://doi.org/10.52756/ijerr.2024.v46.013 *Int. J. Exp. Res. Rev.*, Vol. 46: 165-176 (2024)

Original Article | Peer Reviewed | Open Access

International Journal of Experimental Research and Review (IJERR)
© Copyright by International Academic Publishing House (IAPH)
ISSN: 2455-4855 (Online)
www.iaph.in

ISSN 2455-4855

A Hybrid Deep Learning Framework for MRI-Based Brain Tumor Classification Processing

Check for updates

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Article History:

Received: 15th Aug., 2024
Accepted: 17th Dec., 2024
Published: 30th Dec., 2024

Keywords:

Classification, CNN, Deep Learning, Feature Extraction, Feature Fusion, MRI, SVM, Tumor

How to cite this Article:
Hoshiyar Singh Kanyal, Prakash Joshi, Jitendra Kumar Seth, Arnika and Tarun Kumar Sharma (2024). A Hybrid Deep Learning Framework for MRI-Based Brain Tumor Classification Processing. *International Journal of Experimental Research and Review*, *46*, 165-176.
DOI: https://doi.org/10.52756/ijerr.2024.v46.013

Abstract: Classifying tumors from MRI scans is a key medical imaging and diagnosis task. Conventional feature-based methods and traditional machine learning algorithms are used for tumor classification, which limits their performance and generalization. A hybrid framework is implemented for the classification of brain tumors using MRIs. The framework contains three basic components, i.e., Feature Extraction, Feature Fusion, and Classification. The feature extraction module uses a convolutional neural network (CNN) to automatically extract high-level features from MRI images. The high-level features are combined with clinical and demographic features through a feature fusion module for better discriminative power. The Support vector machine (SVM) was employed to classify the fused features as class label tumors by a classification module. The proposed model obtained 90.67% accuracy, 94.67% precision, 83.82% recall and 83.71% f1-score. Experimental results demonstrate the superiority of our framework over those existing solutions and obtain exceptional accuracy rates compared to all other frequently operated models. This hybrid deep learning framework has promising performance for efficient and reproducible tumor classification within brain MRI scans.

Introduction

Classification of Brain Tumor is an important factor in diagnosing and treating brain tumors. Brain tumor is defined as an abnormal cell growth in the brain, which may be benign (non-cancerous) or malignant (Alanazi et al., 2022; Madhu et al., 2022). Different types of brain tumors exist, and each has unique identification traits. This complexity challenges the classification process (Mehnatkesh et al., 2023). Brain tumors are usually classified by the type of cell or tissue they arise from and their location in the brain. Gliomas, Meningiomas, Metastatic tumors and Pituitary adenomas are the most common types of brain tumors. Gliomas are the most common primary brain tumors, originating in glial cells that surround and support nerve cell activity (Haq et al., 2023). They are then classified into subtypes. Meningiomas are tumors that start in the meninges and include layers (Verma and Singh, 2022). They normally grow slowly and have a lesser possibility of becoming cancerous. Pituitary adenomas are a type of tumor in the pituitary gland, an organ about the size of a pea at the base of your brain that produces hormones (Aamir et al., 2022). These tumors can result in hormonal imbalances that may also interfere with normal physiological activity

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(Raza et al., 2022). Metastatic or secondary brain tumors result from the spreading of cancerous cells to the brain. Glioblastomas are the most common brain tumor in adults and come in several subtypes that make classification difficult based upon characteristics, often depending on what part of the body where an original cancer develops (Kang et al., 2021; Madhu et al., 2023). In addition to their location and cell type, brain tumors are also classified based on their grade, with higher grades signifying more aggressive or malignant behaviour of cancer. Brain tumors are grouped into grades based on how the cells in them look and act, with Grade I being the least aggressive type up to Grade IV (Nassar et al., 2024). Grading is based on the speed at which a tumor grows and its cellular characteristics, vascularity, and ability to invade nearby tissues (Majib et al., 2021). Characterization of brain tumors has been greatly improved through increased-resolution imaging techniques (Qodri et al., 2021).

Our understanding of the genetics and molecular underpinning of this heterogeneous disease is beginning to reveal its diverse underlying biology, facilitating the identification of novel subtypes as well as new therapeutic options (Habiba et al., 2022). Brain tumors are categorized for diagnostic and therapeutic purposes (Taher et al., 2022). It evolves with time regarding technology, research, and three-fold data. A more complete understanding of histopathology among different types and grades will be useful for correct diagnosis and treatment strategies to reduce patient morbidity (Irmak, 2021). Due to variations in brain tumor sizes, locations, and aggression levels among patients from clinical situations which means that this work is critical for a computer-aided diagnosis as the first step toward image-based healthcare (Lakshmi and Nagaraja Rao, 2022). Brain tumor diagnosis is vital for planning effective treatment and management. Commercially available web-based software packages that are widely used for gene expression data analysis have been developed. Integration of this type requires high-dimensional conceptual frameworks to account for tumor intricacies without collapsing them with dimensions linked uniquely or mostly by a healthy brain (Ahmed Hamza et al., 2022). Different computational techniques have been developed for brain tumor classification, including machine learning and image processing to address this. Machine learning is one of the most well-known computational methods for brain tumor classification, and a computer program learns to identify patterns in data and make decisions based on those patterns (Das, 2020). It facilitates learning from training data and generalizes it to unseen cases in brain tumor type classification. Feature extraction is important to extract the specific information related to a class that can separate between healthy and tumor tissue from medical images (Khan et al., 2024). One of the most used methods is wavelet transform, the frequency component that characterizes an image into another set (Mohanty et al., 2024). We use these coefficients as features for classification to create a more informative description of the tumor and its surrounding tissues (Dipu et al., 2021; Saraswat et al., 2024). The key contribution of this research is the following,

#The proposed model uses pre-trained CNN models to benefit from knowledge acquired on large datasets for better feature extraction, enabling it to increase its classification accuracy.

The framework directly embeds multi-modal MRI data, such as T1, T2 and Flair images, to account for all characteristics of brain tumors. This approach increases the neural network model's efficiency and resilience.

The paper uses data augmentation techniques (rotation, flip, and zoom) to expand better and generalize the training set.

The proposed framework uses an attention mechanism to pinpoint the most critical regions of MRIs. This mechanism is useful for training the model to focus on the most important features and maximize classification accuracy.

The remaining parts of this manuscript are organized as follows. Section 2 shows the recent works related to the research. Section 3 explains the proposed model and the different functions of the proposed framework. Section 4 compares the results and discusses current results with other existing models. Finally, section 5 explains the conclusion and future scope of the proposed research work.

Related works

Processing an image plays a vital role in creating an enhanced version of the images and we can also extract features from these images that are invisible to the naked eye (Dang et al., 2022). These techniques include edge detection, which can find the boundaries of tumors, and histogram equalization, which increases the contrast in images (Masood et al., 2022). Using this approach, we can make the features extracted from medical images more tumor-specific, reinforcing traditional classification algorithms. They process the computational issues of brain tumor types, size, and shape of different patterns for image classification (Sharif et al., 2023). Different types of cancer must be classified accurately because the treatment is very distinct, and results may vary enormously (Gab Allah et al., 2021). The other important feature of brain tumor classification is the collaboration between different imaging modalities (Khan et al., 2023). Due to the complementary characteristics of these modalities in describing brain tumors, a fusion of features extracted from versions of diverse imaging techniques can be more valuable for classification (Dataset). Classifying brain tumors involves a complicated process of combining multiple computational methods to enable accurate discrimination between tumor and non-tumor tissues in the normal healthy brain (Gautam et al., 2022; Jain et al., 2023; Himabindu et al., 2024; Bansal et al., 2024; Sagar et al., 2024). As algorithms and techniques in computational methods continue to develop, brain tumor classification will likely become increasingly accurate and less time-consuming for patients obtaining a diagnosis (Tyagi et al., 2024). Table 1 shows the comprehensive analysis of related works.

Research Gaps

Brain tumors are complex and nonuniform in shape. Existing algorithms often fail to recognize and classify the tumor correctly. This is confounded by the heterogeneous imaging appearances of tumors on

Table 1. Comprehensive analysis.

Author	Year	Model	Application	Advantage	Limitation
Lakshmi et al.	2022	Deep Learning	Classification	It can accurately classify brain tumors with less human error.	The application is limited to brain tumor classification
Dang et al.	2022	Deep Learning	Segmentation	Accurate identification and classification of brain tumors in different modalities	It requires a large amount of labelled data for training.
Ahmed Hamza et al.	2022	Deep Learning	Classification	Highly accurate and efficient classification of brain tumors from MRI data.	It requires large amounts of high-quality training data for optimal performance.
Das	2020	Deep Learning	Segmentation	It can detect brain tumors at an earlier stage using tumor segmentation methods.	This does not segment the novel brain tumor types with different modalities.
Khan et al.	2024	Deep Learning	Detection	It can process large amounts of data and analyze complex features at a faster pace.	It makes a resource-intensive process.
Mohanty et al.	2024	Deep Learning	Classification	It can enhance images and reduce noise, which is useful for accurate classification	The complex underlying processes are not easily interpretable.
Dipu et al.	2021	Deep Learning	Detection	It can automate the process of brain tumor detection	It can be sensitive to noise and artifacts in brain tumor images
Dang et al.	2022	Deep Learning	Segmentation	It can eliminate the need for invasive procedures	It can overfit the training data.
Masood et al.	2021	Deep Learning	Classification	It can analyze individual data and provide personalized treatment plans	It may not be able to generalize to new brain tumor types.
Sharif et al.	2021	CNN	Analysis	It can handle a wide variety of brain tumor types and sizes	It may necessitate specialized hardware for efficient processing.
Gab Allah et al.	2021	Deep Learning	Classification	It can reduce the cost of brain tumor detection by automating the process	It may raise ethical concerns
Khan et al.	2023	Ensemble Learning	Prediction	It can improve the quality of brain tumor images for more accurate detection.	It may provide individualized feedback during the detection process.

different modalities.

Many of the current models have a deterministic output, but we want to know how uncertain methods or confidence intervals are in predicted segmentation and classification in medical imaging predictions. This is one of the fundamental difficulties in deep learning research on brain tumors.

Many existing models face the challenge of small and hidden tumors, which might be overlooked in segmentation and classification. This is of particular significance in early managing and treating cerebral tumors.

Imaging of a brain tumor encompasses various modalities. Although deep learning models have presented promising solutions for processing multi-modal data, more research should be conducted on better using the multi-modal information for more accurate segmentation and classification.

Most existing models trained using one dataset may not generalize well when evaluated on another due to variations in image acquisition protocols and tumor characteristics. Based on this, implementing deep learning models in clinical practice remains challenging.

Novelty of the proposed model

We propose a hybrid deep learning framework for MRI-based brain tumor classification that combines the advantages of different deep learning architectures. It provides a basis for comprehensively analysing MRI images and extracting features, resulting in more accurate classification results.

Transfer Learning is an approach to using pre-trained models as a basis for training on another dataset. The knowledge learned by a model on other datasets can be further exploited using transfer learning to enhance brain tumor classification and reduce the training time of the proposed hybrid deep learning framework.

MRI scans usually have several modalities to describe various aspects of the tumor. A hybrid deep learning framework can be designed to effectively combine these disparate modalities, providing a more thorough analysis and, thus, improved classification accuracy.

Proposed model

The proposed hybrid deep learning frameworks intensify the true results of various deep learning models, but tumor classification has been proposed with improved accuracy and sensitivity for MRI-based brains. CNNs are also great at extracting spatial features of pictures, but they may need to be better at capturing sequential information. This is where RNNs are brought into the picture, and basically, they have been designed to deal with sequential data only. The proposed framework could be used to reduce overfitting and make the final model stronger. The hybrid deep learning framework is trained with a large dataset of MRI images labelled as having a brain tumor. After a few training iterations, our model can distinguish between the two classes based on important features learned within MRI images.

Tumor detection

Any data is presented in a very systematic way that represents complete information. It often contains many data points or records, each with a specific property. Pre-processing is the process of cleaning, organizing, and converting raw data (text inputted by a user) into an appropriate format for analysis or as inputs in machine learning algorithms. Normalization is a technique used in

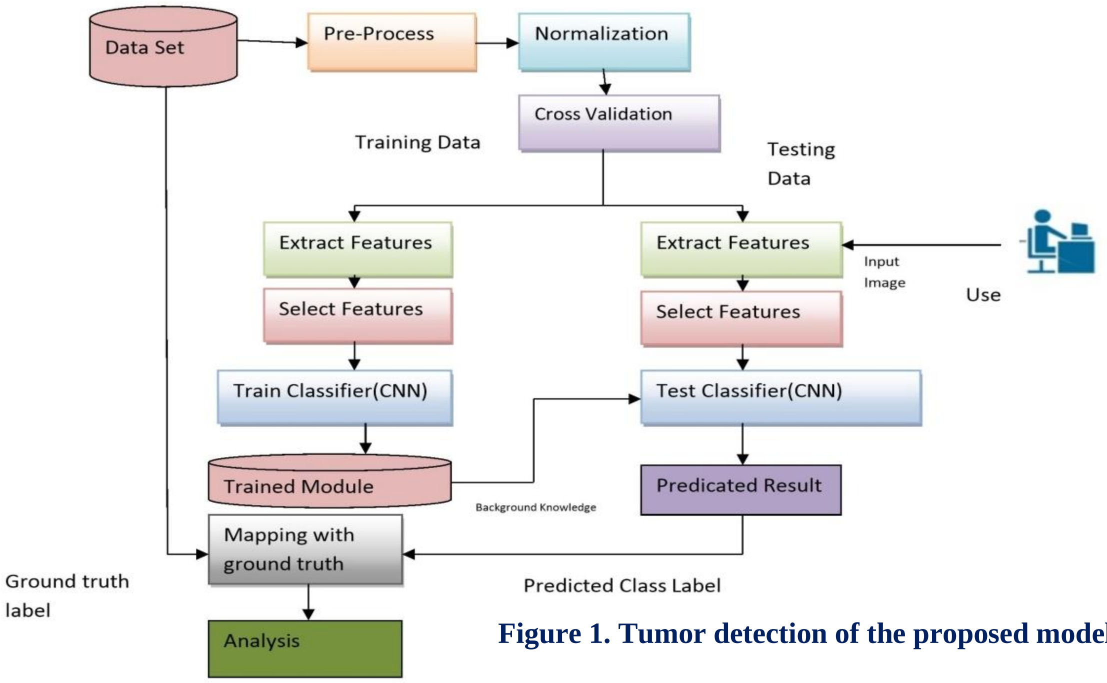

Figure 1. Tumor detection of the proposed model.

DOI: https://doi.org/10.52756/ijerr.2024.v46.013

processing data before training an algorithm when the differences in scales of various features can often mislead to placing too much stress on a few sets. Cross-validation is a statistical method used to estimate the skill of machine learning models. This method involves splitting the data set into several subsets, training with one subset, and testing on another to evaluate the generalization of a model. Training data is a section of the data set used to teach the proposed learning model. It includes Input Data and Output Labels (Target Values). Feature extraction is to study input data and obtain relevant information. The way of choosing a few features from all the variables to get better performance for a model is Feature Selection. Training a classifier requires feeding data through the CNN to predict outputs by updating the CNN parameters and minimizing the error between the predicted and actual outputs. The construction of the proposed model is shown in the following figure 1

The trained module produces the training process containing a trained model with updated parameters according to input data. Testing data is a small part of the set used to determine how well your model has been trained on that dataset. When testing your classifier, take out the extracted and selected features from test data, pass through trained CNN, and compare the predicted output with the actual one. The input image is the data used to predict (feed) into a model classifier, which is either an image or images in a batch. Prediction is the output of the trained classifier when you provide it with an input image. It may be a class label, predicted value, or probability. The actual label is used as a standard against which the performance of a trained model can be evaluated. Mapping from ground truth means predicting with a trained model and comparing the output against the actual label to understand how well our models perform. A predicted class label is the classification label of a data point that our trained classifier has predicted after being fed an input. Analysis can be understood as analysing and interpreting the results of a trained classifier, which helps us to understand why a certain decision is made based on the data provided.

Tumor Classification

MRI images can be used to see different structures and tissues in the brain. Prepare the MRI brain images to analyze the data pre-processing further. This may involve cleaning noise, correcting distortions, and normalizing data to make the results consistent and correct. Augmentation is slightly altering the current dataset to enlarge it artificially. This is usually achieved by rotating, flipping, and sometimes adding noise to the images, which would increase our models' power. The encoder is what processes the input data and extracts its most salient features. In this setup, the encoder is fed with pre-processed MRI brain images, automatically learning how to segment different human brain parts. The tumor classification of the proposed model is shown in the following figure 2

The convolutional layer convolves (applies filters) the input data and thus extracts features. One of the best training techniques for stability and speed is Batch Normalization—ReLU (Rectified Linear Unit) - An activation function that adds non-linearity to the network. Pooling is a sample-based down-sampling technique for reducing the size of feature maps, which, in turn, helps reduce overfitting. It helps to minimize the parameters of the network and overfitting. Pooling indices record the locations of any selected features during max pooling operations. This helps recover activity from that layer more completely during the up-sampling. SoftMax is a central activation function used to classify tasks. This is a function that acts upon the output of your network and helps to convert these results into human-understandable data. The decoder is the part of the network that uses encoded input to recreate output data in its original shape. It does so by reconstructing the original features using up-sampling and other methods. This partitioned outcome is the last yield of the model, which separates an information MRI mind picture into various classes. Mobile Net is a neural network architecture designed specifically for mobile and embedded-based vision applications. It has been optimized for faster computation and is widely used in image classification. It is a way of classifying data into different classes. The model has been trained to identify various structures and tissues within MRI brain images in this particular instance.

Proposed Algorithm

Step 1 defines the size of the image and batch in IMG_SIZE as 256, and BATCH_SIZE is set to 32. We will use these parameters to tell image_dataset that we are processing images in a dataset. In step 2, Load the dataset, which is split into three directories—train, validation, test, and step. 3 Process images using the ImageDataGenerator function, which performs transformations on the image like rescaling, rotating, shifting, and flipping. This is also useful in preventing the model overfitting problem that changes data. Step 4 creat

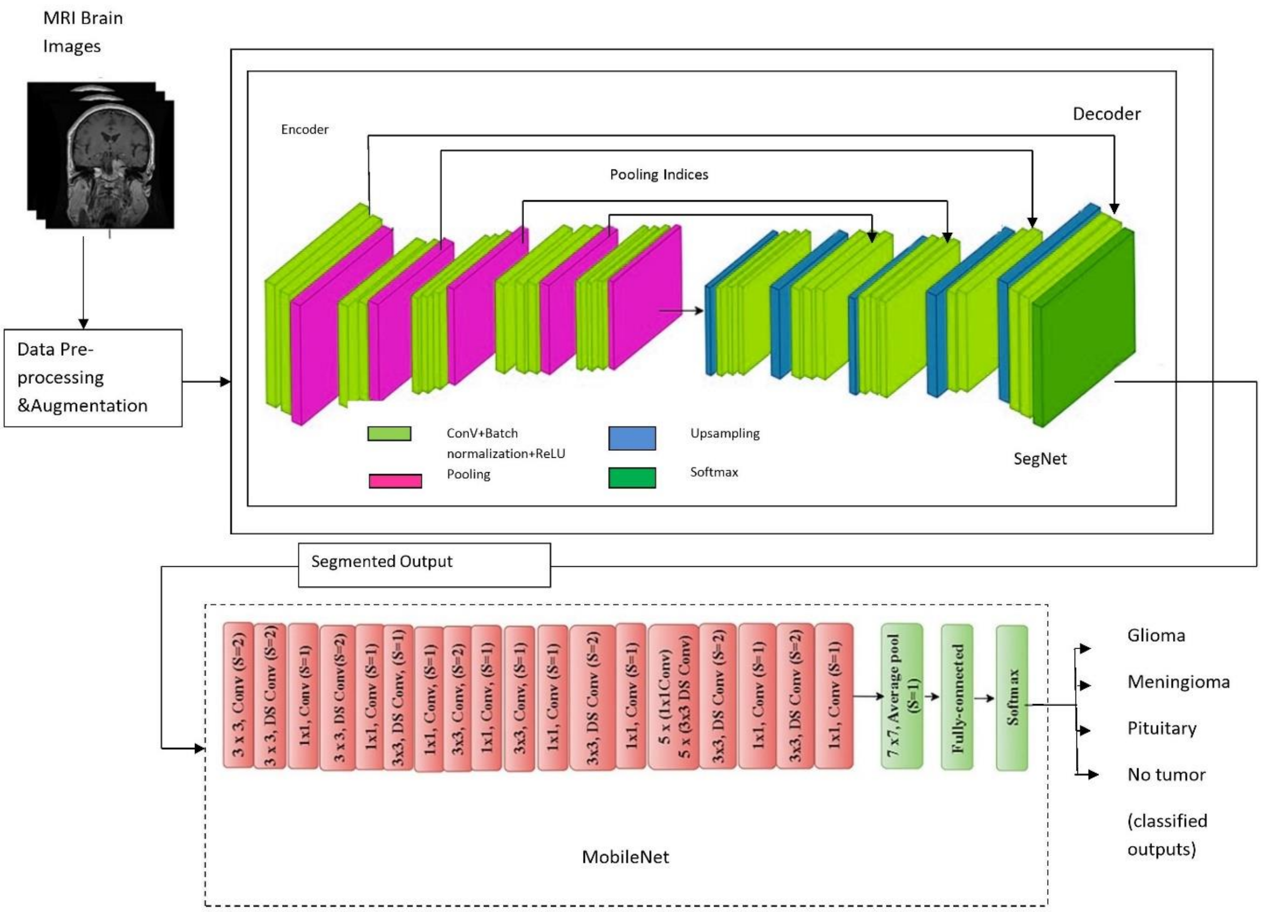

Figure 2. Tumor classification of proposed model.

-es training and validation image batches using the ImageDataGenerator method, which uses the transformations made in Step 3 to generate images on the fly. Step 5 uses the Sequential function to build a linear stack of layers—model. Step 6 adds convolutional layers to the model by calling the Conv2D function and specifying the number of filters and kernel size. To make the output size the same as the input. By convention, the parameter 'input_shape' specifies the shape of images in input, which has been set as (IMG_SIZE, IMG_SIZE,1) for this model. The above code explains all the parameters used, which rely on an activation function used for CNN most of the time. On the other hand, MaxPooling2D is used to reduce the spatial size of a feature map, and BatchNormalization helps with normalizing output from the previous layer.

Algorithm.1: Hybrid Deep Learning Algorithm

Step.1 Define the image size and batch size
    IMG_SIZE = 256
    BATCH_SIZE = 32
Step.2 Load the dataset
    train_dir = "train/"
    val_dir = "val/"
    test_dir = "test/"
Step.3 Preprocess the images
    train_datagen = ImageDataGenerator(rescale=1/255, rotation_range=20, width_shift_range=0.2, height_shift_range=0.2, zoom_range=0.2, horizontal_flip=True)
    val_datagen = ImageDataGenerator(rescale=1/255)
Step.4 Generate batches of training and validation images
    train_generator = train_datagen.flow_from_directory(train_dir),
    validation_generator = val_datagen.flow_from_directory(val_dir)
Step.5 Build the model
    model = Sequential()
Step.6 Add convolutional layers
    model.add(Conv2D(x, (a,b), padding='same', input_shape=(IMG_SIZE, IMG_SIZE, 1)))
    model.add(Activation('relu'))
    model.add(MaxPooling2D((2,2)))
    model.add(BatchNormalization())
Step.7 Flatten the output of the previous layer
    model.add(Flatten())
Step.8 Add fully connected layers
    model.add(Dense(x))
    model.add(Activation('relu'))
Step.9 Add output layer
    model.add(Dense(x, activation='softmax')) # 3 classes: glioma, meningioma, pituitary tumor
Step.10 Compile the model

```
        model.compile(optimizer='adam', loss='categorical_crossentropy', metrics = ['accuracy', precision, recall, 'f1-score'])
Step.11 Train the model
        history = model.fit(train_generator, validation_data=validation_generator, epochs=100-700)
Step.12 Evaluate the model on the test set
        test_datagen = ImageDataGenerator(rescale=1/255)
Step.13 Make predictions on the test set
        predictions = model.predict(test_generator)
```

The output generated from the previous layer will be flattened using the Flatten function, which transforms a multidimensional output into a one-dimensional vector in Steps 7 and 8, adding fully connected layers to the model with a specific neuron count. In this dense layer, we use 'real' as the activation function to add nonlinearity. Step 9 Connect the output layer of the mother del using the e-density function. The nu number of neurons must be equal to. The classes are 3: glioma, meningioma, and pituitary. Tumor. To predict the output, we use the activation function' softmax' to normalize all predictions and give a probability score for all classes.

Step 10 Compile the model using the 'compile' function and oblige an optimizer-loss-metric triplet to determine whether we are underfitting or overfitting. This uses the Adam optimizer, with categorical_crossentropy as the loss function and accuracy precision-recall f1-score metrics. To train our model, we call the fit function, wherein X, Y, or create a mini-batch generator and epochs, like the number of iterations to perform for training. The image data is then fed into the model in batches for training, with the evaluation of validation data in Step 11. Step 12 is to predict new using the ImageDataGenerator function with rescaling as its transformation by testing against a test set. Step 13 provides predictions on the test set for obtaining our desired classes using a trained model.

Results and discussion

The performance of the proposed model has been compared with the existing Brain tumor classification framework (BTCF), deep residual learning framework (DRLF), hybrid deep learning-based approach (HDLBA), machine learning classifiers (MLC) and Feature-enhanced deep learning (FEDL) as shown in table 2 and table 3. Here, the MRI brain tumor dataset (Sagar et al., 2024) has been used and python simulator is used to execute the results.

Computation of Accuracy

The accuracy is calculated by taking the sum of all labels a model predicted correctly and dividing it into the total number of ground-true in the data set. This is done by providing the MRI images to the model and getting it predicted for every image. We then compare the predicted labels with the known same class of all items in dataset and calculate what portion we correctly classified.

Figure 3 shows the comparison of accuracy. The proposed model (HDLF) obtained 90.67% accuracy in a computational point. The same point, existing BTCF reached 67.62%, DRLF reached 82.63%, HDLBA obtained 47.23%, MLC reached 59.34% and FEDL obtained 65.48% accuracy. The more of images where they guessed correctly with the higher accuracy. Many images are used in this process, and the accuracy is averaged across all images to evaluate how well the model is performing.

Table 2. Comparison of accuracy.

Author	Year	Model	No. of Epochs						
			100	200	300	400	500	600	700
Alanazi et al.	2022	BTCF	58.62	60.12	61.62	63.12	64.62	66.12	67.62
Mehnatkeshet al.	2023	DRLF	79.09	79.68	80.27	80.86	81.45	82.04	82.63
Raza et al.	2022	HDLBA	36.01	37.88	39.75	41.62	43.49	45.36	47.23
Kang et al.	2021	MLC	56.34	57.38	57.51	58.47	58.04	58.89	59.34
Mohanty et al.	2024	FEDL	61.41	63.02	63.08	64.06	63.88	64.88	65.48
Proposed	2024	HDLF	85.98	86.76	87.54	88.32	89.10	89.89	90.67

Table 3. Comparison of precision.

Author	Year	Model	No. of Epochs						
			100	200	300	400	500	600	700
Alanazi et al.	2022	BTCF	64.55	65.96	67.18	67.78	69.33	70.37	71.51
Mehnatkesh et al.	2023	DRLF	85.51	86.25	86.66	88.38	88.68	89.64	90.48
Raza et al.	2022	HDLBA	36.77	37.64	38.74	39.74	40.47	41.52	42.47
Kang et al.	2021	MLC	54.72	56.27	56.60	58.24	58.97	60.10	61.15
Mohanty et al.	2024	FEDL	70.39	71.93	72.34	73.93	74.28	75.51	76.48
Proposed	2024	HDLF	88.51	90.24	90.52	92.22	92.38	93.69	94.67

Computation of Precision

Precision is the performance metric that measures how many selected items were relevant (the number of correct positive results divided by the number of all returned positives). It is used within a hybrid deep learning framework for brain tumor classification using MRI, which measures the number of true positive predictions (complete tumoral identification, i.e., correct) to the whole positive prediction made by the model.

Fig.4 shows the comparison of precision. The proposed model (HDLF) obtained 94.67% precision in a computational point. The same point, existing BTCF reached 71.51%, DRLF reached 90.48%, HDLBA obtained 42.47%, MLC reached 61.15% and FEDL obtained 76.48% precision. The algorithm compares this score to the total number of positive cases in your original data set, effectively giving you a precise rate at which our classifier is precise. The same process is repeated for each tumor class (benign and malignant) to obtain precision rates specific to that class.

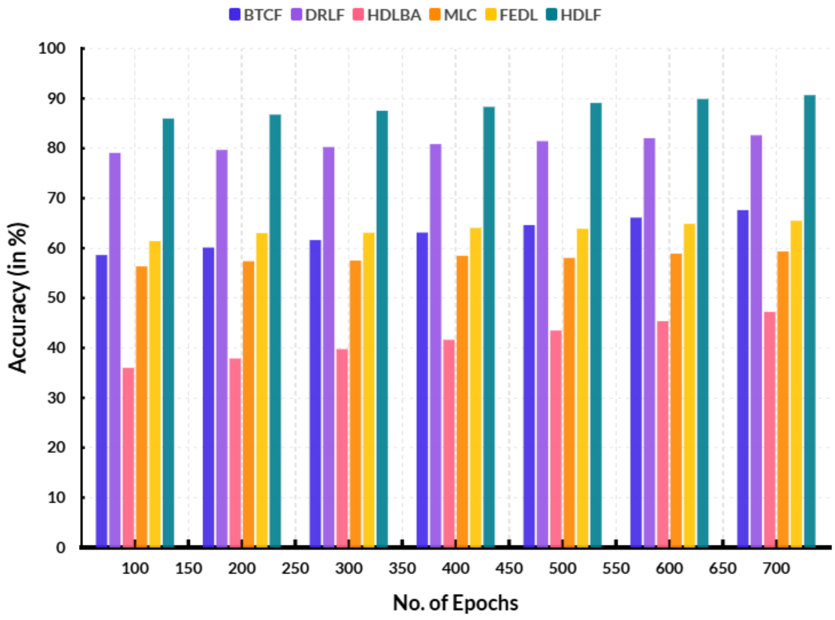

Figure 3. Comparison of accuracy.

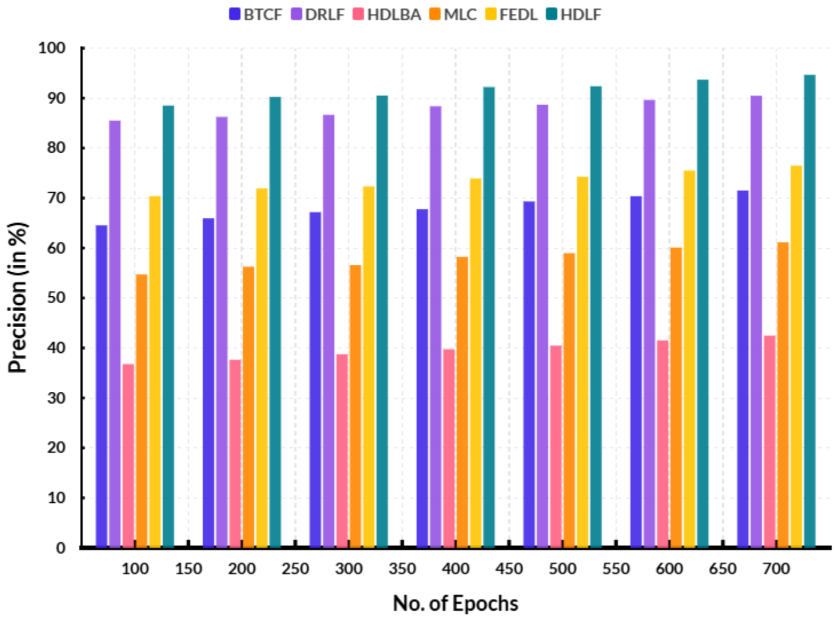

Figure 4. Comparison of precision.

Computation of Recall

Recall is a metric used to evaluate the performance of a classification model at identifying all relevant instances from within an average number of original class constituents. It is calculated for each patch by combining the feature extraction result using a convolutional pre-trained neural network (CNN) and classification based on SVM in a hybrid deep learning framework with MRI images. The recall is then computed by taking the correctly predicted tumor images and dividing them by the total number of real tumors in the dataset.

Table 4. Computation of Recall.

Author	Year	Model	No. of Epochs						
			100	200	300	400	500	600	700
Alanazi et al.	2022	BTCF	62.33	62.00	60.66	59.52	58.47	57.54	56.52
Mehnatkesh et al.	2023	DRLF	60.20	58.70	57.59	57.21	56.20	55.13	54.18
Raza et al.	2022	HDLBA	79.99	79.40	78.42	77.21	76.07	75.21	74.21
Kang et al.	2021	MLC	52.66	51.62	51.49	50.53	50.96	50.10	49.66
Mohanty et al.	2024	FEDL	68.59	66.98	66.91	65.94	66.12	65.12	64.52
Proposed	2024	HDLF	87.40	85.62	85.82	84.84	85.32	84.31	83.82

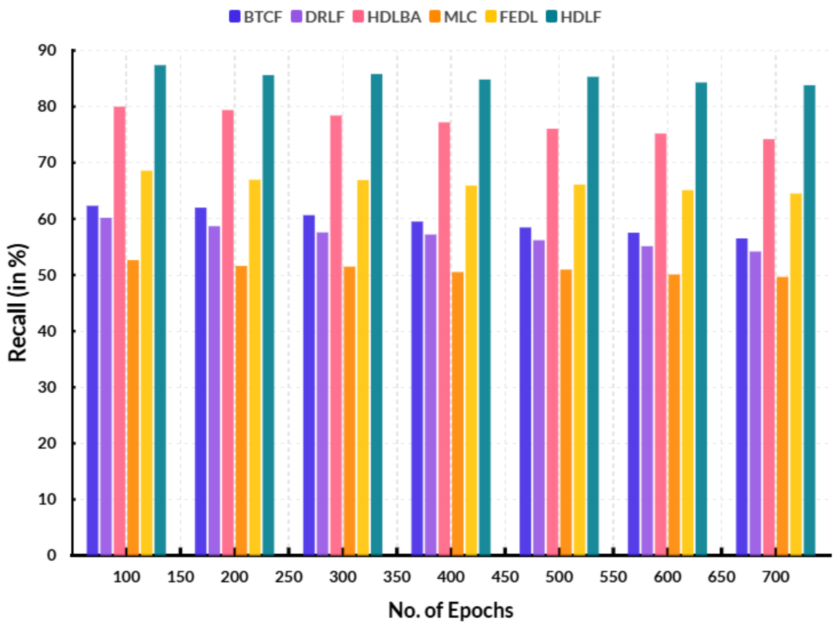

Figure 5. Comparison of Recall.

Figure 5 shows the comparison of recall. The proposed model (HDLF) obtained 83.82% recall in a computational point. The same point, existing BTCF reached 56.52%, DRLF reached 54.18%, HDLBA obtained 74.21%, MLC reached 49.66% and FEDL obtained 64.52% recall. The metric provides a view of how effective the model is at detecting images representing brain tumors, which are critical to delivering correct diagnoses and treatments for patients and shown in table 4.

Computation of F1-Score

F1-score is a performance metric combining Precision and Recall into one metric. It is calculated by comparing predicted results to ground truth labels and comparing the balance between precision and recall in model predictions. The input images are initially pre-processed to augment tumor features and suppress noise, followed by computation of the f1-score. The extracted features from the pictures are then feature-engineered using deep learning techniques. These features are inputted to a classifier like a support vector machine for brain tumor prediction as shown in table 5.

Fig.6 shows the comparison of f1-score. The proposed model (HDLF) obtained an 83.71% f1-score at a computational point. The same point, existing BTCF

Table 5. Comparison of Recall.

Author	Year	Model	No. of Epochs						
			100	200	300	400	500	600	700
Alanazi et al.	2022	BTCF	60.33	59.99	59.07	57.80	56.54	55.81	54.84
Mehnatkesh et al.	2023	DRLF	59.27	57.86	56.64	56.04	54.49	53.45	52.31
Raza et al.	2022	HDLBA	78.57	77.83	77.42	75.70	75.40	74.44	73.60
Kang et al.	2021	MLC	49.28	47.73	47.40	45.76	45.03	43.90	42.85
Mohanty et al.	2024	FEDL	64.61	63.06	62.66	61.07	60.72	59.49	58.52
Proposed	2024	HDLF	89.87	88.14	87.86	86.16	86.00	84.69	83.71

reached 54.84%, DRLF reached 52.31%, HDLBA obtained 73.60%, MLC reached 42.85% and FEDL obtained 58.52% f1-score. This framework combines the advantages of CNN and SVM to optimize brain tumor classification in MRI images. CNNs are known for their ability to extract useful features of pictures, and SVM provides the facility to separate these relevant features. The CNN extracts informative features from MRI images in the hybrid framework, which are directly added to SVM for categorization. CNN can handle complex and high-dimensional data, while SVM makes a more robust classification with high accuracy. The proposed framework combines the strengths of both models and detects improved results for brain tumor classification from MRI. generality and expandability to new datasets. The SVM can be used for dataset-specific fine-tuning while pre-training on a big dataset with CNN. The proposed model obtained 90.67% accuracy, 94.67% precision, 83.82% recall and 83.71% f1-score. MRI-based brain tumor classification using a proposed framework is a very useful system that can help doctors to accurately detect and classify brain tumors. This could improve patient outcomes by making it possible to create better diagnoses, which in turn would make treatment more efficient. This framework could be extended with broader research and development into other medical imaging applications, contributing to deep learning in the healthcare field.

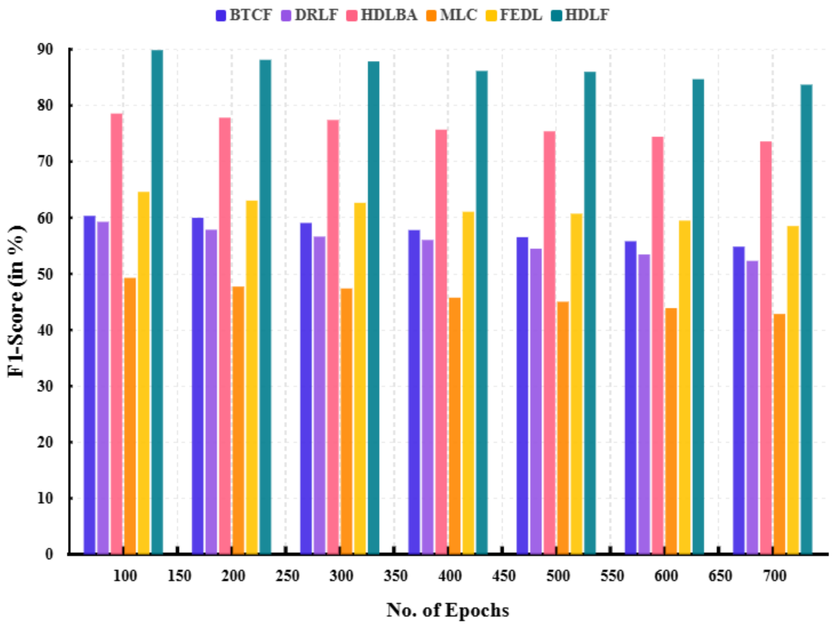

Figure 6. Comparison of F1-score.

Conclusion

This hybrid deep learning framework utilizes powerful machine learning techniques such as CNN and SVM to provide better, consistent results in brain tumor classification on MRI. CNNs are particularly suited for processing MRI images due to the ability of CNN architectures to automatically discern regions useful in detecting a tumor via feature extraction. Conversely, SVMs are known for being adept at working with high-dimensional data and extracting intricate decisions based on this information. The hybrid framework leverages the combined capability of CNN and SVM, which helps to achieve better classification accuracy than simply using one. CNN can discover useful features from the MRI images, which will be used as input nodes of SVM for classification. This hybrid system provides improved

Conflict of interest

None

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How to cite this Article:

Hoshiyar Singh Kanyal, Prakash Joshi, Jitendra Kumar Seth, Arnika and Tarun Kumar Sharma (2024). A Hybrid Deep Learning Framework for MRI-Based Brain Tumor Classification Processing. *International Journal of Experimental Research and Review, 46*, 165-176.

DOI : https://doi.org/10.52756/ijerr.2024.v46.013