FEATURE REDUCTION FOR ENHANCED BRAIN TUMOR DETECTION WITH TRANSFER LEARNING

[1]AMULYA MATTUKOYYA, [2]DR.U.SATHISH KUMAR, DR.K.CHAITANYA[3]

[1]MTech Student, [2]Assistant Professor, [3]Assistant Professor
[1]Department of Computer Science of Engineering,
[1]ANU college of Engineering and Technology, Acharya Nagarjuna University, Guntur, Andhra Pradesh

ABSTRACT *:* An aberrant clump of cells forming tissue is called a tumor, feeding on healthy cells and continuously growing. Brain tumors are particularly significant, as they contribute to a high mortality rate among cancer types. The accurate classification of brain tumors through Magnetic Resonance Imaging (MRI) is crucial for effective treatment. It serves as a critical initial step in identifying abnormal tissue and enabling efficient patient recovery. In this study, we present an in-depth analysis of brain tumor detection and classification. We assess the performance of a deep learning approach using a pre-trained ResNet50 model through transfer learning, coupled with dimensionality reduction techniques. Additionally, we leverage machine learning algorithms to predict brain tumor cells. The pre-trained ResNet50 model is applied to a dataset of MRI brain tumor images. This classification process aids medical professionals and researchers in the early-stage detection of brain tumors, offering valuable insights for timely intervention.

Keywords: BrainTumorDetection, Medical Imaging, MRI Images, Transfer Learning, Dimensionality Reduction, Deep Learning, machine learning algorithm.

1. Introduction:

In the real of medical research, brain tumors represent a critical and potentially fatal ailment. In the year 2019, the American Cancer Society estimated that 23,820 malignant brain or spinal cord tumors would be diagnosed in the United States, affecting 13,410 males and 10,410 females. This calculation excludes benign (non-cancerous) tumors. Their assessment also revealed that an estimated 17,760 individuals, comprising 9,910 males and 7,850 females, would succumb to brain and spinal cord tumors that year. Brain tumor survival rates vary significantly based on the tumor type and the age of the patient.

Medical terminology defines a brain tumor as an aberrant cell growth within the brain. Within the cranial cavity, this development puts pressure on the brain and interferes with its normal function. Primary or secondary brain tumors are possible. Primary brain tumors can develop from inside the brain or from adjacent tissues such the pituitary, meninges, pineal gland, or cranial nerves. On the other hand, malignant cells that originate in other organs such as the lung, kidney, or breast can spread to the brain and cause secondary brain tumors. These tumors may be divided into two main categories: malignant and benign. Malignant tumors are cancerous and constantly spread throughout the brain, perhaps infecting other tissues, whereas benign tumors are not cancerous.

Tumors are categorized by the organization known as the World Health Organization (WHO) into categories I through IV according on anomalous tissue features. Small and generally benign, grade I tumors are frequently treated surgically to ensure long-term survival. Grade II cancers tend to develop and have mild abnormalities. Grade four tumors, which multiply swiftly and offer the greatest threat due to their rapid growth and development of new blood arteries, are more dangerous than Grade III tumors, which are malignant and demonstrate aggressive cell production.

Diagnosing brain tumors is a complex endeavor influenced by factors such as size, shape, location, and tumor type. Early-stage tumors pose challenges in accurately determining their size and resolution. Treatment and prognosis for patients depend heavily on the ability to recognize and differentiate between malignant as well as benign brain tumors. Two MRI pictures of two brains—one in good health and another with a tumor—are displayed in Figure 1.
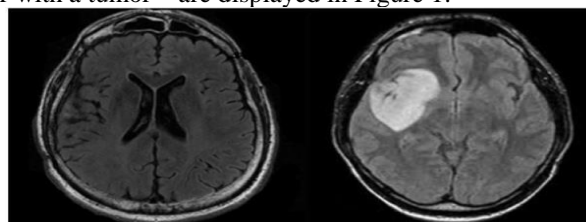

figure 1. healthy and tumor image [4]

Brain cancers are found using medical imaging techniques such as magnetic resonance imaging (MRI), PET/CT, and computer tomography (CT). MRI, in instance, offers a non-invasive way to expose the inside body structure utilizing magnetic

fields and radiofrequency pulses. A useful technique for clinical diagnosis, magnetic resonance imaging (MRI) offers a wide variety of pictures, sequences, and comprehensive information on brain tissues.

Three MRI sequences are commonly used to diagnose brain tumors: T1-weighted, T2-weighted, and FLAIR-weighted (Fluid Attenuated Inversion Recovery). In this work, we provide a novel method for feature extraction using deep learning techniques, namely a Convolutional Neural Network (CNN) model with the transfer learning strategy. Furthermore, we apply dimensionality reduction techniques to improve the accuracy of brain tumor categorization.
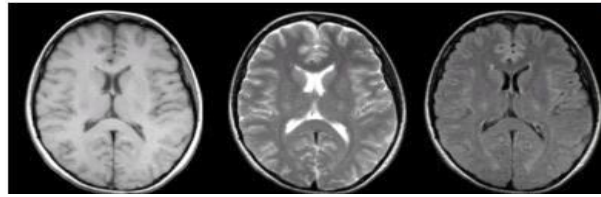

Figure 2. Different MRI Sequences [5]

The following is the order of the remaining portions of the paper: The relevant research that is being done in this field is presented in Section II. The suggested approach and theoretical underpinnings are covered in Section III. The results are thoroughly demonstrated with many performance measures in Section IV. The general conclusion is given in Section V.

2. Related Work:

A CNN (Convolutional Neural Network) was utilized in a study by Das et al. [1] to concentrate on the creation of a model for the categorization of brain cancers utilizing T1-weighted contrast-enhanced MRI scans. There are two main phases to the suggested approach. The photos were first prepared using image preprocessing methods, and then CNN was used to classify the images. The study employed a dataset consisting of 3,064 photos that showcased three discrete categories of brain cancers: gliomas, meningiomas, and pituitary tumors. The researchers' remarkable outcomes, which included an outstanding testing accuracy of 94.39%, a mean precision of 93.00%, and an ordinary recall of 93%, were attained by using the CNN model. Notably, when tested, their suggested approach performed better than a number of well-known current solutions on this dataset.

Brain MRI picture segmentation and classification were carried out by Narayana and Reddy [2] using a support vector machine and an algorithm based on genetics, a metaheuristic efficiency approach. Their experimental results showed an impressive degree of accuracy, with a correctness rate of almost 91% in identifying diseased and normal brain tissues from MRI scans.

Mohsen and colleagues [6] conducted a study wherein they categorized sixty-six brain MRIs into four different groups: glioblastoma, sarcoma, mild, and metastatic bronchogenic carcinoma tumors. For this, they used an architecture of deep neural networks. The Fuzzy C-means clustering algorithm was used to divide the photos into five regions. After the tumor features were recovered from the segmented areas using the wavelet transform method (DWT), the principal component analysis (PCA) method was utilized to efficiently control the feature dimensions. The Deep Neural Network's classification stage then made use of the generated feature vector. This integrated strategy, which combined PCA with DWT as a reliable feature extraction method, produced outstanding results in terms of several performance measures. With the help of a Deep neural network (DNN) classifier, the suggested method produced a 96.97% accuracy rate, 0.97 recall, 0.97 precision, 0.97 F-Measure, and 0.984 AUC (ROC) value.

Kumar and Kumar [7] performed the segmentation and classification of brain tumors using ensemble approaches in a different study. Their method included a number of classifiers into an ensemble framework, such as support vector machines, neural networks, and Extreme Learning Machines (ELM). There were many phases to the procedure, which included segmentation, classification, feature extraction, and preprocessing. Preprocessing operations were performed on the source MRI image using the Median filtering technique in the first step. Then, segmentation was carried out using the Fuzzy C-Means (FCM) clustering technique. Utilizing the Gray Level Co-Occurrence Matrix (GLCM), features were recovered during the third step of the procedure.

An automated technique for classifying brain tumor stages was created by utilizing ensemble classification. With brain imaging analysis, our ensemble classifier successfully discriminates among tumor and non-tumor areas. The technique provides faster performance, more precision, and greater stability, according to experimental data. The suggested approach had an elevated accuracy rate of 91.17% in the testing.

A thorough technique that combines the Grey Level Co-occurrence Matrix (GLCM) and Gaussian Mixture Model (GMM) with a machine learning framework is used in a research article written by Byale et al. [8]. The suggested approach includes a pre-processing stage using a median filter that adapts to efficiently remove noise from the source data. After that, the area of interest is identified by segmentation utilising the GMM model, and various tumor characteristics are extracted based on the fragmented MRI image using the GLCM approach. Next, the tumors are classified using the Neural Network (NN), which can differentiate between benign, malignant, and normal instances. Surprisingly, the research yielded an astounding 93.00% overall accuracy rate when evaluated on a dataset comprised of 60 MR images taken at MS Ramaiah Memorial Hospital in Bangalore.

Hemanth et al. [9] used machine learning techniques in their study to detect malignancies in MRI images.

Their proposed model integrates an automatic MRI image segmentation method that utilizes a CNN model with a compact 3 x 3 kernel. This single technique is applied for both segmentation and classification. The proposed model encompasses several key stages, including data collection, pre-processing, average filtering, segmentation, feature extraction, and classification. Impressively, this model achieved an overall accuracy rate of 91.00% when tested on the UCI dataset.

Shree and Kumar [10] conducted a research study utilizing a combination of Discrete Wavelet Transformation (DWT) and a probabilistic neural network (PNN) to identify and classify brain tumors from MRI images. Their research work introduced a preprocessing stage to address noise removal, image smoothening, and feature extraction, which involved a mixture of DWT, textural analysis, and the Gray-Level Co-occurrence Matrix (GLCM). To eliminate any noise that may emerge following segmentation, morphological operations were applied to the segmented images. The classification and detection of brain tumors in MRI images were accomplished using a probabilistic neural network (PNN) classifier. Experimental results demonstrated the effectiveness of the proposed technique in accurately discerning normal and abnormal brain tissues from MRI images. Impressively, this approach achieved an exceptional accuracy rate of nearly 100% when tested on the diacom dataset.

In their respective research studies, Badisa et al. [17] and Patil et al. [18] introduced different approaches to brain tumor detection and classification. Badisa et al. [17] proposed a CNN model that serves as both a feature extractor and classifier. They incorporated a Gaussian filter in the preprocessing phase before feature extraction.On the other hand, Patil et al. [18] presented a predictive model for brain tumor detection using a deep learning approach. In this approach, a custom CNN model was implemented, and its results were compared to those of a pre-trained CNN model, VGG16, using the brain tumor detection dataset from Kaggle. The proposed model achieved a testing accuracy of 80% and an F1 score of 0.80. Additionally, the fine-tuned VGG16 model demonstrated an accuracy of 90% and an F1 score of 0.85 when evaluated on the same dataset.

In their study, Pashaei et al. [19] introduced a classification approach that combines Kernel Extreme Learning Machines with a CNN model to categorize three distinct types of brain tumors. Their results were subjected to comparison with various other classifiers, including multi-layer perceptron, stacking, XGBoost, support vector machine, radial basis function kernel, and fully connected layers. These evaluations were performed on a brain tumor dataset proposed by Cheng et al. [29], and the accuracy achieved by their method was compared to state-of-the-art results.

In a separate research study, Sajjad et al. [20] put forward a comprehensive augmentation-based model designed to classify brain tumors into four distinct stages. Their approach entailed the segmentation of images using a CNN model, followed by an extensive data augmentation process. Subsequently, these augmented images were input to a pre-trained CNN model, VGG19, for feature extraction and classification.This proposed approach yielded a commendable accuracy rate of 90.67% when assessed using the radiopaedia dataset [28].

Ari and Hanbay [21] introduced an innovative approach for brain tumor detection, employing a deep learning-based model known as Extreme Machine Learning Local Receptive Field (ELM-LRF). In this methodology, the tumor image is initially processed by a CNN model for feature extraction. Subsequently, the pooled features are conveyed to the ELM's hidden layer, followed by the classifier.Their proposed approach demonstrated exceptional performance, achieving an impressive accuracy rate of 97.18% when evaluated on the dataset introduced by Kwan et al. [30].

In their research, Afshar et al. [23] introduced a capsule network as an innovative approach to address the limitations of the CNN model in the categorization of brain tumors. The outcomes of their proposed model were compared with those of a conventional CNN model to demonstrate the effectiveness of their approach.It's worth noting that this approach utilized a single layer capsule network; however, the potential for improvement by increasing the complexity of the network in future work is acknowledged.

Deepak and Ameer [24] have proposed a transfer learning approach in their research. They have employed the pre-trained GoogLeNet model for classification, fine-tuning the last layers of GoogLeNet to achieve state-of-the-art performance on the Figshare brain tumor dataset [31].

Cinarer and Emiroglu [25] conducted a comparative analysis involving four distinct machine learning algorithms, namely K-nearest neighbor, Support Vector Machine, Linear Discriminant Analysis, and Random Forest. They applied these algorithms to the Rembrandt dataset published by the National Cancer Institute in the Cancer Imaging Archive (TCIA) [32]. Among these methods, Support Vector Machine (SVM) demonstrated the highest classification accuracy of 90.00% on the dataset.In a separate study, Choudhury et al. [26] introduced their unique 3-layered CNN model, which boasted a notable 952,278 trainable parameters.

In their research, Bhanothu et al. [27] introduced a methodology that combines a region proposal network and Faster R-CNN for tumor detection. The VGG16 CNN's output is utilized as input for both the region proposal network and the classifier.Remarkably, their approach achieved an average precision of 77.60% when applied to a brain tumor dataset comprising three distinct categories [29].

3. Proposed Methodology:

The method used to divide brain tumor MRI pictures into normal and abnormal categories is thoroughly explained in this section. This study aims to extract important information from MRI images by using a transfer learning (TL) technique in conjunction with deep learning algorithms. To further emphasize the efficacy of the suggested model and achieve remarkable tumor identification accuracy from brain MRI images, a dimensionality reduction technique is also applied.

The technique consists of the following main steps: preprocessing images, extracting features, reducing dimensionality, classifying brain tumors using a specialized classifier, and assessing system outcomes. CNN models that have already been trained are used to extract features, and a softmax layer is added to help in feature categorization. Figure 5 lists the main points of the suggested technique.

The following provides a thorough explanation of each step of the suggested system:

3.1. Data Collection and Initial Processing:

The dataset employed in this study comprises a compilation of brain MRI scan images. It encompasses approximately 256 raw MRI images, each exhibiting various dimensions, typically quantified in pixel values concerning width and height. These MRI brain images have been sourced from the Kaggle dataset and are primarily stored in the Joint Photographic Experts Group (JPEG) format [23]. The image repository is partitioned into two distinct categories: "Yes" and "No," based on the presence or absence of a tumor within an MRI brain image. Among these, approximately 158 brain MRI images depict benign tumors, while the remaining 98 images portray malignant tumors. In our study, we partitioned the dataset into three essential subsets, specifically designed for training, testing, and validation purposes. An illustrative representation of this MRI brain image dataset is presented in Figure 3.
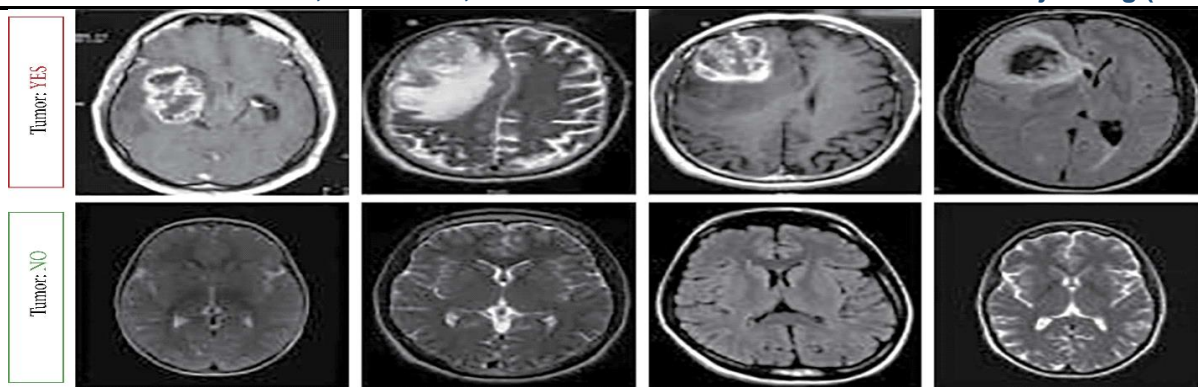
figure 3: sample dataset of brain MRI images

The preparatory steps involved in preprocessing Kaggle's brain image dataset [24] before the application of CNN pretrained models can be summarized as follows:

1. Initialization of the necessary packages.
2. Importing the two distinct data folders labeled as "Yes" and "No."
3. Reading and converting the images into labeled representations, with "Tumor – Yes" and "No Tumor – No."
4. Storing the labeled MRI images in data frames.
5. Resizing the images to the dimensions of 256×256.
6. Normalizing the images through mathematical transformation, specifically image cropping, with the equation $i \rightarrow (i - \mu i) / \sigma i$.

The MRI images available in the dataset were pre-processed in the following manner shown in Figure 4.

figure 4: steps involved in MRI image dataset preprocessing.

3.2 Image Preprocessing

Preprocessing involves the transformation of data prior to its utilization by the model. In the case of the dataset, the images, which initially had varying dimensions, were resized to a consistent size of 224 x 224 as part of the preprocessing procedure. Additionally, we applied image augmentation techniques to generate diverse versions of the images, thereby enhancing the model's ability to generalize.

3.3 Feature Extraction

Within the real of machine learning, there exists a specialized subfield known as deep learning. What sets deep learning apart is its intrinsic ability to autonomously acquire feature extraction during the training process [12]. Deep learning networks, specifically Convolutional Neural Networks (CNNs), have the capability to independently discern and extract visual features by employing kernels or convolutional filters.

Feature extraction, a pivotal step in the development of any classification task, is the process of distilling crucial information from raw data [7]. Its primary objective is to capture the fundamental information that uniquely characterizes each class. Feature vectors are created by extracting important characteristics from photos. Classifiers use these feature vectors as their basis, which enables them to match input units with matching output units. The emphasis on relevant feature extraction from images facilitates the classifier's capacity to differentiate between various classes, as these features are typically distinctive and easily distinguishable.

3.3.1 Convolutional Neural Network (CNN):

In the real of medical disease prediction based on image classification, advanced artificial intelligence models have demonstrated remarkable efficiency, primarily through a deep transfer learning approach [30]. Deep neural networks, particularly those founded on CNN architecture or ConvNets, encompass intricate mathematical operations known as "convolution."

A CNN architecture is characterized by several tiers, each comprising hidden layers, pooling layers, and output layers, often referred to as fully connected (FC) layers. These hidden layers are essentially a sequence of convolution layers equipped with filters (kernels) that execute image classification tasks for disease prediction in patients [31]. Notably, the pooling layer plays a critical role in consecutively reducing spatial size representation and curtailing hyperparameters, effectively mitigating the problem of overfitting in ConvNets. What sets CNN apart is its unique status among artificial neural networks as it obviates the need for pre-established, handcrafted feature extraction for the classification of MRI brain images.

Furthermore, the CNN architecture incorporates segments activated by Rectified Linear Units (ReLU) with dimensions of 3096, 3096, and 1200, respectively. The mathematical expression for ReLU is succinctly defined as:
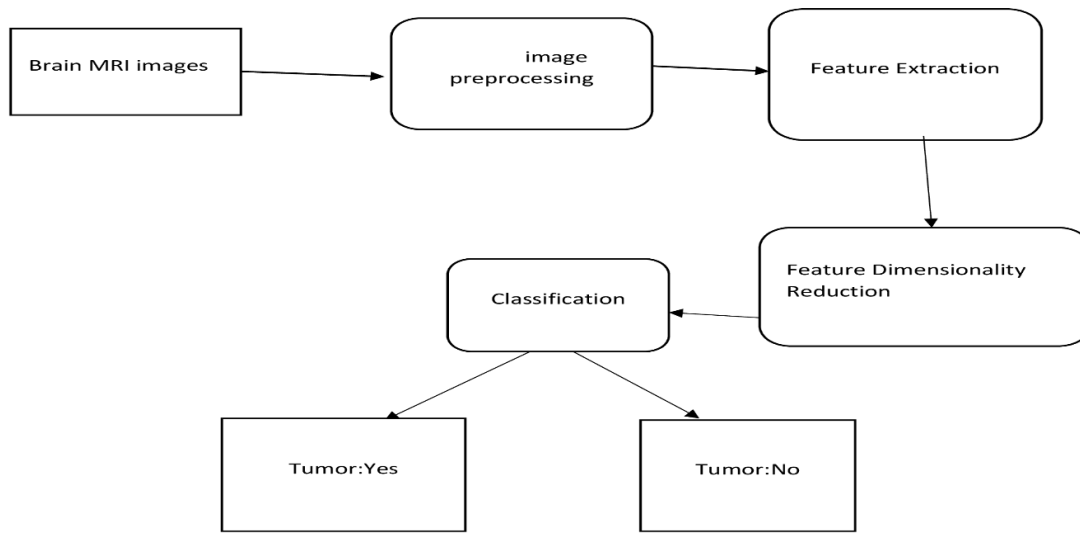
$f(y) \rightarrow \max(0, y)$ [2].

figure 5 . proposed approach architecture

ReLU is a key component in neural network optimization because of its ability to accelerate the training process. Its computational steps are straightforward, featuring the conversion of negative values to zero, while eschewing exponentials, division, or multiplication operations on the training dataset.

The input MRI images are subjected to resizing, transforming them into a standardized format of 256×256, which serves as a strategic measure to address the challenge of overfitting. Within the framework of CNN models, a sequence of layers, often referred to as filters, is meticulously designed to fulfill the dual role of dimension reduction and feature extraction. Consequently, CNNs are aptly dubbed as "feature extractors" capable of autonomously identifying and analyzing salient features, thus facilitating efficient feature classification [32].

To yield the final result, a Fully Connected (FC) layer is harnessed, equipped with the requisite number of classes, to undertake a nonlinear transformation on the extracted features. This FC layer assumes the crucial role of an image classifier, scrutinizing and classifying MRI brain images. The overarching structure of a CNN model is graphically depicted in Figure 6.The feature vectors emanate from the fully connected layers of the CNN and are subsequently funneled as input into a softmax layer comprising 1000 units, specifically designated for classification purposes. The mathematical formulation for the softmax activation function is articulated as follows:

$\sigma(z)_i = e^{z_i} / \Sigma(e^{z_j})$, where:
- "z" signifies the input vector for the softmax function, embodying "n" features pertaining to "n" target values or outcomes.
- "z_i" denotes the ith element of the input vector, which can assume either positive or negative values.
- "e^{z_j}" represents the standard exponential function applied to xi.
- $\Sigma(e^{z_j})$ serves as a normalization term, essential for obtaining a valid probability distribution.
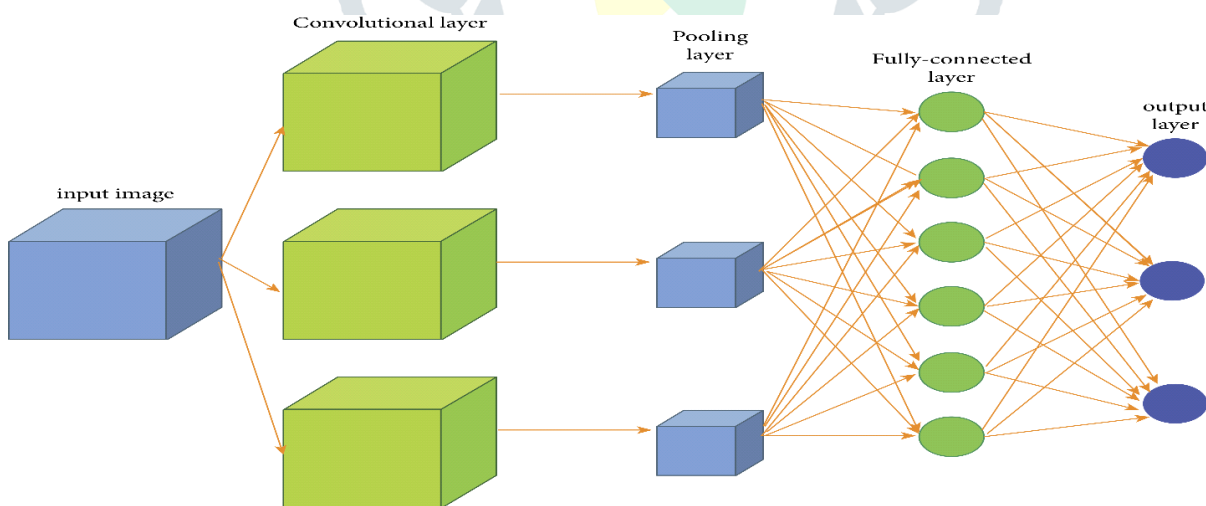

figure 6: General CNN structure.

The implementation of our proposed model is executed within the Python programming language, facilitated by the utilization of Anaconda Jupiter Notebook and Google Colab. The training process spans 120 epochs, incorporating the training, testing, and validation datasets.

3.3.2 Transfer Learning Approach:

In the real of advanced deep learning models [7], the adoption of transfer learning poses specific requirements, notably substantial volumes of training data, significant processing resources, and a considerable amount of time to achieve optimal performance. Transfer learning offers a pragmatic solution by capitalizing on knowledge previously acquired from a different task [27, 33]. It essentially involves the utilization of pretrained CNN models with the focus on parameter fine-tuning, customizing them for specific computational tasks. Within the domain of deep learning, the transfer learning approach is leveraged by employing existing pretrained models that have been trained on extensive and comprehensive datasets like ImageNet, primarily designed for image classification. This obviates the need to initiate the development of a CNN detection model from the ground

up for the purpose of image classification [34].Acquiring healthcare data is typically challenging due to its limited sample size. To address this issue, pretrained models like ImageNet, primarily designed for natural images, are often used. However, since there are significant dissimilarities between natural images and MRI images, it becomes necessary to fine-tune our model using transfer learning techniques with CNN-based pretrained models [5].
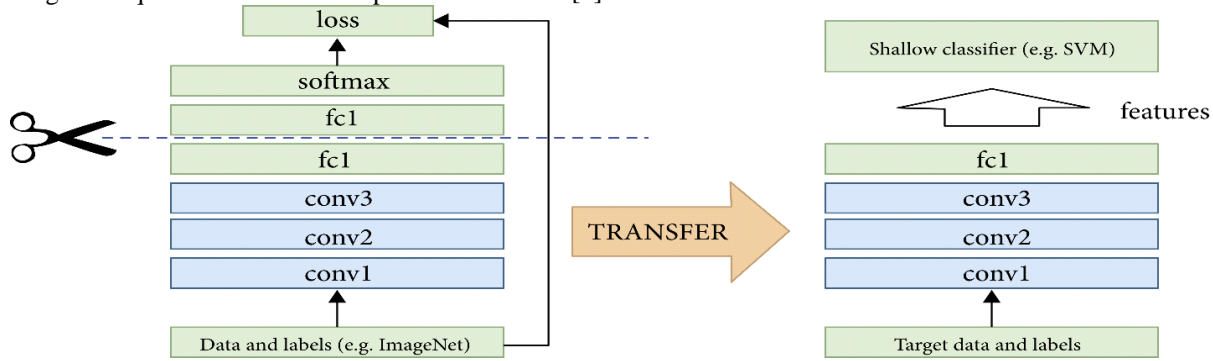

figure 7: transfer learning model

This approach is employed when the dataset for training is small, which is common in computer vision-based problems. Transfer learning usually involves taking the ImageNet dataset as an initial input, freezing convolution layers, and transferring weights from one CNN model to another to produce the final image classification output [22]. In essence, it can be referred to as an enhanced learning model for new tasks by leveraging knowledge obtained from existing tasks. The fundamental working principle of transfer learning is illustrated in Figure 7.

3.3.3 ResNet50 CNN Model:

ResNet50 is a Residual Network consisting of 50 layers and 26 million parameters, which was introduced by Kaiming He and his team at Microsoft Research in 2015 for the purpose of image recognition and classification [12]. In the context of Residual Networks, the term "residual" refers to feature subtraction. Instead of learning new features from scratch, ResNet50 focuses on learning from the features that are subtracted and derived from the input of each layer. In comparison to traditional deep CNNs, ResNet50 is notably easier to train. This pretrained model is trained using the ImageNet database [1].
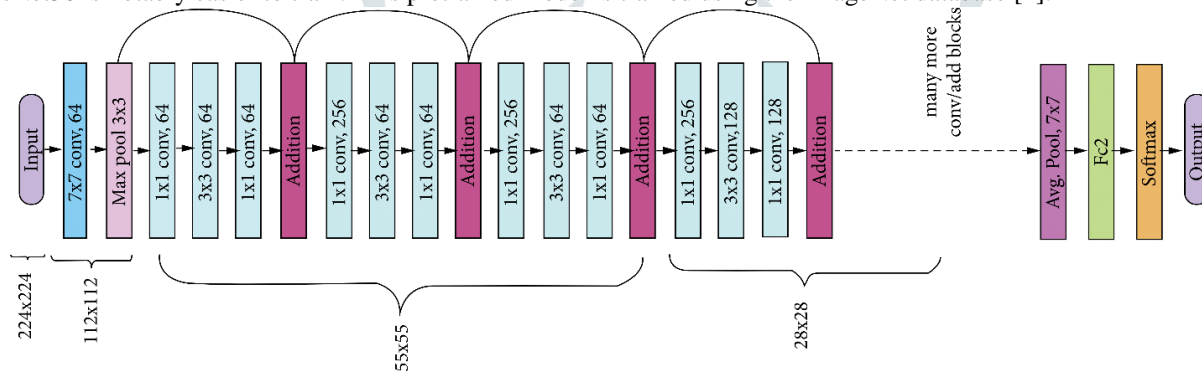

Figure 8: ResNet50 model architecture.

These networks effectively address the problem of diminishing image classification accuracy and incorporate skip connections along with extensive batch normalization. These skip connections are referred to as gated recurrent units or gated units. The ResNet50 network establishes a direct link from the input of the nth layer to the input of some (n + x)th layer, which facilitates the stacking of additional layers to create a deep neural network. This Residual Network offers a lower time complexity when compared to VGG16 or VGG19 models. In our experiment, we adopted a pretrained ResNet50 model and fine-tuned it to suit our input image dataset. The pretrained architecture of ResNet50 is depicted in Figure 8.

3.3.4 ResNet50 CNN Architecture:

During the testing of ResNet50, the training accuracy consistently improves and stabilizes starting from the 2nd epoch and continues to increase, eventually exceeding 95%. However, the validation accuracy exhibits instability and begins to rise around the 5th epoch but experiences a decline in performance after the 8th epoch, settling at 0.78%. This inability to accurately predict new data classes is evident in Figures 9 and 10.
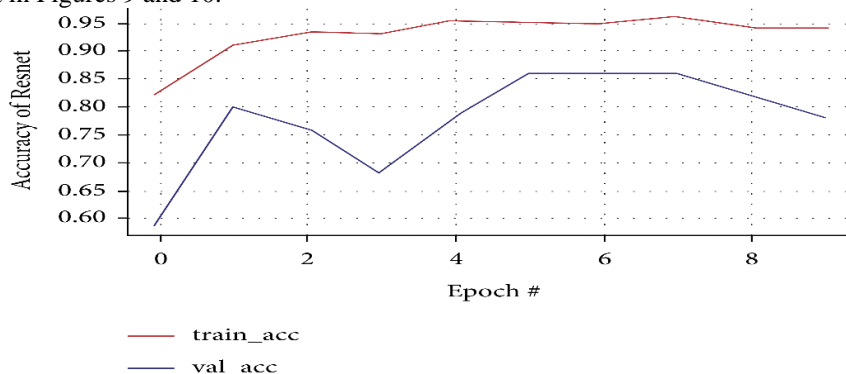

figure 9: Training and validation loss curve of the ResNet50 model.

The performance results of the ResNet50 model are summarized in a confusion matrix, which is used to predict tumors from the testing data. In this assessment, the model misclassifies 11 out of 31 MRI brain images as false negatives, which is a notable limitation of this model, as depicted in Figure 11.
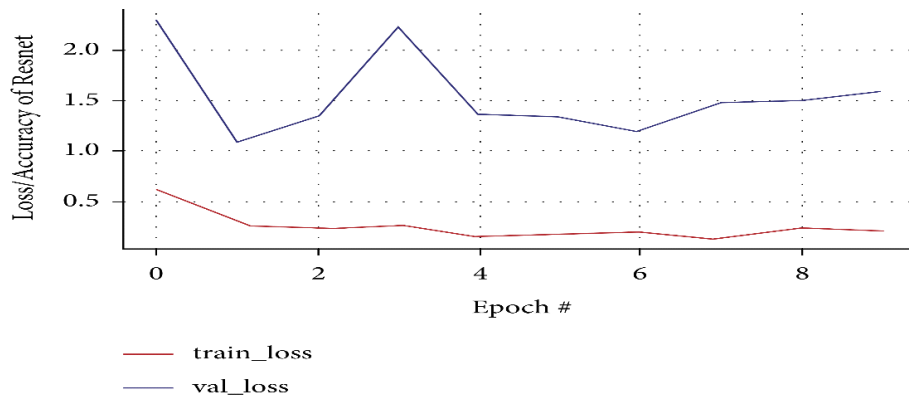

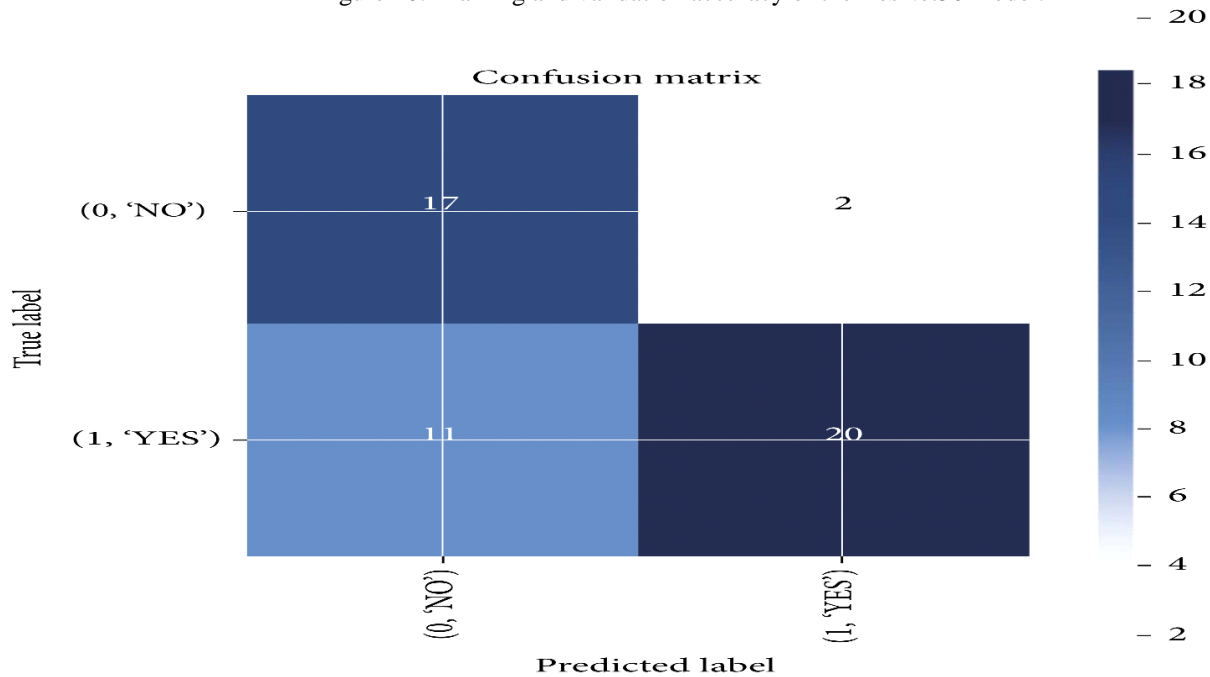figure 10: Training and validation accuracy of the ResNet50 model.

figure 11: Confusion matrix results of the ResNet50 model

3.4 Dimensionality Reduction:

The act of moving data from a space that is high-dimensional to a lower-dimensional one while keeping important information is known as "dimensionality reduction." . When dealing with datasets featuring a multitude of input features, predictions become intricate and less efficient due to the sheer volume of features involved. In such scenarios, the dimensionality reduction technique is applied [13].

Independent Component Analysis (ICA) is another statistical method used for feature reduction and dimensionality reduction in data analysis. Similar to PCA, ICA employs an orthogonal transformation to transform observed features. However, ICA's objective is different. It aims to find statistically independent components within the data, as opposed to PCA's goal of finding uncorrelated components.

Through the ICA process, the observed features are transformed into a new set of features, known as independent components. These independent components capture the underlying statistical independence in the data, making them suitable for various applications, such as blind source separation and feature extraction.

Usually, the amount of distinct elements that are recovered using ICA is either the same as the initial characteristics in the feature input vector, or smaller. These independent components can then be used as inputs for subsequent phases of a data analysis or modeling process.

We have employed Isomap as a feature reduction method. Isomap is a manifold learning technique that focuses on capturing the intrinsic geometry of high-dimensional data. Through a series of steps, it transforms the original data into a lower-dimensional representation that preserves the underlying geometric structure.

Isomap's process involves constructing a neighborhood graph that connects data points based on their pairwise distances, which helps uncover the underlying manifold or intrinsic structure. It then computes geodesic distances on this graph, which represent the true distances between data points while accounting for the manifold's curvature.

The result of Isomap is a lower-dimensional representation of the data, where each data point is positioned in a way that reflects its relationships with other data points in the intrinsic space. This reduced representation, which may have fewer dimensions than the original data, can be used as input for subsequent stages of data analysis or modeling.

3.5 Classification*:*

Classification is the process of identifying and discerning objects or patterns based on their input features [15]. In our context, the classification technique is employed to categorize brain MRI images into two groups: normal and abnormal. To perform this categorization, we have utilized the softmax classifier, which assigns input feature vectors to their respective target categories.

ExperimentalResultsandDiscussion:

The proposed model's outcomes. This section explores the model's generated results. Our goal is to classify brain MRI scans into normal and pathological categories. To do this, we have used the ability to extract features capabilities of the CNN model that has already been trained, ResNet-50. We also performed an independent component analysis (ICA) and The Isometric Mapping (ISOMAP) on the features that were taken out of the model, which resulted in a feature set that was carefully trimmed and suitable for classification tasks. In the realm of deep learning models, the role of hyperparameters is pivotal, as they are instrumental in ensuring optimal results. In order to create a highly effective and well-tuned model, we have utilized two different have been previously trained CNN models, ResNet-50, for this project. We have carefully considered a number of hyperparameters, such as the amount of epochs, training rate, and the size of the batch.

The model itself has been meticulously crafted utilizing the Keras library, seamlessly complemented by the support of Tensor Flow as a backend, all underpinned by the Python programming language. When the pre-trained ResNet-50 CNN model is coupled with ICA and ISOMAP, the remarkable results materialize in the form of a 99.00% training accuracy and an 80.00% validation accuracy. These stellar outcomes have been achieved through the optimization of hyperparameters, where the learning rate is set at 0.0001, the batch size is fixed at 32, and the maximum number of epochs caps at 100.

The assessment of the proposed model's performance hinges on the utilization of a confusion matrix, a structured representation that tabulates both accurate and erroneous classifications [16]. Within this matrix, various metrics are gleaned to gauge the classifier's efficacy for each tumor class, including Precision, Recall (or sensitivity), F1-score, and accuracy.

In Figure 5, we present the comprehensive classification results of our model, revealing precision, recall, F1-score, and accuracy values of 84%, 80%, 79%, and 80%, respectively.

Of primary focus in our evaluation is the accuracy metric, which quantifies the ratio of correctly classified samples to the total number of data samples. The mathematical formulation for accuracy is expressed as:

Accuracy = (TP + TN) / (TP + TN + FP + FN)   (1)

Here, TP represents True Positives, FP signifies False Positives, TN denotes True Negatives, and FN designates False Negatives.

Figure 6 encapsulates the complete confusion matrix of our proposed model. This matrix highlights that 292 positive samples and 186 negative samples have been accurately classified.
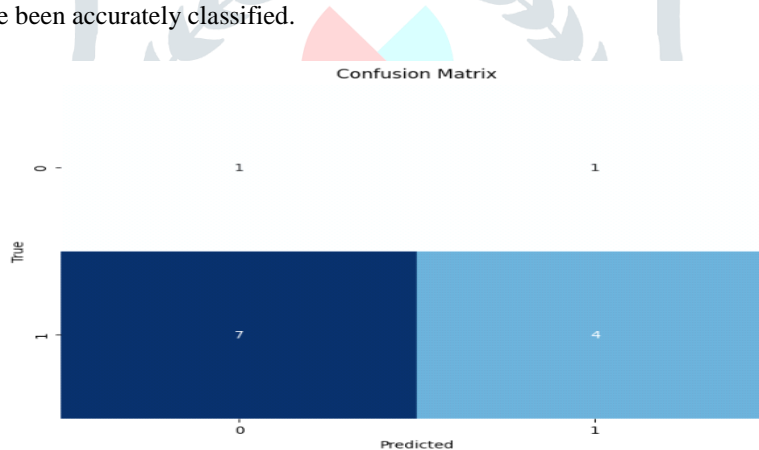

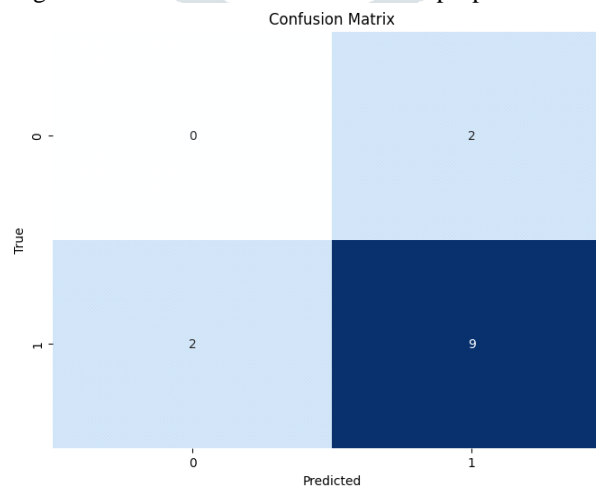figure 12**.** Confusion matrix of the ICA proposed model

Figure 13. Confusion matrix of the isomap proposed model

Support Vector Machines (SVM) : are a subset of guided machine learning algorithms that are employed in regression and classification applications. SVMs work especially effectively in situations where you require to forecast numerical values or divide data into distinct classes. The basic idea behind SVM is

Figure 14. classification results of proposed approaches using dimensionality reduction method of ICA with SVM and random forest classifier and ISOMAP with SVM and RF classifier

	precision	recall	f1-score	support
0.0	0.12	0.50	0.20	2
1.0	0.80	0.36	0.50	11
accuracy			0.38	13
macro avg	0.46	0.43	0.35	13
weighted avg	0.70	0.38	0.45	13

	precision	recall	f1-score	support
0.0	0.00	0.00	0.00	2
1.0	0.82	0.82	0.82	11
accuracy			0.69	13
macro avg	0.41	0.41	0.41	13
weighted avg	0.69	0.69	0.69	13

to find a hyper plane that best separates data points belonging to different classes while maximizing the margin (the distance between the hyper plane and the nearest data points from each class). SVMs are effective in high-dimensional spaces and can handle both linear and non-linear data with the help of kernel functions. If you have specific questions or need more information about SVMs or their applications, please feel free to ask. The accuracy obtain is 84.00% based on dimensionality reduction method for ICA and ISOMAP using SVM .

Random forest:

Random Forest is versatile and can handle a wide range of data types, both numeric and categorical. It is also capable of handling high-dimensional data and can model complex relationships. The concept of Random Forest allows it to work well in both linear and non-linear scenarios without the need for explicit kernel functions. Accuracy achieved by a Random Forest model can vary depending on the dataset, the quality of the data, and the hyper parameters chosen, but it often provides competitive accuracy in many practical machine learning tasks. The accuracy obtain is 64.00% and 39.00% based on dimensionality reduction method for ICA and ISOMAP using RF .

Figure:15 the overall result of our model
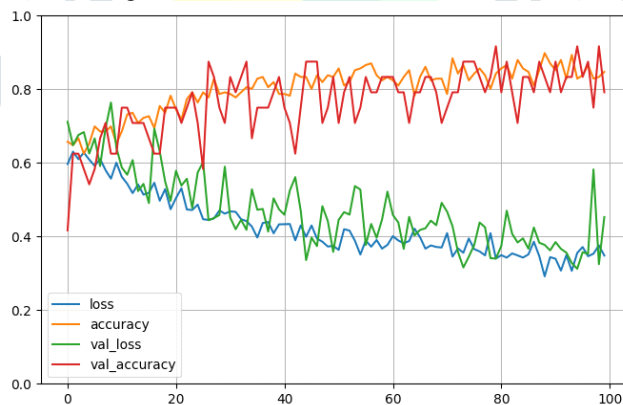
Conclusion

We used the ResNet50 deep learning model that had been trained with the ICA and ISOMAP strategy for feature extraction then used feature reduction in our suggested methodology to categorize brain MRI pictures into either normal or abnormal images. This model was tested using 2000 MRI normal and abnormal pictures from the Kaggle brain tumor detection dataset. The most appropriate feature for more precisely identifying tumors may be obtained by combining features taken from the CNN ResNet50 model with ICA AND ISOMAP. According to our findings, the ResNet50 model with ISOMAP AND ICA outperformed the ResNet50 model with ISOMAP in terms of training accuracy. Furthermore, it has been noted that the CNN model using ISOMAP, a dimensionality reduction technique, produces superior results than the model without ica. Future research on brain tumor classification throughout performance in all and dimensionality reduction techniques may be applied, together with the deep learning methodology. In the prediction study of brain tumors, the research may be expanded for classification using other models such as VGG-19, MobileNet, and Efficient Net-pretrained CNN-based models.

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