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Design of an Iterative Cluster-Based Model for Detection of Brain Tumors Using Deep Transfer Learning Models

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ABSTRACT

A tumor develops when brain cells exhibit abnormal growth patterns within various body locations, characterized by irregular boundaries and shapes. Typically, these tumors exhibit rapid proliferation, increasing at a rate of approximately 1.6% per day. This abnormal cell growth can lead to invisible illnesses and alterations in psychological and behavioral functions, contributing to a rising trend in adult mortality rates worldwide. Therefore, Brain tumors must be detected early. Failure to do so may cause a deadly, incurable condition. Effective brain tumor therapy improves survival if detected early. Magnetic Resonance Imaging (MRI) is essential for finding and classifying brain tumors. The manual nature of brain tumor diagnosis and classification makes it prone to errors, necessitating the development of automated processes for improved accuracy. In light of these considerations, we have devised with a fully automated way to use MR images to find and classify brain tumors. Our approach encompasses three key phases: pre-processing, segmentation, and classification. To detect tumors in the brain, we utilized MRI, employing the deep transfer with the transformed VGG19 model. Notably, our research demonstrates superior growth rates when using other pre-trained Convolutional Neural Network (CNN) models such as AlexNet and VGG-16. The deep transfer learning with the transformed VGG19 model yielded accuracy achieving 98.65% (dataset 1) and 99.18% (dataset 2) for different datasets.

1. INTRODUCTION

Tumors arise as a result of the uncontrolled proliferation of non-functional cells. The human brain, comprising billions of cells, is a highly complex organ that governs the entire nervous system [1]. Due to its intricate cellular composition and pivotal role, the brain has long been considered one of the most vulnerable organs in the human body. It serves as the control center for many essential functions, including regulation, emotions, vision, reactions, and memory. The growth of certain brain tumors (BT) can significantly impair these vital functions.

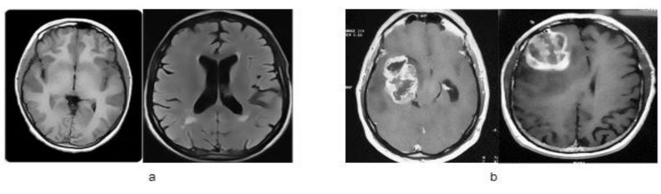


Figure 1. a. Healthy images; b. Tumor images

Figure 1 presents a comparison between healthy images and tumor tissue images. Brain tumors can be categorized into two main types: malignant and benign. Malignant tumors are cancerous and exhibit a rapid tendency to spread to neighboring brain tissues, exacerbating the patient's clinical condition. In contrast, benign tumors lack malignant cells and have a relatively slower rate of proliferation. Typically, they remain localized within a specific area of the brain.

Memory impairment, frequent headaches, focus difficulties, and coordination deficits are often seen as signs of brain tumors [2]. The aggressive nature of brain tumors, particularly malignant ones, contributes to their classification as one of the most severe illnesses among various types of tumors, largely due to their high fatality rates.

Brain and central nervous system (CNS) tumors come in a lot of different types, 120 different types have been discovered. A report from the American Cancer Society in 2021 said that brain and CNS tumors would kill 18,600 people, including 3,460 children under the age of 15. People who are found with brain tumors have a poor outlook. Only 36% of them will be alive after five years, and only 31% will be alive after ten years. In the United States in 2019, the National Cancer Institute found 86,010 cases of cancer in the brain and central nervous system. It is thought that about 0.7 million Americans have brain tumors, with 60,800 cases being normal and 26,180 cases being dangerous. This adds up to 0.86 million cases. The World Health Organization (WHO) reported 9.6 million new cases of cancer around the world in 2018. This shows how important early spotting is for protecting people with brain tumors.

The timely identification of brain tumors is paramount. The conventional approach involves medical professionals, such as doctors or radiologists, visually examining MRI images to detect anomalies and make diagnoses. However, the accuracy of unassisted visual diagnosis is highly dependent on the expertise of the physician, leading to variability in diagnoses. Additionally, the complexity of interpreting images poses challenges, and this process can be time-intensive. Tumors may exhibit diverse morphologies, and MRI images may lack clear anatomical features for precise assessment, further compromising diagnostic accuracy. Misclassification of a brain tumor can hinder appropriate medical interventions and reduce patient survival chances, whereas accurate diagnosis facilitates timely treatment and extends lifespan [3].

This study introduces an enhanced deep-learning model that has been specifically developed to accurately classify the specific category of brain tumor illustrated in an MRI picture. The model has undergone training using a dataset consisting of MRI pictures specifically depicting brain tumors. Its effectiveness is assessed by the use of many measures, including precision, recall, accuracy, and F1-score. These measurements offer valuable insights into the overall efficacy of the model when applied to the complete collection of MRI pictures. The experimental findings suggest that the deep learning model suggested in this study demonstrates comparable performance to existing approaches, hence showing potential for improved accuracy and efficiency in the detection of brain tumors.

1.1 Background

Throughout the years of deep learning, significant achievements have been realized across various domains, including computer vision (utilizing tools like OpenCV), text recognition, robotics, speech recognition, and computer-aided detection. Deep learning models have proven their effectiveness in acquiring diverse levels of abstraction, representation, and knowledge from large datasets when provided with raw data samples.

One key technology that has made a substantial impact is Convolutional Neural Networks (CNNs), which find applications in image and audio processing, video identification, and natural language processing (NLP). CNNs draw inspiration from the visual processing mechanisms in the brains of species like felines and monkeys, particularly Ateles. Their expertise in the domain of image processing can be attributed to their inherent aptitude for identifying and differentiating patterns within visual datasets. The fundamental component of a CNN is the convolutional layer, which plays a crucial role in extracting visual characteristics from pictures, such as lines and colors. This layer employs teachable kernels, often with a small spatial extent but distributed uniformly throughout the depth of the input. By integrating the input with the spatial dimensions, the convolutional layer generates feature maps. Following the convolutional layer, there is typically a pooling layer whose primary role is to reduce the dimensionality of the convolved features. This results in a decrease in both model parameters and computational requirements.

The final layer in the neural network architecture is the fully connected layer, where neurons establish direct connections with neurons in the subsequent layers but not within their layer. This layer promotes linearity within the network, facilitating higher-order cognitive processes. It has been observed that the depth of a CNN positively correlates with its ability to address more complex tasks and enhance model accuracy. In the structure of the article, the second section delves into related works, providing a comprehensive overview of prior research in the field. The third section outlines the proposed methodology, detailing the techniques and approaches employed. The fourth section is dedicated to the analysis of the results obtained from the research. Discussion of the findings and their implications takes place in the fifth section. Finally, in the last section, the article concludes, and future research directions are considered and discussed.

Paper structure: Section 1 represents the introduction, Section 2: Related works, Section 3 represents the proposed methodology, Section 4 represents the results analysis, Section 5 represents the conclusion and future scope.

2. RELATED WORKS

Saurav et al. [4] suggested a novel lightweight Attention-Guided Convolutional Neural Network (AG-CNN) for brain tumor classification in magnetic resonance (MR) images as a solution to these problems. By using skip connections and channel-attention blocks through global-average pooling, this AG-CNN architecture improves feature extraction and classification while demonstrating its computational robustness and efficiency compared to other approaches. The model's applicability for implementation in resource-constrained clinical settings is highlighted by the authors' evaluation of their findings on four benchmark brain tumor MRI datasets.

A different study [5] underscored how difficult it is to categorize brain tumors because of their wide range of features and stresses how important a precise diagnosis is for patient care. This work proposes a hybrid classifier that combines Random Forest, K-Nearest Neighbour, and Decision Tree classifiers with feature extraction techniques like shape-based features and Grey Level Co-occurrence Matrix. The authors demonstrate the effectiveness of their method and its potential as a better diagnostic tool by reporting impressive accuracy rates for various datasets.

Shahin et al. [6] discussed the difficulties caused by the nonlinear morphological and textural features of brain tumors in a different study project. With adjustments to the PCANet model to improve feature extraction, they present a multi-class brain tumor classification technique that consists of an unsupervised convolutional PCANet module and a supervised CNN module. Their approach outperforms existing methods on a variety of benchmark datasets, demonstrating its superiority and encouraging its use in medical imaging diagnosis.

In addition, a brain tumor detection system that is automated is presented to address the challenges that come with manual diagnosis. To achieve an impressive accuracy rate, the authors combine the Salp swarm algorithm, deep convolutional networks, and feature selection techniques. Their research shows how deep learning can improve the early detection and classification of brain tumors [7].

An alternative method involves the proposal of a hybrid model based on CNNs for the classification of various types of brain tumors, such as gliomas, meningiomas, pituitary tumors, and normal brain images with the astounding accuracy of 95.4%, this hybrid model uses pre-trained architectures for Support Vector Machine classification, mRMR feature reduction, and feature extraction. The model performs better than earlier architectures, according to the authors [8].

Furthermore, a three-stage hybrid classification framework for pituitary, glioma, and meningioma brain tumor classification is presented. This framework is based on YOLO, DenseNet, and Bi-LSTM. The suggested model shows exceptional accuracy rates, establishing it as a useful instrument for field specialists and enhancing patient outcomes [9].

The study [10] also addressed the detection and classification of brain tumors using a deep CNN technique in conjunction with an improved LuNet classifier algorithm. The authors achieve a high accuracy rate of 99.7% by utilizing a variety of techniques, such as Laplacian Gaussian filtering and Fuzzy C Means with Gaussian mixture modeling for segmentation. When compared to other traditional methods, their approach is thought to be advantageous in terms of computational complexity and performance.

Finally, a safe framework for the diagnosis of brain tumors is suggested, emphasizing quantum models and patient data encryption. This method outperforms recent research in terms of accuracy and security and exhibits a high dice similarity coefficient (DSC) [11].

A different study [12] introduced a novel method for classifying brain tumors that combines dense, accelerated robust features, histogram of gradient techniques, and normalization. By using a support vector machine classifier, the authors surpass more recent systems, achieving an accuracy rate of 90.27%.

Additionally, a radial basis neural network (RBNN) enhanced whale optimization algorithm (IWOA) is suggested for the classification of brain tumors. The authors stress the significance of early diagnosis and achieve high accuracy using RBNN with IWOA, image segmentation, feature extraction, and pre-processing steps. Their approach holds the potential for precise and effective diagnosis [13].

The accurate classification of brain tumors from MRI images is the main focus of the study cited as, acknowledging the critical importance of a precise diagnosis for successful clinical treatment. Gliomas are a major target for MRI diagnosis; brain tumor classification entails identifying and labeling malignant brain tissues based on tumor types. The enormous amount of MRI data generated makes manual classification impractical, as the paper acknowledges. Therefore, segmentation and classification require automated techniques. However, because brain tumors differ greatly in terms of both location and structure, MRI image segmentation is challenging. The authors present a novel CNN architecture intended for the classification of three different kinds of brain tumors to overcome these difficulties. In contrast to earlier models, the CNN model employs contrast-enhanced T1 images to streamline the network architecture to increase performance and efficiency. When applied to record-wise cross-validation, the model exhibits a high accuracy rating of 92.50%, as demonstrated by two ten-fold cross-validation procedures conducted across various datasets. The findings indicate that radiologists working in the field of medical diagnostics may find this CNN architecture to be a useful decision-support tool [14].

In a different study, the authors stress the value of prompt diagnosis in cases of brain tumors, particularly malignant tumors, which have a greater death rate. They stress that despite advancements in computer-aided diagnosis systems, problems with current approaches such as low accuracy and computational time persist. They suggest an end-to-end optimized deep learning system for multimodal brain tumor classification to allay these worries. By employing a hybrid division histogram equalization and ant colony optimization technique, the suggested system improves image contrast. A newly created nine-layered CNN model is then trained. The second fully connected layer is used for feature extraction and moth flame and differential evolution are used for optimization. After fusing the features from these two approaches, a multi-class support vector machine (MC-SVM) is used. The method outperforms existing methods with impressive accuracy rates across multiple datasets [15].

The authors of a different study [16] also seek to address the problem of labeled data acquisition for supervised models in the context of MRI scans for brain tumor diagnosis. Acknowledging that supervised models heavily rely on labeled data, which is frequently scarce and necessitates domain expertise for annotation, they propose a novel self-supervised framework for the unsupervised classification of brain MRIs. Without requiring a large amount of labeled data, the framework presents contrastive learning with an interleaved structure, dynamic weighting mechanisms, and a jigsaw puzzle solver to aid in feature representation and enhance classification. The authors carry out extensive tests that show the suggested model performs better than others, both in terms of quality and quantity.

In a separate study, the authors provide a three-phase processing technique for accurate MR image-based brain tumor diagnosis. The procedure involves pre-processing, fuzzy C-mean-based segmentation for brain tumor localization, and statistical feature extraction. The Relevance Vector Machine (RVM), an enhanced Support Vector Machine (SVM) classifier, is introduced in the last stage. The suggested method outperforms previous methods in terms of accuracy and is experimentally validated on benchmark datasets [17].

Additionally, the authors [18] use the Sparrow Search Algorithm (SpaSA) to describe an automatic discriminative learning-based method for segmenting and classifying brain tumors. CNN models that have already been trained are used for learning, while UNet models are used for segmentation. The method outperforms other approaches with impressive accuracy and specificity across different datasets.
Comparative analysis of the reviewed models is presented in Table 1.

Table 1. Comparative analysis of the reviewed models

Reference Number	Name of Method	Advantages	Details of Work	Future Scope
[4]	AG-CNN for Brain Tumor Classification	-Lightweight architecture-Improved feature extraction-Computational efficiency	-Novel AG-CNN architecture for MRI images-Evaluation of benchmark datasets	Implementation in clinical settings
[5]	Hybrid Classifier	-Effectiveness in brain tumor classification-High accuracy	-Hybrid classifier combining RF, K-NN, and DT-Feature extraction techniques	Better diagnostic tool
[6]	PCANet-CNN for Brain Tumor Classification	-Outperforms existing methods-Improved feature extraction	-Unsupervised convolutional PCANet module-Supervised CNN module	Use in medical imaging diagnosis

[7]	Automated Brain Tumor Detection	-High accuracy	-Combination of algorithms and techniques-Emphasis on early detection	Improved early detection
[8]	Hybrid Model for Brain Tumor Classification	-High accuracy	-Hybrid model using pre-trained architectures-Multiple tumor types	Continued improvement
[9]	Three-Stage Hybrid Classification Framework	-Exceptional accuracy	-Framework based on YOLO, DenseNet, and Bi-LSTM	Useful instrument for specialists
[10]	DL with LuNet Classifier	-High accuracy-Low computational complexity	-Deep learning with image processing techniques	Advancements in computational methods
[11]	Quantum-Based Brain Tumor Diagnosis	-High accuracy and security	-Quantum models and encryption	Further security enhancements
[12]	SVM Classifier with Feature Techniques	-High accuracy	-SVM classifier with feature extraction techniques	Enhanced diagnostic tool
[13]	RBNN with IWOA for Brain Tumor Classification	-High accuracy	-RBNN with IWOA, image segmentation, and feature extraction	Precise diagnosis
[14]	CNN Architecture for Brain Tumor Classification	-High accuracy-Streamlined network architecture	-Novel CNN architecture for brain tumor classification-Utilization of contrast-enhanced T1 images	Useful decision-support tool
[15]	DL for Multimodal Brain Tumor Classification	-Improved accuracy-End-to-end optimization	-Deep learning system with optimization techniques-Multimodal classification	Enhanced diagnostic accuracy
[16]	Self-Supervised Framework for Brain MRI Classification	-Reduced dependence on labelled data-Quality and quantity improvement	-Self-supervised framework for unsupervised classification	Less reliance on labelled data
[17]	RVM-Based MR Image-Based Brain Tumor Diagnosis	-High accuracy	-Three-phase processing technique-RVM-based classification	Improved accuracy
[18]	SpaSA for Brain Tumor Segmentation and Classification	-High accuracy and specificity	-Automatic discriminative learning-based method-Use of CNN and UNet models	Enhanced segmentation and classification

3. PROPOSED METHODOLOGY

3.1 Methodology

Detailed descriptions of each phase of the proposed system are provided below:

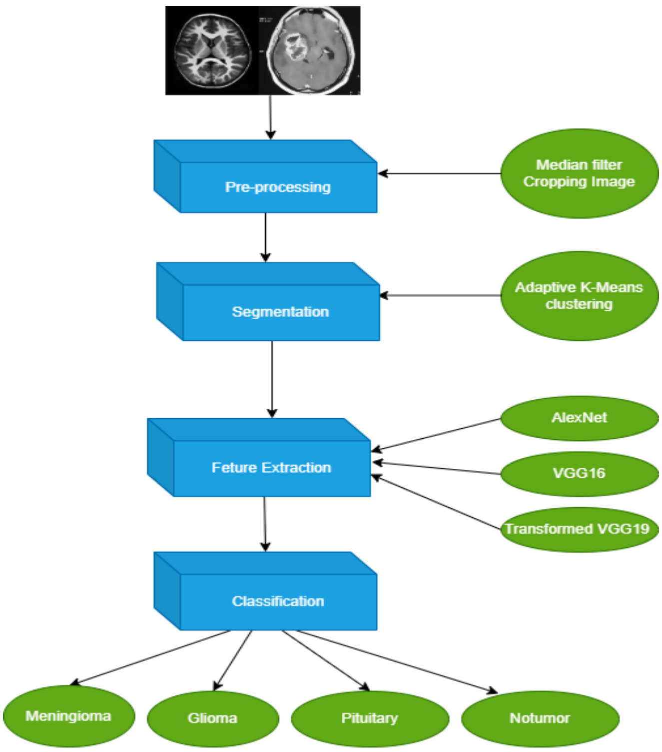


Figure 2. Proposed approach architecture

In Figure 2 The procedure consists of the following steps: input dataset, pre-processing, segmentation, feature extractions, classification of BT using a classifier, and system performance measurements deep transfer with the transformed VGG19 model is used to extract the features, which is classified by a SoftMax layer.

3.1.1 Pre-processing

Figure 3 illustrates MRI images of various brain tumor types, including glioma, meningioma, pituitary tumor, and a normal brain without a tumor. Magnetic resonance image during the picture capture procedure, pulse interference introduced significant noise. Pre-processing the image with nonlinear smoothed median filtering helps get rid of these distractions. Noise can be reduced using a nonlinear processing technique called median filtering. The median filter uses the midpoint of this data column to get the template's median value in Figure 4. Median filtering is a powerful tool for eliminating visual artifacts like salt and pepper. While the border is more reliably protected when using a median filter, picture detail processing is less than optimal, leading to the occasional loss of fine lines and small target areas. Median filtering can keep track of information about the edges while removing noise.

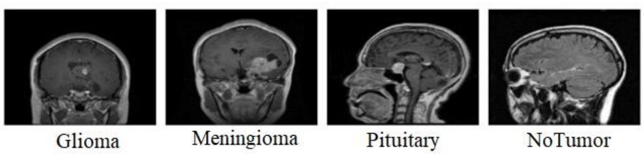


Figure 3. Tumor images

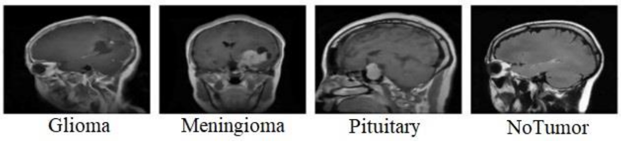


Figure 4. Preprocessed tumor images

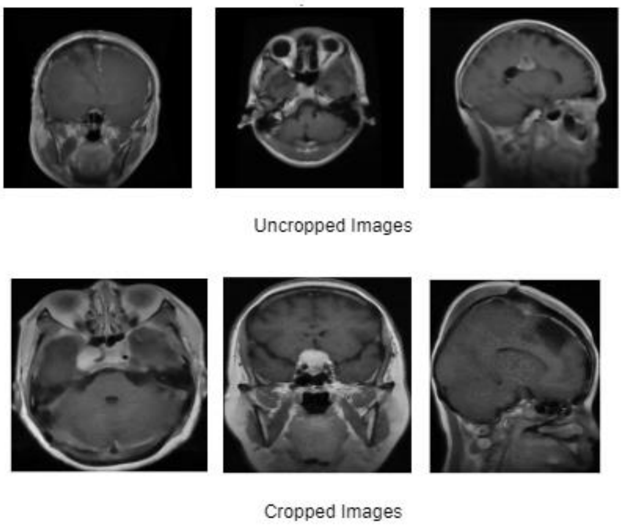


Figure 5. Uncropped and cropped images

In Figure 5, the process of cropping images is essential for eliminating unnecessary space and optimizing the use of pertinent data samples.

3.1.2 Segmentation

Adaptive K-Means Clustering: The number of clusters in adaptive K-Means clustering is constantly adjusted according to the properties of the data, making it a variant of the original K-Means clustering technique. This flexible strategy is helpful when the precise number of clusters is unknown or subject to change.

Adaptive K-Means Clustering Algorithm

I. Select the desired number of clusters, denoted as k, to be identified.
II. The data points are randomly assigned to one of the k clusters.
III. Next, proceed to compute the centroids of the clusters.
IV. Determine the Euclidean distance between the data points and the centroids of each cluster.
V. The process of reassigning data points to their nearest clusters is dependent on the calculation of the distance between each data point and the cluster.
VI. Subsequently, compute the updated cluster centroid.
VII. Continue to repeat steps IV, V, and VI until the data points cease to modify the clusters, or until the predetermined number of iterations has been attained.

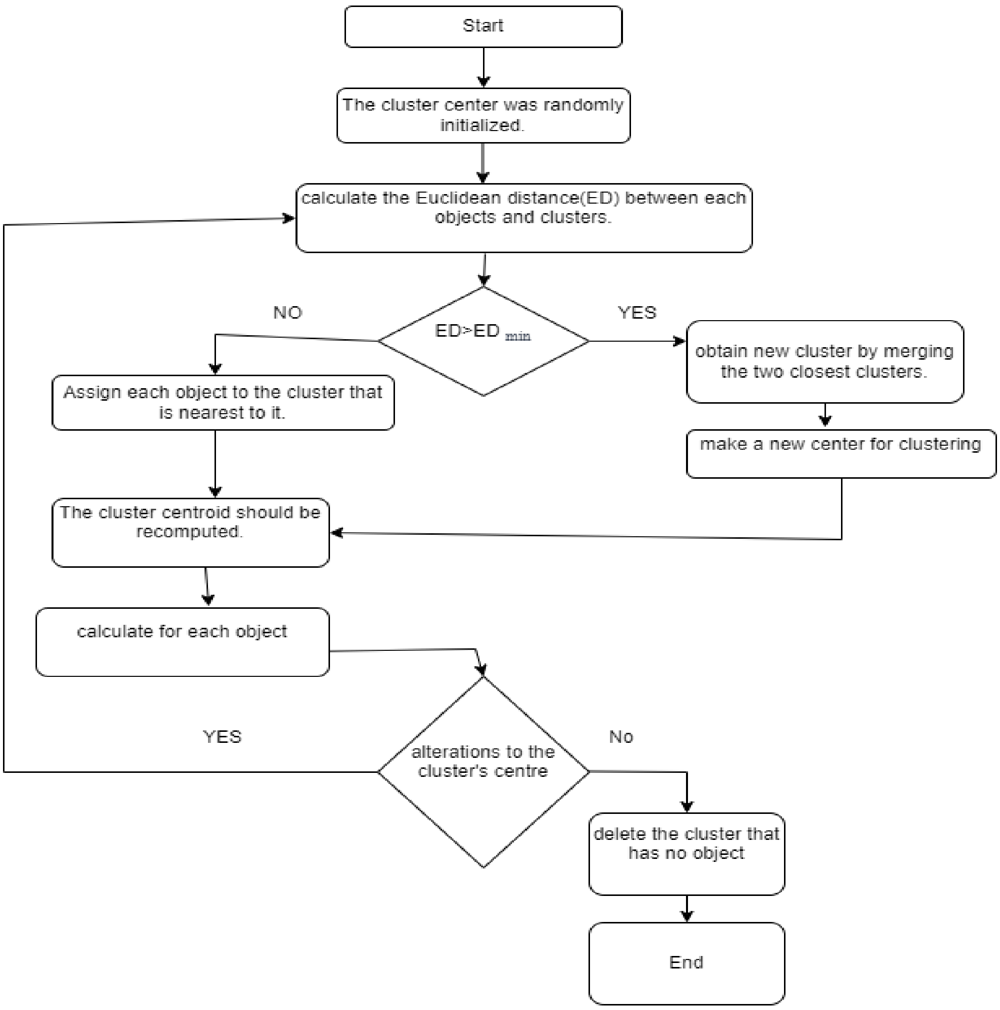


Figure 6. Flowchart of the adaptive K-Means clustering process

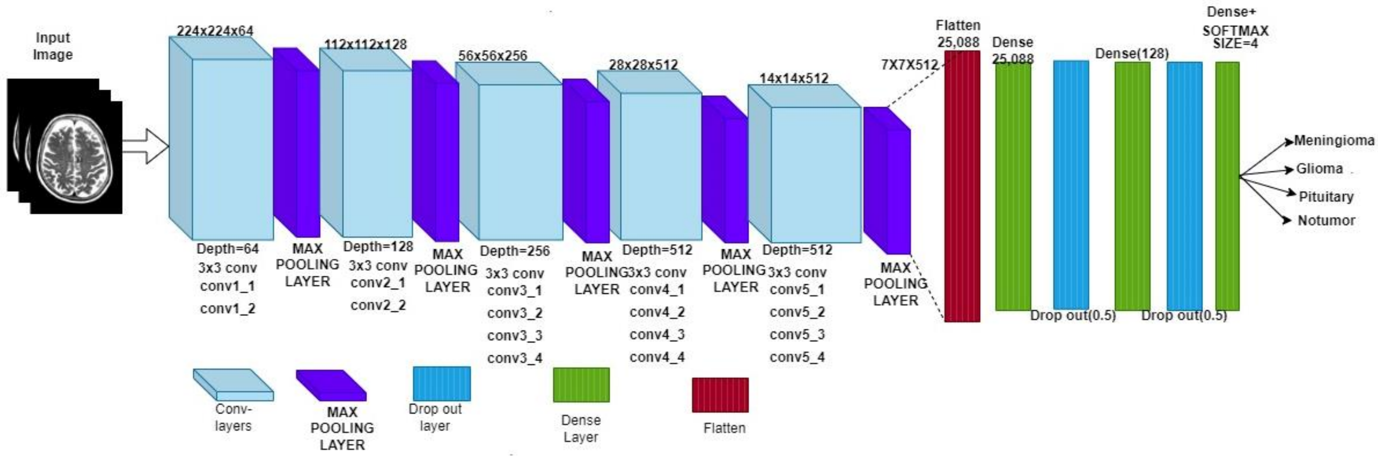


Figure 7. The architecture of deep transfer with the transformed VGG19 model

In the realm of medical imaging, the segmentation of brain tumors from MRI scans is crucial for diagnosis, treatment planning, and patient monitoring. One method that has shown promise for this task is an adaptive K-Means clustering algorithm. Unlike traditional K-Means clustering, the adaptive version is tailored to account for the unique characteristics and heterogeneity of brain tumors, making it more suitable for MRI image segmentation [19].

To begin with, the MRI images serve as the input to the algorithm. These images typically contain pixels with varying intensity values, representing different tissues, fluids, and abnormalities within the brain.

Figure 6 illustrates the adaptive K-Means clustering process in flowchart format.

The objective is to partition these pixels into distinct clusters, where each cluster represents a specific region or type of tissue. In the context of brain tumor segmentation, one of these clusters will ideally correspond to the tumor region.

The adaptive K-Means clustering process commences by initializing K centroids, where K represents the number of desired clusters. These centroids can be initialized randomly or based on some heuristic. The main idea behind K-Means is to assign each pixel in the MRI image to the nearest centroid based on its intensity value. The similarity between a pixel's intensity and a centroid is typically measured using the Euclidean distance, given by:

$$d(p,c) = \sqrt{(p-c)^2}$$

where, d is the distance, p is the pixel intensity, and c is the centroid intensity levels. Once all pixels are assigned to their respective clusters, the next step is to update the centroids. Each centroid is recalculated as the mean intensity value of all the pixels currently assigned to its cluster:

$$ci = \frac{1}{ni} \sum nipj$$

where, ci is the new centroid for cluster i, ni is the number of pixels in cluster i, and pj is the intensity of the jth pixel in cluster i sets.

However, what makes this algorithm adaptive is the incorporation of spatial information. Recognizing that neighboring pixels in MRI images often belong to the same tissue type, a spatial constraint is introduced. This constraint adjusts the clustering process such that spatially close pixels with similar intensities are more likely to be grouped. This is achieved by incorporating a spatial weight into the distance calculation:

$$d(p,c) = \sqrt{(p-c)^2 + \lambda \times spatial(p,p')}$$

where, $spatial(p, p')$ is a function that returns a value based on the spatial proximity of pixel p to another pixel p' in the same cluster, and λ is denoted as a weighting parameter that controls the dominance of the spatial term.

The algorithm iteratively allocates pixels to clusters and updates centroids until a combination is attained. Combination is typically identified when the alteration in centroids between iterations cascades below a predefined threshold or when a maximum number of iterations is reached. Upon completion of the clustering process, the resultant clusters signify distinct regions within the sets of MRI images. One of these clusters, characterized by its unique intensity distribution, corresponds to the brain tumor sets. This cluster can then be extracted to produce the final segmented image, which highlights the tumor region against the background.

3.1.3 Deep transfer with the transformed VGG19 model

The objective of this study is to employ deep learning algorithms and a transfer learning (TL) strategy to extract optimal features from MRI images. Additionally, a dimensionality reduction method is incorporated to demonstrate the capability of the proposed model in accurately detecting brain tumors within MRI images with a high level of precision.

Figure 7 illustrates deep transfer using the transformed VGG19 model, with the final layer designed for four distinct classes that correspond to the categories in the MRI dataset. Deep transfer with the transformed VGG19 model is made up of sixteen layers with convolutions and two drop-out layers, two dense layers that are fully linked. The final layer of VGG19 comprises 1000 neurons, each specifically corresponding to distinct classes within the ImageNet datasets. In this case, the final fully connected layer was modified to accommodate the classification of four distinct classes, corresponding to the classes present in the MRI dataset samples [20].

For the network, MRI data, represented as X, was processed through a modified VGG19 architecture incorporating a deep transfer learning process. The feature map obtained after processing can be mathematically represented via Eq. (1):

$$V(X) = ReLU(Wpre * X + bpre) \quad (1)$$

where, $V(X)$ is the output feature map, *Wpre* and *bpre* are the pre-trained weights and biases from ImageNet, respectively, and $ReLU$ is the Rectified Linear Unit activation function of the VGG19 network [21].

Following this, the feature map $V(X)$ was transformed through additional layers to adapt the model to the task of brain tumor classification, which is represented via Eq. (2):

$$T\big(V(X)\big) = LReLU(Wtrans * V(X) + btrans) \quad (2)$$

In this equation, $T(V(X))$ represents the transformed feature map, *Wtrans* and *btrans* denote the weights and biases associated with the additional layers, respectively, and LReLU is the Leaky Rectified Linear Unit function which controls activation of these layers. The last step involved classifying the transformed feature map $T(V(X))$ into different brain tumor classes, which is done via Eq. (3):

$$C\left(T\big(V(X)\big)\right) = SoftMax\big(Wclass * T\big(V(X)\big) + bclass\big) \quad (3)$$

where, $C(T(V(X)))$ is the output representing the brain tumor classes, *Wclass* and *bclass* denote the weights and biases associated with the classification layers, respectively. In addition, SoftMax is the activation function that assists in the prediction of tumor classes. Through this comprehensive methodology, this work successfully inputs MRI images and outputs the corresponding brain tumor classes, achieving the objective of identifying brain tumors using a Deep Transfer Learning-Based VGG19 modeling process [22].

A model can remember training data but not be able to use it in new situations. By removing randomly chosen nodes and links during network training, the dropout layer stops the network from learning too much. This procedure prevents weights from exceedingly mirroring the data samples. The dropout layer can only be utilized during training to prevent overlearning scenarios. Not utilized for testing and verification purposes [23].

3.1.4 Performance evaluation

Accuracy: Accuracy is considered the principal performance assessment parameter for classification tasks. The accuracy is computed by dividing the count of accurate predictions by the total number of predictions and then multiplying the quotient by 100.

$$Accurcy = \frac{TP + TN}{TP + FP + TN + FN}$$

Precision: When the data set exhibits uneven observation points, the accuracy of the classification may not serve as a reliable measure of model performance. In this scenario, if all samples are predicted as the highest-ranking class, the resulting accuracy rate would be unreasonably high and devoid of meaningful interpretation. Consequently, the model lacks knowledge and can only provide projections at the most general level. Therefore, it is necessary to have a performance metric that is particular to the class to ensure validation.

$$Precision = \frac{TP}{TP + FP}$$

Recall: It is another important measure, defined as the percentage of observations from a class that the model predicts correctly.

$$Recall = True\ Positive\ (TP)/True\ positive\ (TP) + False\ Negative\ (FN)$$

$$Recall = \frac{TP}{TP + FN}$$

F1-Score: Another important measure is putting both accuracy and memory into a single number. It is the point where accuracy and memory come together.

$$F1-Score = 2 * recall * precision/recall + Precision$$

4. RESULTS ANALYSIS

This section provides a concise overview of the experimental setup and the data achieved. The experimental configuration encompasses the specificities employed in the current study regarding the training of the model and the software framework.

4.1 Experimental setup

The dataset was partitioned into training validation and testing subsets, and the specified model was constructed utilizing Tensor Flow technology and the Keras framework. It was then run in the Colab Pro setting. Google Colab is a great tool that makes it easy for data scientists and experts in the field of artificial intelligence to share their work online. Python code can be written and run over the internet without any setup. It also has easy sharing options and free access to graphics processing units (GPUs). This process can be refined through the Google Drive interface within the collective space offered by Collaboratory. The training of the relocated models involved the utilization of a loss measure and algorithm. Specifically, Categorical Cross entropy was employed as the loss measure, and Adam served as the optimizer with a learning rate set at 0.001. The selection of a mini-batch size of 32 and a maximum of 100 epochs was determined for this purpose.

Table 2 lists the hyperparameters and configuration settings used for training the deep learning model in dataset 1.

Table 2. Model training hyper parameters for dataset 1

S. No	Parameter Used	Value
1	Training Epochs	100
2	Optimizer	Adam
3	Learning Rate	0.001
4	Batch Size	32
5	Loss Function	Categorical Cross Entropy
6	Activation Function	ReLU, SoftMax

The experiment was conducted in two distinct phases. The initial stage involved training the MR images using the AlexNet and VGG-16 architecture. In the subsequent phase, the deep transfer with the transformed VGG19 model was trained to utilize the identical dataset. The pre-trained CNNs achieved a Accuracy of 92.36% for the AlexNet model and 95.45% for the VGG-16 model. In the subsequent phase, the deep transfer with the transformed VGG19 model was employed to train the identical dataset. The proposed model achieved notable results, with a sensitivity of 98.12%, a specificity of 99.45%, Precision of 98.45%, F1-Score of 97.87% and an overall accuracy of 98.65%. Figure 8 shows the Accuracy Comparison of AlexNet, VGG16, Transformed VGG19 model. Figure 9 illustrates the training and validation accuracy graph and the training and validation loss graph of the suggested model on the dataset. Experimental outcomes revealed superior performance compared to pre-trained convolutional networks. Figure 10 shows the variation of accuracy with 25Epochs, 50Epochs and 100Epochs (dataset 1).

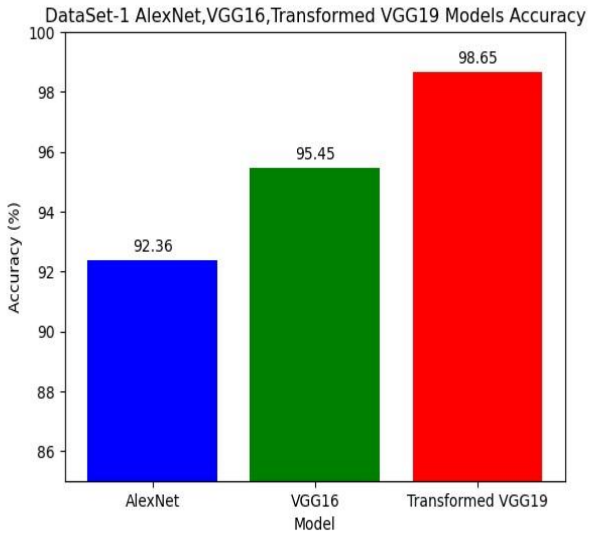


Figure 8. Accuracy comparison of AlexNet, VGG16, transformed VGG19 in dataset 1

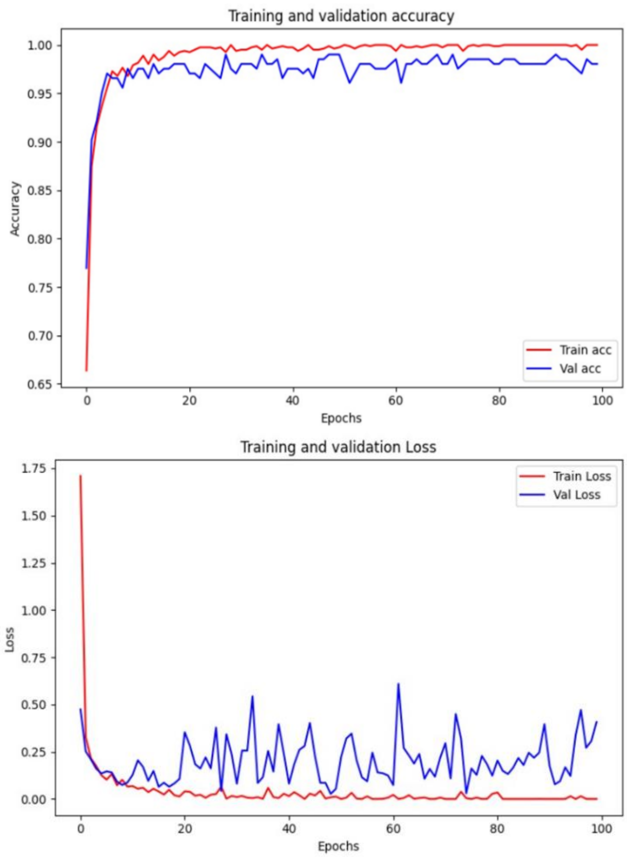


Figure 9. The model accuracy and loss graph of the deep transfer with the TransformedVGG19 model (dataset 1)

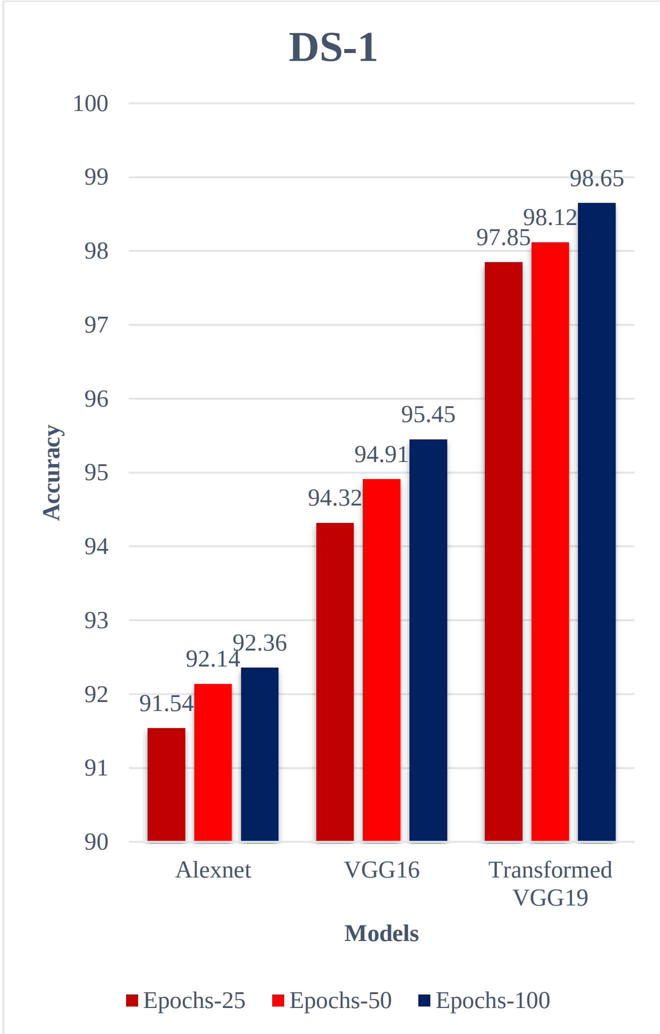


Figure 10. Variation of accuracy with epochs (dataset 1)

4.2 The details of a dataset 1

In this study, the publicly available Kaggle Brain tumor MRI dataset is used The Training dataset has a total of samples, out of which 1339 samples correspond to Meningioma, 1321 Glioma samples, 1457 Pituitary samples, and 1595 No tumor samples. The Testing dataset contains a total sample from which 306 Meningioma samples, 300 Glioma samples, 300 Pituitary samples, and 405 No tumor samples. The MRI brain tumor dataset is an openly accessible research community for academic purposes. To combine both Training and testing data sets 1645 Meningioma Images, 1621 Glioma Images, 1757 pituitary Images, and 2000 No tumor images. Table 3 presents the details of the brain tumor MRI dataset and the distribution of images used for training, validation, and testing phases.

Table 3. Brain tumor MRI dataset for using splitting training, validation and testing phases

Classification	Training Images (70%)	Testing Images (15%)	Validation Images (15%)	Total
Meningioma	1151	247	247	1645
Glioma	1135	243	243	1621
Pituitary	1231	263	263	1757
No Tumor	1400	300	300	2000
Total	4917	1053	1053	7023

You can access Dataset-1 in Kaggle by clicking on the URL. https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset.

4.2.1 Comparatively analysis AlexNet, VGG16, VGG19

Additionally, a comparative analysis was conducted to assess the classification productiveness of two pre-trained CNN models: AlexNet, VGG16, and Deep Transfer using the TransformedVGG19 model. The models employed in this investigation underwent training with the MRI dataset-1. The Deep Transfer with the TransformedVGG19 model, depicted in the above mentioned graphic, represents a CNN architecture consisting of 19 layers. In contrast, the AlexNet model comprises eight layers, while the VGG16 model consists of 16 layers. Transfer learning and fine-tuning methodologies were consistently applied to the AlexNet, VGG16, and VGG19 models in the tests conducted on the MRI dataset. The AlexNet architecture can be considered somewhat shallow in comparison to the VGG16 and VGG19 models [24]. Consequently, the fine-tuning process of AlexNet was conducted in a layer-wise fashion [25]. The AlexNet and VGG16 models have accuracies of 92.36% and 95.45%, respectively. The VGG19 model exhibits superior performance across all classification criteria when compared to the other two pre-trained models.

AlexNet: AlexNet is composed of a total of eight layers, which comprise five convolutional layers and three fully linked layers. AlexNet pioneered the utilization of Rectified Linear Unit (ReLU) activation functions, dropout regularization, and data augmentation approaches, which were groundbreaking at the time. The architecture contains over 60 million parameters [26].

VGG16: VGG16 has a more intricate structure in comparison to AlexNet, which consists of 16 layers, which encompass 13 convolutional layers followed by three fully connected layers. The VGG16 model always uses 3×3 convolutional filters across the network, which makes it easier to get more detailed and complete feature representations. Although VGG16 is a straightforward model, it demonstrated remarkable performance on the ImageNet dataset. The model possesses an estimated 138 million parameters [27].

VGG19: VGG19 shares the same architectural design as VGG16, but it incorporates a greater number of layers, specifically 19 layers in total. VGG19 consists of 16 convolutional layers and three fully linked layers. Similar to VGG16, it employs 3×3 convolutional filters throughout the whole network. VGG19 has extra layers that result in somewhat higher accuracy than VGG16, but this improvement comes at the expense of increased computational cost. The VGG19 model consists of around 144 million parameters.

- Depth: VGG16 and VGG19 possess greater depth in their network architecture when compared to AlexNet.
- The number of parameters: VGG16 and VGG19 is higher than that in AlexNet because of their more complex designs. Among the three models, VGG19 has the maximum number of parameters.
- Performance: Typically, as the network gets deeper, it can extract more intricate characteristics from the input images, which may result in improved performance. VGG16 and VGG19 exhibit superior performance compared to AlexNet in diverse picture classification tasks but at the cost of increased computational complexity.
- Training Time: Because of their higher parameter count, VGG16 and VGG19 often require more computer resources and time for training than AlexNet.
- Memory usage: VGG16 and VGG19 models are higher than that of AlexNet during both training and inference. This is because VGG16 and VGG19 have more layers and parameters.

The Transformed VGG19 model achieved higher accuracy compared to the AlexNet and VGG16 models [28].

The VGG19 model was chosen for adoption due to its deeper architecture, which allows for an exploration of the effects of deep fine-tuning. Additionally, this particular model is very appropriate for feature representation in the context of localizing or identifying specific material.

The examinations were conducted on pre-trained CNNs, specifically AlexNet, VGG16, and VGG19. As depicted in Figure 8, the findings reveal that VGG19 outperformed both AlexNet and VGG16. The present study mostly centers around the classification of brain tumors in 2D pictures, given that CNN models inherently operate in a two-dimensional framework. The performance evaluation of fine-tuning in 3D magnetic resonance (MR) pictures was not conducted because of the substantial quantity of 3D medical datasets. Previous studies have demonstrated promising results in using CNNs trained from scratch for these datasets. The focus of our study is on 2D pictures, therefore rendering 3D pre-trained CNN models unsuitable for the analysis of the 2D-MRI dataset. The VGG19 pre-trained model is widely acknowledged as a particularly effective choice for classifying 2D brain tumor MRI images. This is accomplished by employing transfer learning and block-wise fine-tuning techniques on the CE-MRI dataset.

4.3 The details of a dataset-2

The dataset of brain MRI images was sourced from Kaggle, an openly accessible database, encompassing a total of 253 images. These images were organized into a single folder with two subfolders: one labeled "no tumor," comprising 98 images, and the other labeled "tumor," comprising 155 images. Figure 11 illustrates representative images from the dataset, showcasing examples of both tumor and non-tumor (healthy) images. The brain tumor dataset utilized includes 253 authentic brain images obtained from the Kaggle website, with 177 images allocated for training, 38 for validation, and 38 for testing. You can access Dataset-1 in Kaggle by clicking on the URL. https://www.kaggle.com/datasets/navoneel/brain-mri-images-for-brain-tumor-detection.

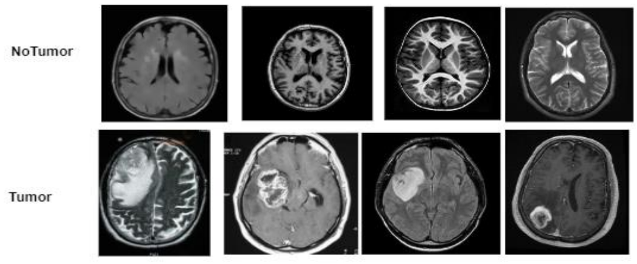


Figure 11. Tumor and No tumor images

The deep transfer with the TransformedVGG19 model comprises sixteen layers, including two dropout layers and two connected dense layers. The final layer of VGG19 contains one thousand neurons, representing the classes in the ImageNet dataset. To adapt to the Brain MRI dataset, the last fully connected layer is modified to accommodate two classes, as determined by the classes present in the dataset.

The pre-trained CNNs achieved an Accuracy of 96.58% for the AlexNet model and 97.65% for the VGG-16 model. In the subsequent phase, the deep transfer with the transformed VGG19 model was employed to train dataset 2. The proposed model achieved notable results, with a sensitivity of 98.62%, a specificity of 99.45%, a Precision of 98.45%, an F1-Score of 97.87% and an overall accuracy of 99.18%. Figure 12 shows the Accuracy Comparison of AlexNet, VGG16, Transformed VGG19 model. Figures 13 illustrates the training and validation accuracy graph and Figure 14 shows the training and validation loss graph of the proposed model on the dataset. Experimental outcomes revealed superior performance compared to pre-trained convolutional networks. Figure 15 shows the variation of accuracy with 25Epochs, 50Epochs and 100 Epochs (dataset 2). Table 4 presents the details of the brain tumor MRI dataset and the distribution of images used for training, validation, and testing phases.

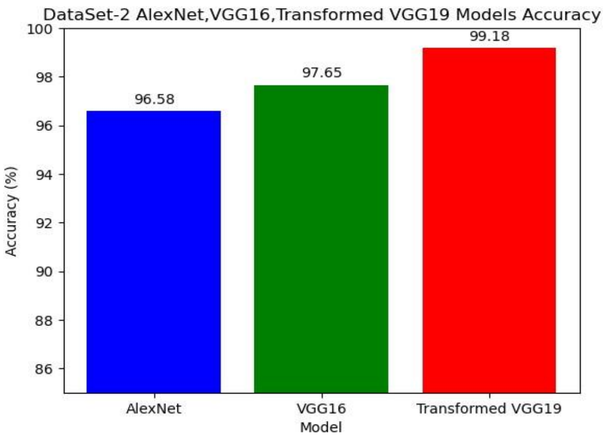


Figure 12. Accuracy comparison of AlexNet, VGG16, transformed VGG19 (dataset-2)

Table 4. Brain MRI image dataset for using splitting training, validation and testing phases

Classification	Training Images (70%)	Testing Images (15%)	Validation Images (15%)	Total
No tumor	68	15	15	98
Tumor	109	23	23	155
Total	177	38	38	253

Table 5 lists the hyperparameters and configuration settings used for training the deep learning model in dataset 1.

Table 5. Model training hyper parameters for dataset 2

S.No	Parameter Used	Value
1	Training Epochs	100
2	Optimizer	Adam
3	Learning Rate	0.001
4	Batch Size	32
5	Loss Function	Binary Cross Entropy
6	Activation Function	ReLU, Softmax

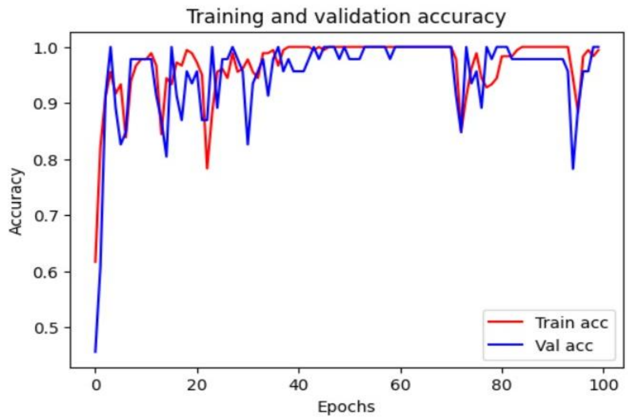


Figure 13. Accuracy for training and validation (dataset 2)

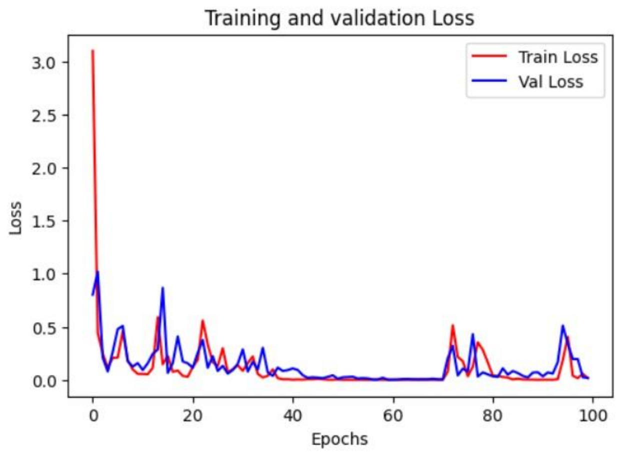


Figure 14. Loss for training and validation (dataset 2)

Early and accurate diagnosis is pivotal in devising effective treatment plans and improving the prognosis for patients suffering from these malignancies. With the rapid advancements in deep learning and image processing techniques, there is a growing emphasis on leveraging these technologies to enhance the accuracy and speed of brain tumor diagnoses.

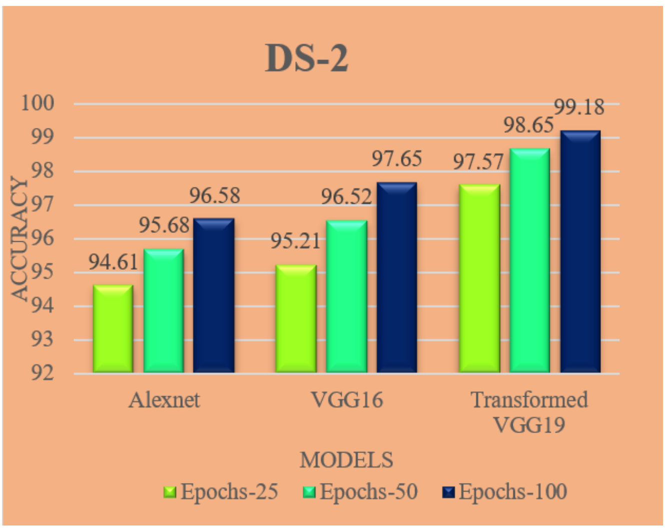


Figure15. Variation of accuracy with epochs (dataset 2)

Figure 15 presents on a dataset known as "DS-2," the graph compares the accuracy performance of three different models (AlexNet, VGG16, and Transformed VGG19) at various training epochs (25, 50, and 100).

Figure 16 presents the confusion matrices for the three models evaluated (A) AlexNet, (B) VGG16 and (C) Transformed VGG19 model on dataset 1, (D) AlexNet, (E) VGG16 and (F) Transformed VGG19 model on dataset 2. The confusion matrices provide a visual representation of the model's performance in terms of classifying samples correctly. Dataset-1, The model's task in this case is to classify brain tumors into four categories: meningioma, glioma, pituitary, and no tumor. Dataset-2, The model's task in this case is to classify brain tumors into two categories: tumor and no tumor. Rows Represent the samples' true labels. Columns represent the model's predicted labels. The diagonal elements display the number of correctly classified samples.

Figure 17 is a bar chart that compares the accuracy of different models on two datasets: dataset-1 and dataset-2. The x-axis represents the models (AlexNet, VGG16, and Transformed VGG19), and the y-axis represents the accuracy in percentage.

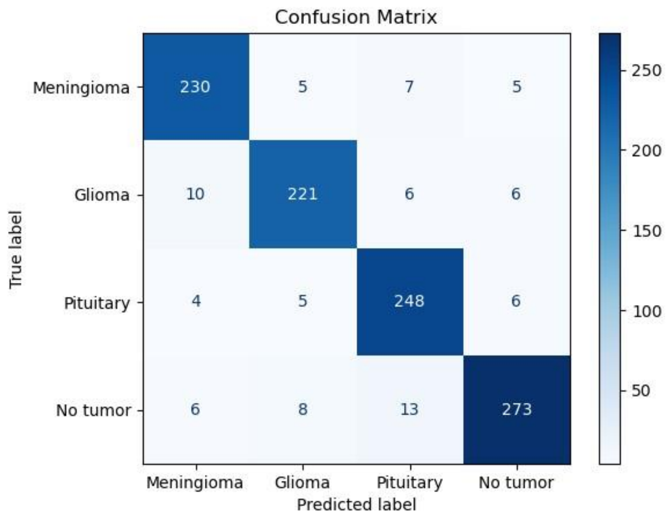
Table 6 presents a comparative analysis of three deep learning models AlexNet, VGG16, and Transformed VGG19. These models were evaluated on two datasets, dataset-1 and dataset-2, to assess their performance in terms of accuracy.

Table 7 shows the results of different deep learning models for a specific task. The first column lists the authors of each model, the second column lists the techniques used in the model; and the third column lists the model's accuracy. The last row shows the results of the proposed model for two different datasets.

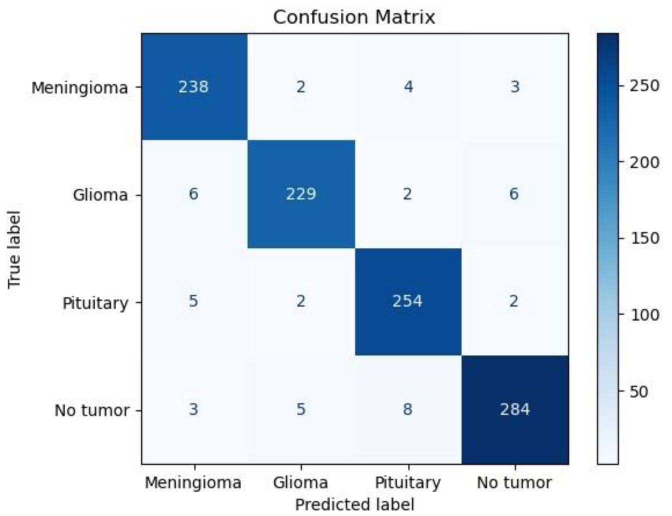
The proposed model, Deep Transfer Learning with the Transformed VGG19, achieved an accuracy of 98.65% on the multi-class dataset and 99.18% on the binary-class dataset. This is the highest accuracy among all the models listed in the table.

The application of deep learning models in medical imaging has demonstrated significant promise in detecting and classifying abnormalities, including brain tumors. However, the proliferating range of models and techniques emphasizes the pressing need for a systematic, empirical evaluation to discern their efficacy, precision, scalability, and complexity in real-world scenarios.

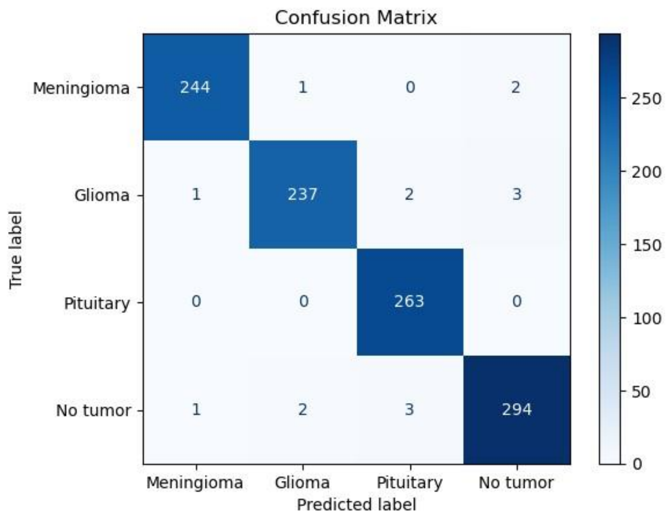
The Transformed VGG19 architecture has proven to be superior to other architectures. The Transformed VGG19 model confusion matrix Figure 16 (C) shows that the developed model was able to detect 244 out of 247 Meningioma patients, 237 out of 243 Glioma patients, 263 out of 263 Pituitary Patients, 294 out of 300 normal patients as healthy.



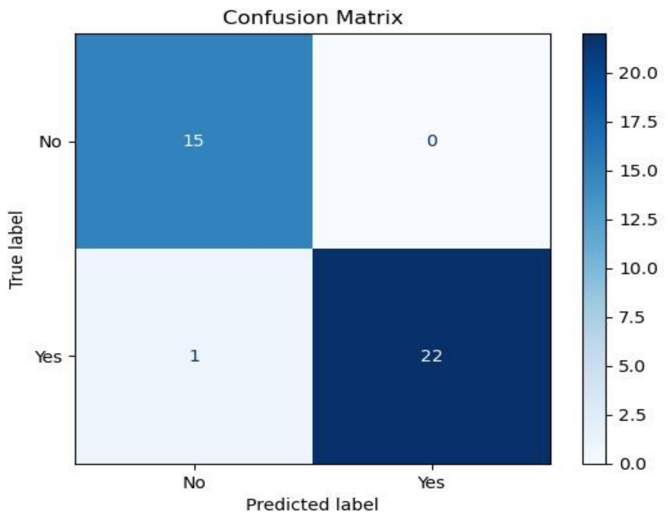
(A)



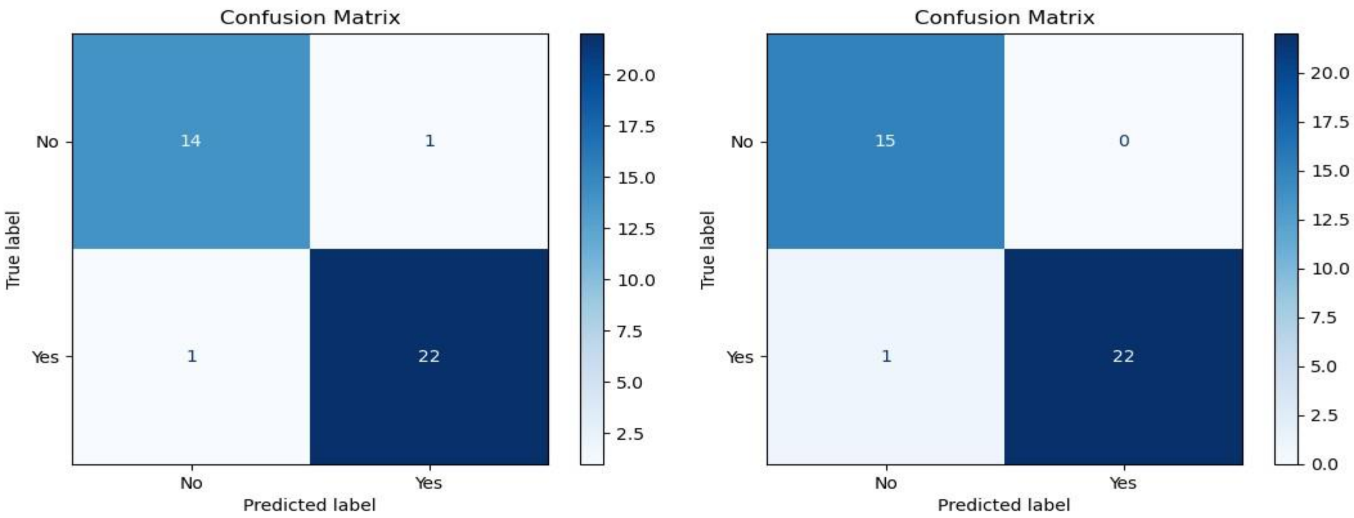
(B)



(C)



(D)



(E) (F)

Figure 16. Dataset-1: Confusion matrices (A) AlexNet, (B) VGG16, (C) Transformed VGG19 model
Dataset-2: Confusion matrices (D)VGG16, (E) AlexNet, (F)Transformed VGG19 model

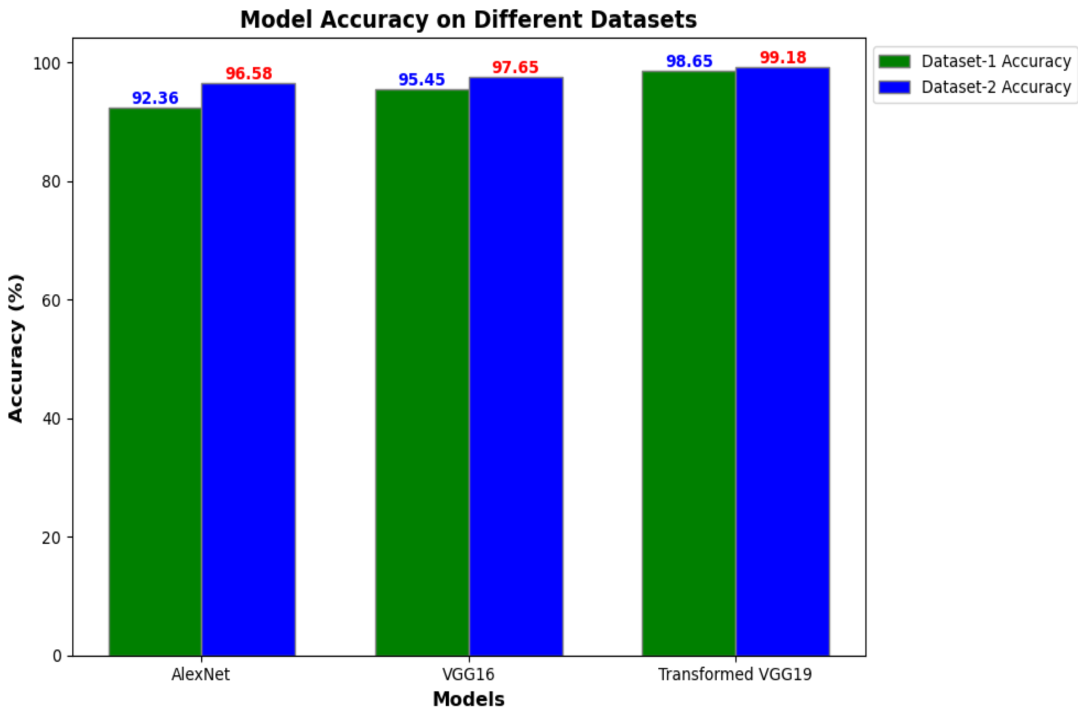


Figure 17. Accuracy comparison of AlexNet, VGG16, and Transformed VGG19-(dataset-1, dataset-2)

Table 6. Accuracy comparison Table Alexnet, VGG16, Transformed VGG19-(dataset-1, and dataset-2)

Sno	Model	Epochs	Batch Size	Learning Rate	Optimizer	Dataset-1 Accuracy	Dataset-2 Accuracy
1	AlexNet	100	32	0.001	Adam	92.36	96.58
2	VGG16	100	32	0.001	Adam	95.45	97.65
3	Transformed VGG19	100	32	0.001	Adam	**98.65**	**99.18**

Table 7. Results for the proposed model for different samples

Author	Techniques	Accuracy
Anaraki et al. [29]	GA-CNN	94.02%
Swati et al. [30]	VGG19	94.84%
Sultan et al. [31]	CNN	96.13%
Proposed approach	Deep Transfer Learning with the Transformed VGG19 Multi-class dataset-1 Binary-class dataset-2	**98.65%** **99.18%**

5. CONCLUSION AND FUTURE SCOPE

In this study, a variety of techniques was assessed for their accuracy in identifying brain tumors from MRI images. The deep transfer learning approach utilizing the transformed VGG19 model demonstrated promising results, showcasing its capability to distinguish between multiple classes and binary classes of brain tumors with high precision. When benchmarked against other prevalent methods, such as VGG19, GA-CNN, and CNN, the proposed approach stood out in terms of performance, especially for binary class datasets and samples.

The robustness of this study is evident in its thoughtful customization of the VGG19 model, adjusting it to fulfill the distinctive needs of tumor classification based on MRI. While the conventional VGG19 showed commendable results, the customizations made to it in the proposed approach unlocked further potential, making the algorithm more attuned to the subtle nuances of MRI images.

Future Scope:

The promising results from this research pave the way for several future endeavors:

1) **Data Augmentation:** To further improve the accuracy, future studies can employ advanced data augmentation techniques. These can help the model recognize tumors under various conditions and transformations, making the algorithm even more robust.
2) **Integration with AI-based Radiology Systems:** The proposed model can be integrated into AI-driven radiology diagnostic systems, offering real-time suggestions to medical professionals and aiding them in their diagnostic process.
3) **Expanding the Dataset:** By introducing a wider variety of tumor classes and stages, the model can be made more comprehensive. Future research should focus on expanding the dataset to include rare tumors and borderline cases.
4) **Model Optimization:** While the transformed VGG19 shows promise, there is always room for optimization. With the rise of newer architectures and optimization algorithms, future works can fine-tune the existing model or explore hybrid models for better results.
5) **Real-world Testing:** The ultimate test for any model is its performance in real-world scenarios. Future endeavors should focus on clinical trials and collaborations with hospitals to evaluate the model's efficacy in live environments.

By building on the foundation laid by this research, future studies can push the boundaries of AI in medical imaging, ensuring quicker, more accurate diagnoses, and better patient care scenarios.

- **Explainable AI:** While AI-driven models have demonstrated impressive diagnostic capabilities, the opacity of these models remains a concern in clinical practice. Future efforts should focus on developing explainable AI methods that provide clinicians with insights into how AI systems arrive at their decisions. This will foster trust and enhance the adoption of AI technologies in healthcare.
- **Real-Time Diagnostics:** The reduction of diagnostic delay is of paramount importance. Future research should aim to develop real-time diagnostic systems that can quickly and accurately detect and classify brain tumors. These systems could potentially be integrated into operating rooms to aid surgeons during procedures, improving patient outcomes.
- **Personalized Medicine:** Tailoring treatment plans to individual patients is a growing trend in healthcare. Future studies could explore how AI and machine learning can contribute to the development of personalized treatment strategies for brain tumor patients. This may involve predicting treatment responses and outcomes based on patient-specific data.
- **Data Augmentation and Quality:** The availability of high-quality, diverse, and well-annotated datasets is essential for training robust AI models. Future research should prioritize data augmentation techniques to address data scarcity issues. Additionally, ensuring data privacy and security will be crucial as healthcare systems become more data-driven.
- **Clinical Validation and Adoption:** The transition from research to clinical practice is a significant challenge. Future efforts should focus on rigorous clinical validation of AI-based diagnostic tools to ensure their safety, efficacy, and compliance with regulatory standards. Collaboration between researchers, healthcare institutions, and regulatory bodies is essential in this regard.

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