An Efficient Methodology for Brain Tumor Segmentation & Detection Using K-means clustering & Fine-Tuned Efficient Net model

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Abstract. A brain cancer or tumor is a condition occurred due to the expansion of unnatural nerve cells. Because tumors are rare and can take many different forms, it is challenging to estimate the survival rate of a patient who has been impacted. These tumors can be found using Magnetic Resonance (MRI) Images, which are crucial for locating the tumor placement; however, non-automatic recognition is a labor-intensive & difficult process that may yield inaccurate findings. Segmentation is also required to calculate the tumor's size and other prognostic parameters. Adopting computer-aided methods is crucial to assisting in overcoming these limitations. Various models of Deep learning are utilized in medical image analysis to detect brain tumor employing MRI images as artificial intelligence (AI) technology progresses. This paper presents a deep learning convolutional neural network fine-tuned Efficient Net baseline model and K-means clustering based segmentation are utilized to effectively detect and segment images of brain tumors, respectively. In order to boost the number of data samples for our suggested model's training, data augmentation techniques are used. The tumor is separated from the MRI images using K-means clustering. Brain tumor detection is carried out using fine-tuned Efficient-B0. The findings demonstrate that the state-of-the-art EfficientNet-B0 model, which has been suggested and fine-tuned, has obtained excellent classification accuracy, precision, and recall values, with final accuracy of 98.66% for overall segmentation and detection.

Keywords: Brain tumors, Deep learning, Segmentation, Convolutional neural network.

1. Introduction

The immensely prevalent intracranial cancers or tumors that cause major mortality and morbidity are brain tumors, which constitute a diverse group. The malignant tumors are extremely fatal as well as aggressive neoplasms in persons of each & every ages. The World Health Organization's 2021 Classification of different tumors in the Central Nervous System divides brain lesions in four categories (I, II, III, IV), each one having a deteriorating prognostication and a progressively aggressive malignity. Glioblastoma is the extremely antagonistic primary tumor among World Health Organization's Grade IV tumors, with 12- to 15-month median survival time following diagnosis.

The benchmark for diagnosing and evaluating tumors is the pathological evaluation of tissue samples. However, a non-invasive technique that could precisely identify the tumor kind and predict its grade would be greatly desired because of the huge effect this would have on the surrounding structures [1]

Since MRI plays a very important role in the segmentation, identification, and management of brain tumors, it has recently become a very common technology for their detection and classification. Different types of machine learning as well as deep learning (DL) strategies are now universally employed in the medical profession and healthcare administration for the automatic diagnosis and segmentation of all diseases.

Brain tumor segmentation is investigated for diagnosing shape and different range of tumor in brainMRI image. Existing segmentation methods involves thresholding, edge and region, clustering, and neural network based strategies. The cluster-based method is among the extremely efficacious ones among the various techniques. Again, there are other clustering techniques, including the mountain clustering approach, fuzzy clustering, K-means clustering, Watershed clustering. K-means clustering is widely used & most popular clustering strategy. It is easier to use and performs computations more quickly than hierarchical clustering. It can also be used with a lot of different variables.

In terms of diagnosing medical picture records, the detection of brain tumors is crucial in the realm of biomedical application. A patient's chance of survival may increase with earlier brain tumor discovery. Even though there have been numerous important developments in this field, tumor identification remains an extremely difficult task. The position, size, and structural characteristics of the tumor varygreatly from patient to patient, making segmentation an extremely difficult task. . By involving thefeature extraction and selection phases in the training process, deep and transfer learning has overcome the difficulties listed above with an unparalleled level of success[2].

The deep learning (DL)methods that have been extensively used for solving medical image analysis issues are the convolutional neural network (CNN) models. It addresses the shortcomings of earlier deep learning techniques. Due to its exceptional performance and extremely high accuracy in a research environment, CNNs have recently grown in favor for the categorization of brain tumors and is well recognized for operating images. Some of the extremely renowned CNN designs include ResNet, ZfNet, VGGNet, GoogLeNet, and AlexNet. A CNN can automatically extract significant and associated characteristics from images. Even with a small amount of training data, a CNN can nevertheless generate high recognition accuracy. No longer necessary are design specifics or prior knowledge of attributes. The main advantage of utilizing a CNN model to achieve excellent recognition results is the use of topological details already present in the input. The results of themodel's detection algorithms are mostly unaffected by the rotation and translation of the input images.

2. Literature Survey

CNN was used to apply the approach that Ghassemi et al. recommended that focuses on pretraining. As a result, the main emphasis is placed on pretraining the model using various publicly accessible datasets, after which the model is applied. The resulting prototype is then tested employing the primary dataset, which contains three discrete variations of tumor, and it attained an accuracy of 95.60%. [3, 4]

Recently, a number of unique designs have been introduced with the overarching goal of utilizing the CNN technique to the graph domain, particularly in the categorization of medical imaging.Although there are different proposed methods for classifying brain tumors, this methodology has the following problems. The accuracy obtained by prevailing strategies is inadequate due to the significance of MRI categorization in the medical field. Some classification methods required manual tumor region identification, inhibiting full automation. [4]

The clustering reliability analysis served as the foundation for the authors' enhanced K-means algorithm. The approach successfully addresses the issue of unequal density and significant variations in the amount of data clustering. [5]

K-mean clustering was employed by the author of this research to distinguish between benign and malignant aberrant cells. This research uses K-mean clustering to efficiently assess the aberrant cell to discover if it is cancerous or non-cancerous.The BRATS 2018 dataset is utilized in this investigation for experimenting the approach the approach. After using the suggested methods, it is possible to distinguish between malignant and non-cancerous tumors using MR images. [6]

The automated segmentation procedure and identification strategy employing ANN from MR images was provided in a research investigation that was conducted to detect and identify the abnormal behavior of brain tumors. Improved automated segmentation and identification techniques were thought to be beneficial in detecting cases of brain tumors without the need for human intervention. And it was done so by making the enhancements listed below while taking into account earlier methods: K-mean clustering improved greyscale region identification in MR images, ANN was employed in the training phase by selecting the right object view, and texture features were used to examine and separate benign from malignant brain tumor cases. [7]

Although threshold-based OTSU segmentation was utilized in this publication, color-based segmentation approaches are typically used in brain tumor research. The outcomes demonstrated that this approach is superior to the established use of color segmentation and grey scaling. On many datasets, this article offered a minimum of 87% accuracy. When it came to separating the tumor location from the rest of the brain, the procedure outperformed previously used techniques. [8]

In this study, two deep learning models are proposed to recognize binary class (abnormal and normal) and multiclass (glioma, pituitary &meningioma) tumors on two datasets that each contains 152 and 3064 MRI images. The author combined our proposed "23 layers CNN" architecture with the VGG16 design using transfer learning, and then compared the proposed models to those that had been previously published in the literature. The findings show that the models outperform all other models in terms of the dataset's correctness. [9]

The authors of this study summarized more than 30 contributions to this topic and examined the various methods used in the pre-processing, segmentation, localization, feature extraction, andclassification of tumors. They have addressed the gaps in current knowledge, issues, and prospective application in this field. [10]

This article describes a deep learning CNN strategy for classifying tumors with the assistance of MRI image pre-processing. The recommended strategy consists of three primary phases: preprocessing, brain tumor segmentation using k-means cluster-based technique, and brain tumor classification utilizing MRI images on a refined VGGNet (19) model. Additionally, the data augmentation concept was developed in order to increase the measure of data attainable for training in order to refine model's accuracy. Through careful experimentation, the proposed technique was assessed using the BraTS 2015 benchmark data sets. The outcomes support the proposed strategy's efficacy and show that it was more accurate than previously reported state-of-the-art methods. [11]

The authors provided a thorough overview of all clustering methods known for medical field segmentation. Appropriate clustering algorithms in the medical area might lessen the enormous strain on medical science by processing patient data effectively and precisely identifying disorders. [12]

3. Proposed Methodology

The proposed model strategies will be agitated in the ensuing sections. Fig1 illustrates the flow chart of the proposed methodology

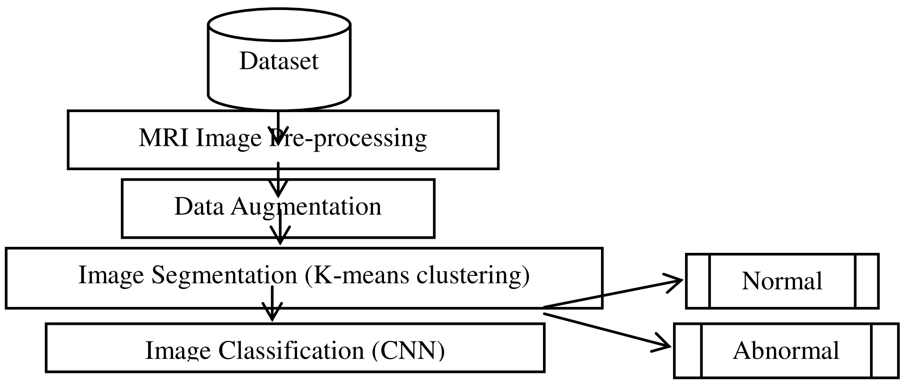


Fig 1.Flow chart of the proposed methodology

3.1 Dataset

There were 3000 MRI pictures in the dataset. 1500 were given the tumor designation of YES. 1500 more scans were classified as NO (non-tumor). The dataset was equally split between the two classes in order to prevent class dominance, with 90% (2700) of the scans going for training and 10% (300) for validation. In order to select our subset, we must eliminate any photos that might have deceived the model during training. There are no set dimensions for the image collection. Since all input photos were automatically enlarged into 224 224 dimensions using the Keras automated resizing script, all image samples were normalized and resized as a result. The pictures dataset utilized in these tests is a publicly accessible dataset on Kaggle.

3.2 Image Pre-processing

To make a picture effective for producing accurate results, excess noise is eliminated from it before it is utilized for categorization. Additionally, pre-processing methods such mean normalization, standardization, noise reduction, image scaling, and geometric modifications are used to pre-process photos. The development of the features found in certain photographs is accomplished by image processing. Since every outcome in computer vision depends on the features, image processing is primarily used in this field. Some people think that picture pre-processing can change an image's genuine characteristics.

3.3 Data Augmentation

While analyzing data, a technique called data augmentation is employed to enhance the portion of data by appending copies of the existing data that have been significantly updated or new aggregated data that have been produced from the existent data. This serves as regularization and lowers over fitting when machine learning models are trained. This and oversampling in data analysis are closely related. A common method for enhancing deep neural networks' generality is known as data augmentation, which can be compared to implicit regularization. When there is a lack of trustworthy, high-quality data and finding new examples is costly and time-consuming, it is crucial. It increases the model's resistance to minute changes. Cropping, flipping, padding, rotation, shifting, brightness, rescaling, shear intensity, zoom range, and preprocessing functions are some of the numerous augmentation techniques.

3.4 Kmeans Clustering

The most popular algorithm for the unlabeled dataset is K-means cluster-based technique. It is used in unsupervised learning techniques to address drawbacks of clustering. When using K-means, separate clusters are formed based on specific criteria, with the number of clusters (k) being predetermined. It is sometimes referred to as an iterative algorithm since it employs an iterative process to create k distinct clusters based on shared characteristics. That method also qualifies as a centroid-based algorithm because each cluster is connected to a specific centroid. The total of the distances between each data point and cluster is reduced with the aid of this approach. Traditional k-means just needs a few steps.First, choose k centroids at random, where k is equal to the number of clusters you want to use. The center of a cluster is represented by centroids, which are data points.

The algorithm's major component operates via a two-step procedure known as expectation-maximization. Each data point is assigned to the closest centroid during the expectation stage. The new centroid is then determined by computing the mean of all the points for each cluster during the maximization step.Fig2 shows the flow-chart of k-means clustering technique.

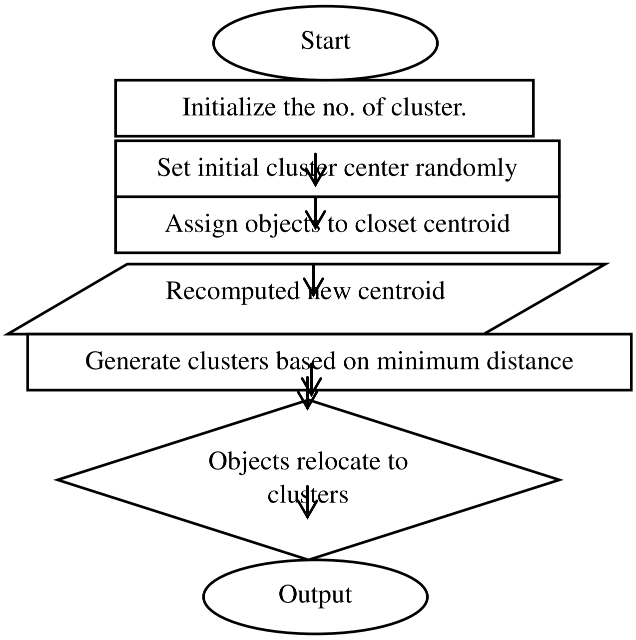


Fig 2. Flow chart of K-means clustering

3.5 Convolutional neural network (CNN)

An image processing neural network type is a convolutional neural network (CNN). Because they can extract features from photos and learn to recognize patterns, CNNs are efficient for classifying and recognizing images.

They are renowned for their capacity to use data to learn intricate traits.The success of CNN is attributable to their capability to use densely connected layers to extract information from data. Additionally, the comparatively low number of weights per layer enables the network to pick up complicated features fast.

CNNs are frequently employed in two applications: speech recognition and image recognition. It is a great tool for these kinds of tasks despite its complicated feature learning capabilities and thick connection structure.

Convolutional neural networks (CNNs) are often built at a permanent resource cost and then weighed up when extra resources become available to attain higher accuracy. There are different architectures of CNN. These are LeNet, VGG16, Xception, Inception, DenseNet, GoogleNet, MobileNet, EfficientNet(B0-B7), etc. We are implementing fine-tuned EfficientNet B0 model for this study.

3.6 Efficient Net B0 Baseline model

The Google Brain Team created the EfficientNet CNN model [13]. When looking at network scaling, these researchers discovered that performance can be reinforced by optimizing network's depth, width as well as resolution. The researchersscaled a neural network to assemble more deep learning models, which have a significantly progressive efficacy as well as classification accuracy than the CNN models that were earlier in use, to generate a new model. EfficientNet successfully and consistently carried out extensive visual recognition for the ImageNet. These designs are approximately eight times lesser and six times quicker to infer than the most notable existing techniques, such as VGGNets, GoogleNet, Xception, ResNetsand InceptionResNet [14]. Different models in the convolution neural network family are produced by EfficientNet-B0 using a composite scaling technique of network's number of tiers. Figure3 shows the baseline EfficientNet B0 model architecture.

The network depth is basically the total number of layers in a network. The width of CNN gives information about number of filters present in the model. The resolutionof CNN model is deduced by the image's height as well as breadth. The most recent EfficientNet baseline model, which takes a 224* 224* 3 as input image, is shown in Fig3 [15]. This technique uses multiple convolutional layers along with 33 receptive fields and inverted bottlenet residual MonileNet to capture properties across layers.

EfficientNet-B0 outperformed other pioneering models that were trained on the ImageNet by adjusting each dimension using a specified set of scaling coefficients, unlike other deep CNNs. EfficientNet unveiled exceptional results even working with the transfer learning strategy, demonstrating its utilityfor other datasets. With scales from 0 to 7, the model was made public, suggesting an improvement in parameter size and accuracy. As a result of the recent development of EfficientNet, users and developers may now take advantage of and deliver enhanced ubiquitous connection equipped with DL capabilities across many platforms to satisfy a variety of purposes.

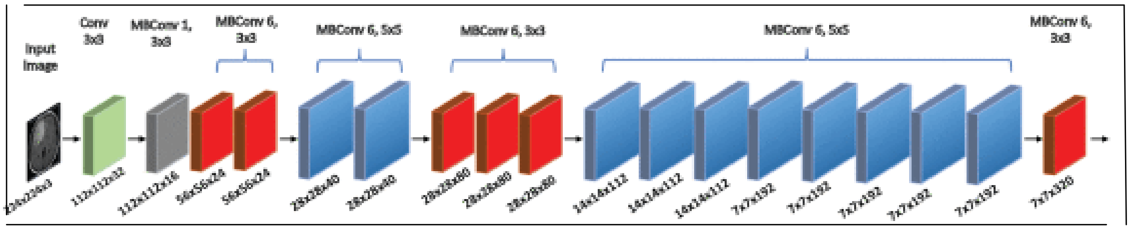


Fig 3.Baseline Efficient Net B0 model architecture

3.7 Fine-tuned Efficient Net model

The main goal of the presented study is to discourse the challenging classification and diagnosis of brain tumors in MRI images by using the baseline EfficientNet model with little updation in layers added by fine-tuning & training phase. Images sized 224 x 224 x 3 were given data enhancement and augmentation before being passed to the pre-trained baseline EfficientNet model, which impetuously performs feature extraction. This quality involves descriptors of coloras well as shape, circularity, roundness, and conciseness. The EfficientNet-B0's presumed final layers, which include a sigmoid classifier, dropout, an activation layer, two fully connected (FC) layer, and global average pooling, are shown in the figure. We used a flattened layer to direct the feature estimates from the sixth MBConv layer and transformed them into a one dimensional array. Further it is transmitted to the dense layer with 128 hidden units after flattening. Before predicting the outcomes, we employed an activation named rectified linear unit, coupled to pooling and next thick layer with one of the neurons depicting our supplied labels. By linearly smearingnew estimates of weights as well as biases to each& every feature map, this technique produced a probability.

In addition, to get rid of the over fitting, we annexed a dropout layer with an estimate of 0.5 after the hidden layer of 128 neurons. As our chosen classifier, we ultimately used the sigmoid. Equation 1 depicts the sigmoid classifier's mathematical function, which has an easily identifiable S-shaped curve. A logistic function called sigmoid performs binary classification.Fig4 shows the architecture of fine-tuned EfficientNet B0 model.By establishing a threshold value of 0.5, it assigns values to 0 or 1, where 0 denotes non-tumor images and 1 denotes tumor images. These classes are represented by the neuron in the final dense layer.

$$\text{Sigmoid}(x) = f(x) = \frac{1}{1+e^{-x}} \quad (1)$$

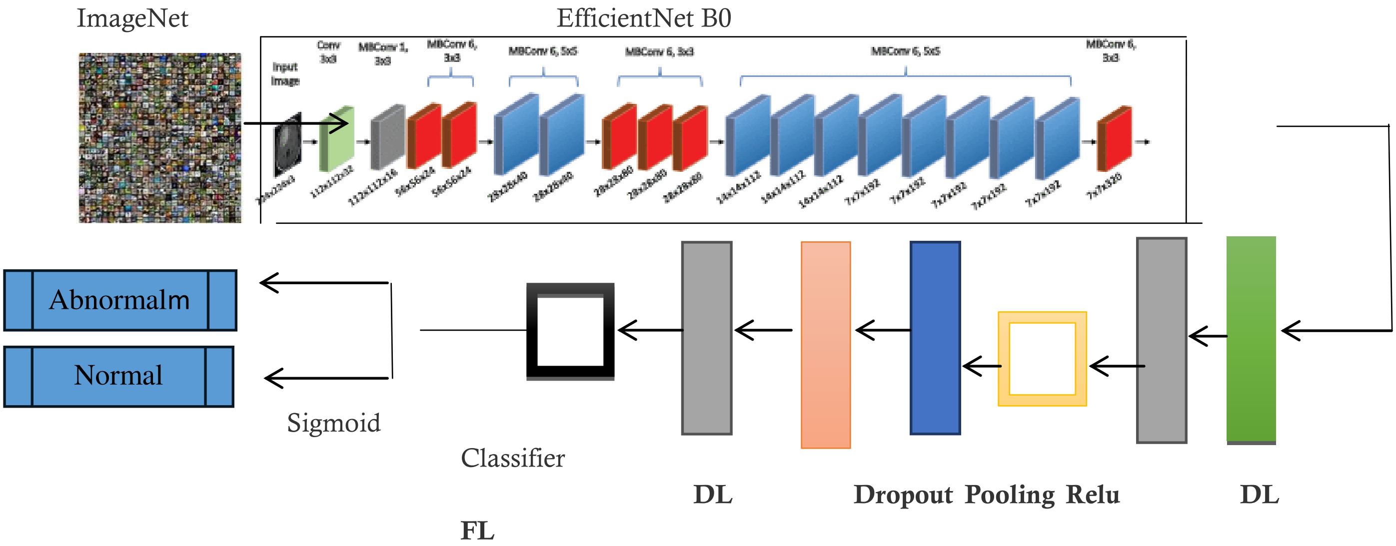


Fig 4.Architecture of fine-tuned EfficientNet B0 model.

4. Experimental set-up

The open-access dataset was employed for experimentation of the suggested model. Python implementation of the optimized Efficient Netbaseline model was built on top of the TensorFlow as well as Keras infrastructures. The general network underwent training on the computer system that met the subsequent requirements: 2.60 GHz Intel Core i5-11400 processor. Our setup had a 128 GB SSD, 1 TB HDD and a 64-bit operating system with 16 GB of memory. Fig5 shows some of the images of the input dataset.

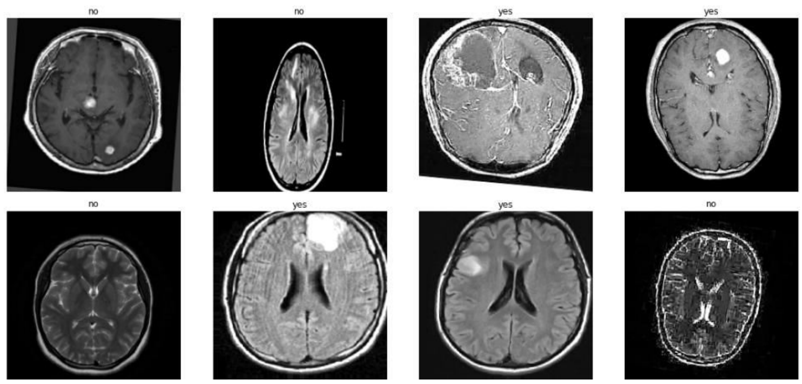


Fig 5. Samples from image dataset

4.1 Hyper parameters & Loss Function

The hyper-parameter as well as loss function settings employed for the job to generate productive results are illustrated in this segment. A DL model's performance is influenced by both accuracy and loss. Since a model with a high loss is worse, the primary objective of a designed model is to attain the minimal rate of mistakes. To calculate the average difference between the expected and predicted values, we employed cross-entropy (CE). Equation 2 illustrates the loss measurement for the binary classification, here y denotes binary estimates of 0/1, & p denotes probability. [16]

$$\text{Loss} = (1 - y)\log(1 - p)) - (y\log(p)) \qquad (2)$$

In order to get the best possible loss reduction during training, we used Adam [40] as our optimizer. This optimisation method helps the weights get closer to the local minima more swiftly by employingan adaptive gradient descent function. Adam was chosen over competing optimisation methods like SGD and RMSProp because of its simpleness, effectual usage of memory, & quick learning curve. Recently, Adam optimizer had great DL programmes that trained models to help with medical image interpretation. The values of the hyper-parameters are shown in Table 1, along with a tiny learning rate (LR) that has been modified to work with the other hyper-parameters. Adam worked more swiftly and effectively to achieve a rapid convergence.

Table1. Training hyper-parameters for training

Hyperparameters	Value
Optimizer	Adam
Batch_size	32
No. of epochs	20
Loss function	Binary CE
Intial learning rate	$10e^{-3}$
Reduced learning rate	$10e^{-5}$

We were able to transmit data over the network because of the batch size of 32 without using all of our computational memory. Additionally, 20 epochs were used to train each model.

4.2 Data Augmentation

In computer vision, the augmentations of the original dataset go through a number of visual modifications to enhance the data samples, which helps model training and reduces over fitting. Geometric transformations, colour space, cropping, random rotation, and noise injections are some of these processes. This method of training models improves generalizability and the accuracy of predictions made using distributions other than the training set [17]. Using an open-source Python library called Albumenatations, image augmentations were carried out to increase the dataset's size by generating new sets of images using different transformation techniques, including random rotation (90, 180, and 270 degrees), horizontal and vertical flips, and transposition [18]. Albumenatations were used with the intention of preserving the pixel-by-pixel data required for medical imaging activities.Data augmentation parameters are shown in Table2.

Table2: Data Augmentation strategy

Techniques	Parameter Value
Width shift range	0.1
Shear_range	0.2
Zoom_range	0.2
Rotation	90 degree
Height_shift_range	0.1
Vertical_flip	True
Horizontal_flip	True

5. Performance Evaluation Metrics

A research study's evaluation of the CNN algorithm's classification performance is crucial. Here, we include the evaluation metrics— sensitivity, accuracy, precision and area under curve (AUC) that are most frequently disputed in the literature on the categorization of brain tumors. True positive (TP) in classification tasks refers to the dataset that is accurately categorized into positive instances. Similar to this, a true negative (TN) result occurs when the model correctly places an imagined in the negative category. Contrarily, a false positive (FP) means when the designed model wrongly assigns a positive classification to an image when the actual classification is a negative classification. A false negative (FN) is a result when our model projected a negative result for a positive class.

1. Accuracy of model: Percentage of absolute right classifications divided by absolute number of MRI images is the statistic used to quantify how well the designed model performs in appropriately identifying the classes in the dataset.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FN + FP} \quad (3)$$

2. Precision of the model: The precision is the sum of all true positives divided by all detected positives.

$$\text{Precision} = \frac{TP}{TP + FP} \quad (4)$$

3. Recall: Sensitivity or Recall gauges a proposed model's capacity to recognize positive instances. It displays the proportion of actual positive instances in the data that are true positives.

$$\text{Recall} = \frac{TP}{TP + FN} \quad (5)$$

4. Area under curve: It is defined as Area under the ROC curve. Therefore, there is a strong likelihood that the predictions will be TP and TN when AUC is high. AUC = 0. 8 indicate, for instance, that there is an 80% chance the model will correctly distinguish between the positive and negative classes. AUC = 0.5 indicates that the model is unable to distinguish between these two classes.

5. Results and Discussion

The segmentation on MRI image was performed for 10 iterations. The number of clusters used for segmentation is six. Fig 6 shows the input image. Fig7 shows segmentation result for the input image. Fig 8 shows different grey levels corresponding to six clusters.

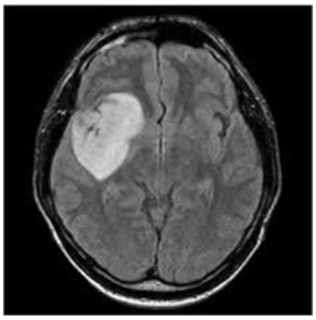
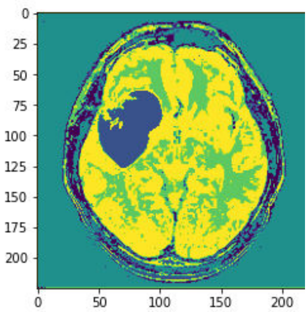


Fig 6.Input image



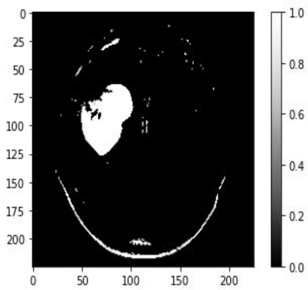
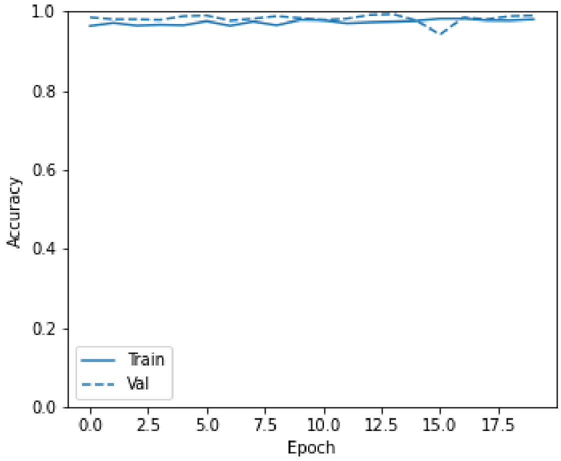


Fig 7.Segmentation result **Fig 8. Different grey levels corresponding to clusters**

The posed fine tunedEfficientNet model was trained on MRI images obtained fromKaggle. The outcomes of the training and validation are covered in this part.

The suggested model was trained to use data 90 percent of the time for training and 10 percent for validation. The training as well as validation accuracy is shown in Fig8. The loss curves with training epochs are shown in Fig9. The training as well as validation recall is shown in Fig10. The training as well as validation precision is shown in Fig11. The training as well as validation area under curve is shown in

Fig12. The graph for the proposed model shows that as number of epochs rose, the classification accuracy of the validation as well as training sets rapidly increased in very less time with the provided hyper-parameters till it reaches stability.



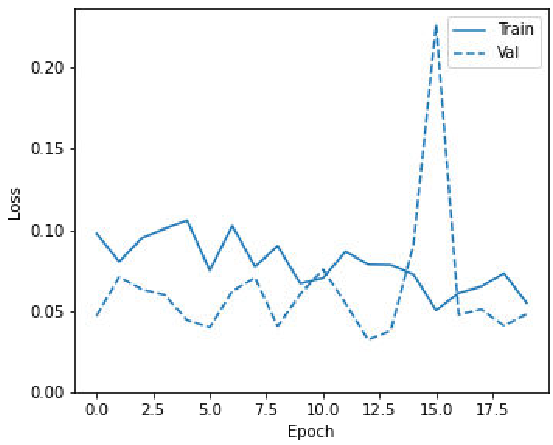
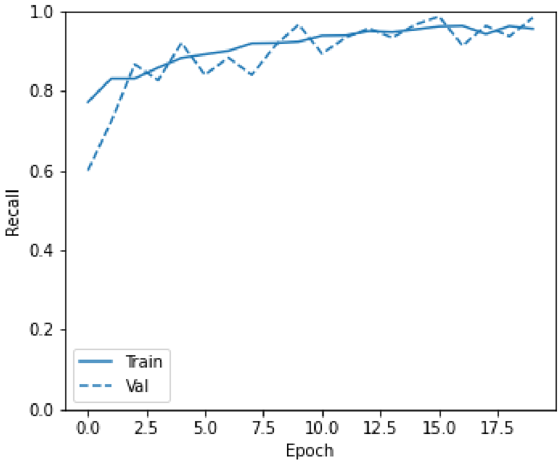


Fig 8.Training and validation accuracy curves Fig9. Training and validation loss curves



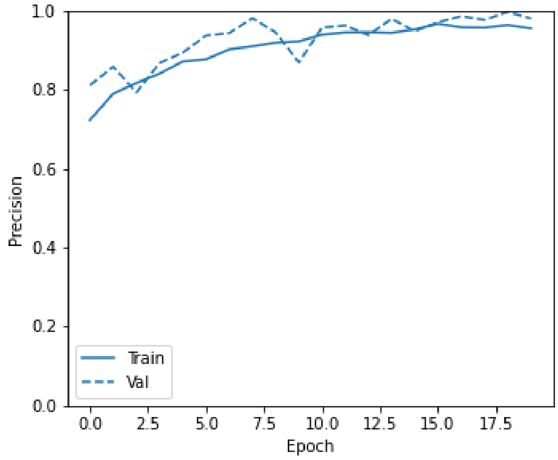
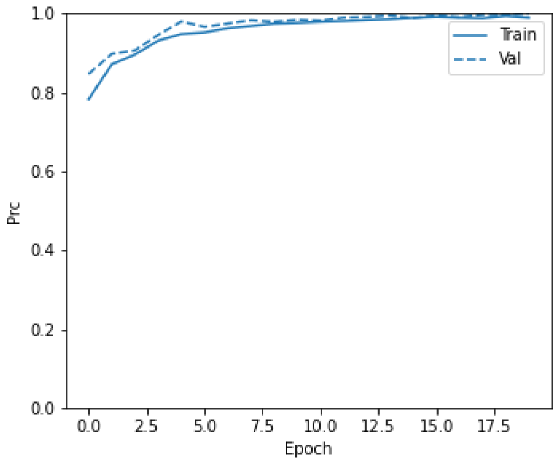


Fig 10.Training and validation recall curves Fig 11. Training and validation precision curves



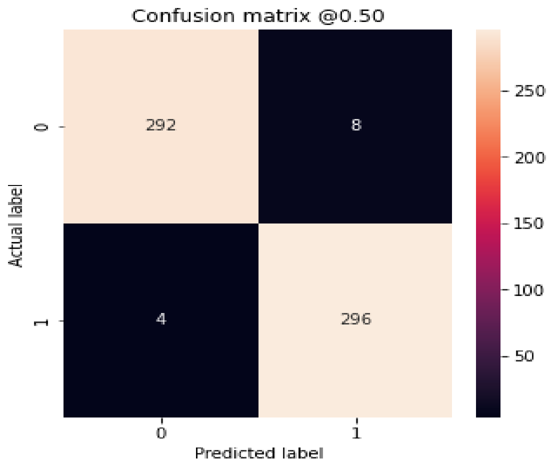


Fig 12.Training and validation AUC curves Fig 13. Confusion matrix of the proposed model

A confusion-matrix was employed for counting the quantity of successfully and incorrectly classified data &to estimate the performance of our proposed model using the aforementioned evaluation metrics. Fig 13 demonstrates that the proposed model's CM correctly classified 296 images as tumors while missing four.

Eight images were missed by the second-class model, which correctly classified 292 images as being free of tumors.

The proposed model shows good segmentation result. Also proposed model shows 98.66% accuracy, 97.71% precision, 99.66 % recall and AUC of 99.87% for proposed model. The proposed segmentation and detection model produced a great performance in terms of evaluation metrics.

Conclusion

The progressing requirement for an empirical and well-grounded evaluation of enormous amounts of data has led to a considerable increase in popularity of MR imaging for the identification and segmentation of brain tumor research. A brain tumor is an incurable condition, and non-automatic detection needs time depending upon medical competency. To find problems in MRI pictures and segment them, an automatic diagnostic system will be needed. To identify and segment brain tumors from MRI scans, this study developed a hybrid technique using k-means clustering and an EfficientNetB0 based transfer learning architecture. With a validation accuracy of 98.66%, the suggested technique demonstrated the highest performance in the identification of brain tumors. Although this paper concentrated on a few medical imaging models for brain tumors, more work is required. In the future, we'll look at more powerful and influential deep CNN models to classify brain tumors and segment them with less time complexity. We will also accelerate the amount of brain tumorimages in the dataset utilized for the exploration in order to improve the suggested model's accuracy. Additionally, in order to provide the groundwork for future study, we will also apply the suggested method to other medical pictures such as ultrasound, computed tomography (CT), and x-ray.

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