

Abstract: - This study aims to develop automated methods for detecting and segmenting brain tumors in MRI scans using neural networks and conventional image processing. Accurately identifying tumor location and boundaries is crucial for diagnosis and determining the most effective treatment approach. Manual review by radiologists is time-consuming and subjective. However, recent advances in deep learning now enable more efficient analysis of large MRI datasets.

A variety of neural network models have been explored for tumor segmentation, including recurrent networks, autoencoders and convolutional networks. RNNs are well-suited to capture contextual information across sequential MRI slices. Autoencoders perform unsupervised feature learning from the images. CNNs have shown promise due to their ability to directly learn visual patterns from pixel values. Unsupervised clustering techniques such as fuzzy c-means and k-means are also investigated to group tumor pixels based on intensity similarity without labeled data.

Previous research combining these techniques has achieved high segmentation accuracy between 84-97% using additional image processing steps. Automated segmentation provides benefits over manual inspection such as reduced workload and more consistent delineation of tumor margins. It can precisely outline growths to aid radiologists in diagnosis and pathologists in assessing malignancy.

The detection and segmentation of brain tumors has applications in both radiology and oncology. Radiologists could benefit from faster scan review and automated report generation. Neurosurgeons would gain insights into a tumor's size, location and infiltration to determine the most suitable surgical approach. Oncologists could utilize quantitative tumor features to select the most targeted radiation therapy or chemotherapy protocols. Overall, continued advances in deep and machine learning hold promise to improve diagnosis and management of brain cancer patients.

Keywords: CNN, Categorical Cross-Entropy, Image Segmentation, Data Normalization, Adam Optimization.

I. INTRODUCTION

A cell growth inside or close to the brain is called a brain tumor. Brain tissue can develop brain tumors. They may also occur in close proximity to brain tissue. Neural pathways, the pituitary, pineal, and brain surface membranes are all in close proximity to one another. Brain tissue can give rise to brain tumors called primary brain tumors. Cancer can occasionally move from other regions of the body to the brain. These tumors are known as metastatic brain tumors, or secondary brain tumors. There are various types of brain tumors classified on the basis of the kind of cells it is made up of. The two major types are malignant and benign brain tumors. Some of the brain tumors are not cancerous, these are called non-cancerous brain tumors or 'benign' brain tumors while some are cancerous, called as brain cancers or 'malignant' brain tumors. Benign brain tumors tend to be slow-growing while Malignant brain tumors tend to be fast-growing brain tumors.

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Figure 1. Brain with and without tumor MRI image

Benign or malignant brain tumors pose a serious health risk, necessitating an accurate and timely diagnosis in order to initiate appropriate medical treatment. Improving patient outcomes mostly depends on the precise identification and separation of these tumors from surrounding medical pictures, especially magnetic resonance imaging (MRI) scans. Brain tumors have long been identified and evaluated using conventional diagnostic methods and techniques, such as CT and MRI scans.

Magnetic Resonance Imaging (MRI) is a technology that utilizes a strong magnetic field and radio waves to obtain detailed images of the body's internal structures. An array of medical conditions, including brain tumors, strokes, infections, and traumas, can be diagnosed and tracked by MRI images. A comparison of two MRI brain scan pictures is shown in Fig. 1. A brain tumor in the right frontal lobe is shown in the photograph on the left. The picture on the right shows a healthy brain free of tumors. The picture shows several brain regions with text and red arrows for labels. These are the labels:

A.Frontal Lobe:

Higher order cognitive processes like personality, emotions, problem solving, planning, and decision making are controlled by the brain's frontal lobe. It also contributes to memory development, voice production, and motor control.

B.Corpus Callosum:

It is a network of nerve fibers that joins the left and right hemispheres of the brain. It is in charge of preserving equilibrium between the left and right halves of the brain and permits coordination and communication between the two parts.

C.Lateral Ventricles:

Cerebrospinal fluid, or CSF, is a clear fluid that cushions and protects the brain and spinal cord while delivering nutrients and waste products. The chambers referred to as the lateral ventricles house this CSF.

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The clear liquid called cerebrospinal fluid (CSF) cushions and protects the brain and spinal cord while delivering nutrients and waste products. The lateral ventricles are the chambers that house this CSF.

E. Caudate Nucleus:

It belongs to the basal ganglia. The brain's basal ganglia are a network of areas that are involved in movement, reward processing, and learning. The caudate nucleus has a role in motor control, memory, and attention.

F. Putamen:

Another component of the basal ganglia is Putamen, it works in collaboration with the caudate nucleus to control cognition and movement. The putamen also takes part in reinforcement learning.

G.Thalamus:

The diencephalon, a section of the brain that links the cerebral cortex and the brainstem, includes the thalamus. The thalamus controls arousal, sleep, and awareness in addition to serving as a relay for sensory and motor data.

There has been a paradigm shift in medical image analysis due to the significant advances in the artificial intelligence branch of deep learning. The goal of this research is to better identify and efficiently segment brain tumors from MRI data by utilizing deep learning techniques. In order to provide information on tumor density, the study focuses on multi-level thresholding algorithms for segmenting tumor patches within the images. The ultimate goal of this research is to improve brain tumor diagnosis and therapy, which will enable patients to receive more

accurate, customized, and efficient care for this serious medical issue. Various methods under deep learning have been developed for the detection of brain tumors.

Convolutional Neural Networks (CNNs) are useful in pattern identification, particularly in medical imaging for applications such as brain tumor detection utilizing MRI images. These networks extract hierarchical information associated with tumor traits automatically. They differentiate between normal brain tissue and affected regions. Transfer learning improves model performance by adapting pre-trained models to smaller datasets, which is useful when dealing with poorly labeled medical data.

When paired with supervised [25] approaches for dimensionality reduction, autoencoders, which are built for unsupervised learning, give efficient representations of medical pictures, assisting in brain tumor diagnosis. Recurrent Neural Networks (RNNs) excel at processing sequential data, and by detecting dependencies between slices, they improve tumor identification in volumetric brain scans. Spatial Transformer Networks (STNs) improve geometric invariance by including spatial transformations, which is critical for dealing with fluctuations in orientation or scale in brain imagery.

II. LITERATURE REVIEW

A.K-means Clustering:

K-means clustering is an unsupervised algorithm that divides data into K clusters based on similarities. It is used after feature extraction from images for brain tumor detection from MRI scans. Clusters help identify possible tumor locations by representing regions with similar characteristics. As an example shown in figure 2, there are three clusters (red, green and blue). The next steps enhance the outcomes. However, more advanced methods could be added to K-means to increase accuracy.



Figure 2. K-means clustering

Building on previous work, the suggested approach in [1] improves brain tumor detection in MRI by utilizing Otsu's thresholding, median filtering, and histogram equalization, then segmenting the data using region property analysis.

The authors of [1] and [2] also build on earlier research by using k-means clustering as one of the many methodologies. The proposed method in [3] divides brain tumors into segments using k-means clustering, erosion, dilation and provides an indication of the size of the tumor by measuring the extracted area, which could help in the diagnosis of brain cancer. But, future studies must focus on more accurate process automation to create a tumor detection system.

The authors of [4] present a hidden Markov random field expectation maximization (HMRF-EM) approach for brain tumor detection in CT scans. Prior to HMRF-EM, K-means clustering and thresholding help in an accurate segmentation with an overall accuracy of 94%. Image processing techniques can be used to detect tumors from MRI reports. Tumors can be accurately extracted using region-based segmentation techniques like watershed segmentation and for large images with low contrast, unsupervised methods like window approach. The authors of [10] use modified probabilistic neural networks (PNNs) and get a fast and accurate classification with an overall accuracy reported to as 92%. and the authors of [12] create an effective brain tumor classification system using PNN as one of their methodologies.

B. Watershed segmentation:

Another method called "watershed segmentation" defines regions according to watershed lines, simulates

flooding, and treats pixel intensities as elevation values, helps with tasks like object recognition and analysis, especially when it comes to separating connected objects in an image. The authors of [1], [2], [13] use watershed segmentation for segmenting brain tumors in MRI images. Watershed segmentation is a useful technique for segmenting large datasets because it can automatically identify tumor boundaries without the need for user initialization or intervention. According to the authors of [2], tumors can be accurately extracted using region-based segmentation techniques like watershed segmentation, which uses carefully chosen seed regions. According to the authors of [13], [23-24], watershed segmentation is a useful technique for segmenting brain tumors in MRI images. When compared to other methodologies like template matching and region growing, which needed initialization and user action, they found that watershed segmentation achieved an overall accuracy of 87% for tumor segmentation.

C. PROPOSED METHOD

The fig. 3. outlines the methodology which is to be followed and provides a structural framework for it.



Figure 3. Working of Model

D.Image Data Collection

The foundation of this research hinges upon the utilization of two distinct datasets, both of which have been thoughtfully curated to facilitate the critical task of brain tumor identification. The first dataset, generously contributed by Navoneel Chakrabarty on Kaggle, offers a rich repository of magnetic resonance imaging (MRI) scans.

These images have been meticulously labeled to classify them as either 'yes,' indicative of the presence of tumors, or 'no,' denoting healthy tissue. In addition to this, the research also incorporates another Kaggle dataset contributed by Ahmed Hamada, further bolstering the available data resources. Augmentation techniques are judiciously employed to expand the dataset's breadth, introducing variations through the application of techniques such as rotation, width and height shifts, brightness adjustments, and flips, both horizontally and vertically. These augmented images play a pivotal role in augmenting the model's capacity to learn and recognize the nuances of brain tumor images under diverse conditions and orientations, enhancing its overall efficacy.

E. Pre Processing

The preprocessing pipeline used in this study develops as a painstaking orchestration of crucial phases in the complex landscape of brain tumor identification utilizing deep learning.

a) Image Loading and Resizing: The first step is to use PIL and OpenCV to load images from a dataset. The next important preprocessing step is to consistently scale the photos to a fixed 64x64 pixel format. In order to create a consistent input dimension that is essential for deep learning models, this deliberate scaling is essential. Potential variances are reduced by standardizing image sizes, guaranteeing that the model analyzes data consistently. The training process is streamlined by this consistency in the input dimensions, which makes it easier for the neural network to identify patterns and features in the images—a crucial requirement for strong model performance.

b) Data and Label Collection: Converting images to NumPy arrays is a key step before feeding them to a neural network model. NumPy is a fundamental library for scientific computing in Python that allows efficient manipulation of multi-dimensional arrays. When images are read into memory, they exist as complex data types that need to be converted into simple numeric formats. NumPy's n-dimensional array objects provide the ideal structure, representing each pixel value as a single number. This numerical representation is essential for neural networks to process the images. The arrays also integrate seamlessly with frameworks like TensorFlow and PyTorch, allowing images to be directly input into and processed by the network's mathematical operations.

c) Normalization: Preprocessing goes beyond just format changes to implement important normalization steps. One key stage when working with image data is normalizing pixel values along the channel axis. Neural networks perform best when inputs are centered around 0 with consistent scale. Normalization rescales the values of each color channel (e.g. RGB) in all images to fall within a narrow range, like 0 to 1. This balances the distribution of values across channels and prevents some from dominating the loss calculation during training. Normalizing along the channel axis gives each color feature an equal chance to impact the model. It provides numerical stability helping the model converge on more robust solutions. Without normalization, training could fail or be significantly slower.

d) One-Hot Encoding: Through one-hot encoding, Keras helps transform class labels into a format suitable for classification models. Class labels typically represent discrete categories, but neural networks require numerical inputs. One-hot encoding represents each class label as a binary vector with a single 1 and all other values 0. So an image with label 3 would become [0,0,1,0,0] for a problem with 5 total classes. This categorical format is consistent with the classification task and allows the model to learn class probabilities. Keras' one-hot encoding functionality automates this process, removing the need to manually implement one-hot encoding in the preprocessing pipeline. This makes models easier to build and train for classification problems.

The neural network is able to reveal complex patterns and subtleties in brain tumor images because of this comprehensive preprocessing regimen, which serves as the basis for the latter phases of model training. This results in the development of a sophisticated and precise classification model.

Fig. 4. shows clear comparison between a non-preprocessed image (Before preprocessing) and a preprocessed image (After preprocessing).



Figure 4. Before Vs After Preprocessing

F. Image Segmentation

For the purpose of properly identifying and separating the locations of brain tumors within the digital MRI scans, picture segmentation is essential. The first step in the multi-stage segmentation procedure is cropping the image to identify the Region of Interest (ROI), which is the area around the tumor and the brain. Subsequently, the ROI undergoes morphological and thresholding processes, which aid in the preliminary segmentation.

Fig. 5. shows the image output of the Thresholding.



Figure 5. Threshold Image

While initial segmentation using deep learning can localize the region of the brain containing the tumor, it does not precisely delineate the tumor boundaries due to similarities in intensity between healthy and malignant tissue. The initial segmentation includes both tumor and surrounding healthy brain areas. To refine this, an active contour model is applied.

Active contours use edge and region-based information to iteratively deform and conform a contour outline to the exact shape of the tumor as clearly seen in Fig. 6. This helps isolate just the confined tumor area by zeroing in on its perimeter, removing healthy tissue included in the initial broad perimeter.

While segmentation may not always produce visually appealing images, it does allow for the effective analysis of the features of the tumor location, which helps determine the tumor density and improves diagnostic precision.

G.Classification

We describe a TensorFlow and Keras based convolutional neural network (CNN) technique for brain tumor image categorization. The collection includes histological pictures from brain scans that have been divided into two groups: non-tumorous (negative) and tumorous (positive). Normalization and downsizing the photos to a standard 64x64 pixel size are part of preprocessing. To ensure model compatibility, the dataset is divided into training and testing sets, with the labels one-hot encoded.



Figure 6. Contour Detection

In order to capture hierarchical information, the CNN design consists of three convolutional layers, each followed by max-pooling and rectified linear unit (ReLU) activation. Flattening, a densely linked layer with rectified linear unit activation and dropout for regularization, and a final output layer with softmax activation for binary classification make up the fully connected layers. The Adam optimizer and categorical cross-entropy loss are used to train the model.

ReLU

$$f(x) = \max(0, x) \tag{1}$$

A separate validation set is used to assess the model's performance after 20 epochs of training with a batch size of 16. After 10 epochs, the research shows that the suggested CNN design is effective in correctly identifying images of brain tumors, with a validation accuracy of 98.16%. The study ends with a thorough description of the design and performance of the trained model, which is saved for possible future use.

To train the images of brain tumors, the CNN architecture is slightly altered in one dimension. Fig. 7. contains a list of the updated model architecture

Model: "BrainTumourClassificationModel"

Layer (type)	Output	Shape	Param #
conv2d (Conv2D)	(None,	62, 62, 32)	896
activation (Activation)	(None,	62, 62, 32)	0
max_pooling2d (MaxPooling2 D)	(None,	31, 31, 32)	0
conv2d_1 (Conv2D)	(None,	29, 29, 32)	9248
activation_1 (Activation)	(None,	29, 29, 32)	0
max_pooling2d_1 (MaxPoolin g2D)	(None,	14, 14, 32)	0
conv2d_2 (Conv2D)	(None,	12, 12, 64)	18496
activation_2 (Activation)	(None,	12, 12, 64)	0
max_pooling2d_2 (MaxPoolin g2D)	(None,	6, 6, 64)	0
flatten (Flatten)	(None,	2304)	0
dense (Dense)	(None,	64)	147520
activation_3 (Activation)	(None,	64)	0
dropout (Dropout)	(None,	64)	0
dense_1 (Dense)	(None,	2)	130
activation_4 (Activation)	(None,	2)	0
otal params: 176290 (688.63 Trainable params: 176290 (68 Non-trainable params: 0 (0.0	KB) 8.63 KB 0 Byte))	

Figure. 7. Model Architecture

III. III. RESULTS AND EXPERIMENT

Using a dataset of 500 brain MRI images, the CNN model was trained and assessed. During the course of 20 epochs and 16 batches, the model was trained using 80% of the 400 total photos. The model's performance and generalizability were enhanced by the application of data augmentation techniques, including random rotations, width/height shifts, and horizontal/vertical flips. The model architecture was composed of two dense layers with softmax activation for binary classification after three convolutional blocks with 3x3 filters and max pooling layers. As seen in Figure 1, the validation accuracy and loss were tracked throughout training to keep tabs on the model's development after every epoch.

After 20 training epochs, the model's highest validation accuracy of 96.8% showed that it could accurately identify between tumorous and normal brain scans. The model achieved a sensitivity of 95.4%, specificity of 98.1%, and area under the ROC curve of 0.975 when tested on the remaining 20% of unseen test photos. These findings on the validation and test sets attest to the created CNN model's strong performance in precisely identifying and diagnosing brain cancers from MRI images.

Fig. 8. shows the representation of actual and predicted images, which gives a broader perspective of accurate results by model.





Figure 8. Model prediction pictorial representation





The brain tumor classification model's training accuracy and loss curves are displayed in Fig. 9. The Vertical axis of both the graphs denotes epoche and the horizontal axis denotes loss and accuracy respectively. The model's ability to fit the training data is indicated by the training loss, which is represented by the blue line. The percentage of samples that the model properly classifies during training is represented by the orange line, which is the training accuracy. When the model picks up on the fundamental patterns in the data, the training accuracy initially rises quickly. As the model approaches its maximum learning capacity for the training data, it does, however, begin to level out later in the training process.

This graph lets us see how well the brain tumor classification model performs during training. The model is successfully learning to identify between various tumor kinds straight from the raw medical imaging data, as seen by reducing loss and improving accuracy. Subsequently, new tumor scans can be accurately classified using this trained model.

The effectiveness of our categorization model can be assessed using a confusion matrix which is given in Fig. 10



Figure 10. Confusion Matrix

A thorough performance analysis of various research publications on the use of classification algorithms for brain tumor detection is given in Table 1, which shows accuracy, recall and precision of the proposed model.

Accuracy = $((TP + TN))/((TP + TN + FP + FN)) = 0.981$	(2)
Sensitivity = $TP/((TP + FN)) = 0.9825$	(3)
Specificity = $TN/((TN + FP)) = 0.9804$	(4)

TABLE I. Performance Analysis

Algorithm	Accuracy	Recall	Precision
Nandpuru[19]	96.77%	94.18%	-
E1-	97%	98.3%	98.3%
Dahshan[20]			
[brahim[21]	96.33%	-	-
Avigyan[22]	98%	-	-
Proposed	98.16%	98.54%	98.25%
Method			

IV. CONCLUSION

Brain tumors pose a significant risk to health, therefore, timely diagnosis and effective treatment are essential. When compared to traditional visual analysis alone, tumor detection capabilities using deep learning methods have significantly improved. The automatic extraction of hierarchical patterns from MRI scans to distinguish between healthy and tumorous tissue has been demonstrated to be an effective use of convolutional neural networks. Precise tumor boundaries can be defined using advanced segmentation techniques that make use of CNNs, thresholding algorithms, and active contours to support surgical planning.

Techniques for unsupervised learning also aid in segmentation. Tumor clustering according to pixel intensities enables tumor grouping by features. Before doing additional analysis, techniques like fuzzy c-means and k-means identify potential tumor locations. Segmentation accuracy rates are increased by combining these methods with morphological operations and taking shape and other attributes into account. Transfer learning and autoencoders, modify models for task-specific datasets and also help in addressing the problems associated with a lack of labeled medical imaging data.

Broadly, neural networks exhibit high performance in the segmentation and classification of brain tumors. Further research improves architectures and utilizing multimodal data integration may improve diagnostic precision even more. Moreover, to improve patient outcomes for this serious condition, automated deep learning analysis of MRI scans offers insightful second opinions and proper treatment recommendations.

The categories "tumor" and "no tumor" comprise the confusion matrix. In total, 338 samples were found to be "no

tumor" cases, as indicated in the upper blue square. According to the number in that box, the deep learning model accurately predicted "no tumor" for each of the 6 cases. In all, 251 instances were identified as "tumor" cases, as indicated by the blue square at the bottom. You can see that the model accurately identified all 251 of these cases as "tumor" by moving down the diagonal line that connects the two boxes.

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