Brain Tumour Detection With Threat Analysis Using U-Net Architecture

Shital Raut[1], Divyam Gupta[2], Prashik Dupare[3], Rutvik Ghode[4]

[1]Department of Electronics and Telecommunications, Vishwakarma Institute of Technology, Pune, India
shital.raut@vit.edu

[2]Department of Electronics and Telecommunications, Vishwakarma Institute of Technology, Pune, India
gupta.divyam21@vit.edu

[3]Department of Electronics and Telecommunications, Vishwakarma Institute of Technology, Pune, India
prashik.dupare21@vit.edu

[4]Department of Electronics and Telecommunications, Vishwakarma Institute of Technology, Pune, India
rutvik.ghode21@vit.edu

Abstract – **Brain tumours are the main reason for 85% - 90% of all the primary CNS (central nervous system) tumours. Nearly 70% to 75% of Brain Tumours are undetected in early stages. The implemented model used Deep CNN and U-Net architecture to reduce this problem. The model includes detecting threat levels with lower resource requirements. The dataset is stored in NifTl-1 format (DICOM), and it uses the NiBabel Library to access the files. The U-Net Architecture using Deep CNN performs Biomedical image segmentation and the Dice Coefficient, Specificity, and Sensitivity are utilized to check the segmentation predictions. This project is an attempt with the goal of scanning a tumour, extracting its threat level, and proposing a model to deliver a more accurate result to determine the affected brain region. It is a project aimed to scan and extract the threat level of the tumour and further propose the model to provide a more accurate and reliable result for determining the affected region in the brain. The research further achieved an excellent accuracy of 96% in detecting affected areas. Also, a comparative study was performed to showcase the efficacy and dependability of a novel approach suggested in the research. Hence, the conducted research can be a success in the medical industry.**

Keywords: Deep CNN, MRI, Brain Tumour, Image Segmentation, U-Net Architecture

INTRODUCTION

Medical image processing exploded extensively in the last few years. It became a popular research field that attracted researchers from various domains such as biology, medicine, engineering, computer science, and mathematics, with applications in biomedical imaging and clinical practice to check and support diagnoses and therapy in patients. One of the essential levels for processing medical images is image segmentation, which is seen as a tough process, particularly with brain images because of the complexity of the images. The brain has a complex structure and more precise segmentation is mandatory for accurate detection of tumours, and oedema to describe therapy. The oedema is related to intracranial brain tumours and is caused by leakage of plasma into the parenchyma through dysfunctional cerebral capillaries. Precise and effective brain tumour picture segmentation from neuroimaging scans is a crucial step toward better disease diagnosis along with appropriate treatment planning, both of which enhance the prognosis for patients. The brain is very diverse in size, location, and structure, making segmentation difficult in the case of brain tumours. In addition, brain tumours frequently invade large areas of the brain, making it challenging to tell them apart from healthy brain tissue. Manually segmenting brain tumours from MRI scans is laborious, time-consuming, and less reliable. Because of this, automatic brain image segmentation has garnered a lot of interest over the past 20 years due to its consistency.

The very recent automated segmentation techniques are built on CNNs (convolutional neural networks) which are trained using manually collected datasets of many patients. The major focus of the implemented research is to construct and evaluate an automated algorithm for identifying the exact location of tumours in MRI brain slices and identifying the most salient slices of pathological patients to focus the attention of clinicians/doctors on these slices.

LITERATURE REVIEW

Method for categorizing MRI of the human brain that is based on unsupervised learning is presented in this study using neural networks. A thorough histological study is necessary for the identification of brain tumours, and this procedure entails invasive surgery, which can be uncomfortable and traumatic for patients. The diagnosis process for brain tumours is broken down into the following steps in this study.

Image pre-processing, which includes thresholding, noise filtering, edge identification, histogram equalization, and other techniques, makes up the initial step. Later, in the second step, ICA (Independent Component Analysis) is used to extract characteristics from the MR brain photograph. The third step involves the use of a self-organised map (SOM) to diagnose brain tumours. Lastly, the brain is divided into several tissues using the k-means clustering technique. This approach shows promise based on classification findings for various disorders on a range of MR images [1].

Before segmentation, the input image is pre-processed in this suggested method by using the Fuzzy C Means and K Means clustering techniques. It is evident from a comparison of these two methods that Fuzzy C Means clustering yields superior segmentation. Additional characteristics are recovered from the tumorous region of the fuzzy C Means segmented image, including magnitude, direction, and area. MRI images are categorized based on the retrieved characteristics. The supervised neural networks known as the Generalized Regression neural network (GRNN), Probabilistic neural network (PNN), and Radial Basis Function (RBF) are used for classification. A comparison of the sensitivity, specificity, and accuracy is made in this suggested technique, which makes use of the fuzzy probabilistic neural network classifier (FPNNC) to distinguish an MRI image as normal or abnormal. Hence, the suggested approach outperforms the latest classifiers considering the accuracy and model efficiency[2].

The primary objective of this implemented research is to implement dependable and common techniques for glioma classification, brain tumour detection, and feature extraction with the utilization of MRI (Magnetic Resonance Imaging). The created technology, which uses artificial neural networks and image processing, aids in the automated identification of brain tumours. Analyzing and modifying an image, essentially to enhance its quality, is a very important step of image processing. The Histogram Equalization (HE) technique is implemented in the given suggested method to enhance the contrast of the source picture. Later, feature extraction is used for the pre-processed picture by utilizing the Gray Level Co-occurrence Matrix (GLCM). Then, the acquired characteristics are transferred into a Probabilistic Neural Network (PNN) classifier, which is then employed to train and evaluate the accuracy of the tumour site detection in brain MRI images. This method has allowed the classifier (PNN) to achieve an accuracy of around 90.9% [3].

This proposed approach is predicated on the categorization of each superpixel and the superpixel methodology. FLAIR MRI employs an array of newer image features, including Gabor textons, intensity-based curvatures, and fractal analysis, which are produced from every single superpixel inside the entire brain region, in order to deliver a strong and precise classification.. Two datasets are used to assess the suggested method: MRI FLAIR pictures of patients having grade II to IV gliomas from the clinical dataset; and the BRATS-2012 dataset, which consists of thirty FLAIR images with ten high-grade and twenty low-grade gliomas. The suggested strategy utilizing the ERT classifier has excellent detection and segmentation performance. The segmented tumour's detection sensitivity, Dice overlap measure, and balanced error rate against the actual truth for our cohort are, 89.48%, 0.91, and 6%; respectively; similar assessment findings for the BRATS dataset are, meanwhile, 88.09 %, 0.88, and 6% [4].

This study presents an entirely automated brain tumour identification using MRI and a segmentation approach that uses wavelet transform, entropy segmentation, active contour, fuzzy C-Means, and Gaussian mixture model as a robust clinical-aided machine. Having scores of 0.957, 0.913, and 0.954 for the Sensitivity, Jaccard index, and Dice coefficient, respectively, our suggested technique beats the top-ranked popular brain extraction algorithms in the first stage of the evaluation, which was conducted using the OASIS, LPBA40, and BSR databases. The BRATS database was used to analyze the second half of the approach, which produced an accurate result of 69% for real analysis and a false detection rate of about 22% for non-diagnosed cases and 9% for cancer cases identified as healthy patients, respectively. Thus, the tumour segmentation technique achieved a 0.69 Dice coefficient and a 0.67 Jaccard index. This approach is discovered to be quick, efficient, precise, and entirely automated [5].

Presenting an automated technique to aid in the diagnosis of both abnormal and normal MR images is the goal of this work. Preprocessing of MR images, skull stripping, classification, feature reduction, and feature extraction, are the four major steps of the diagnostic procedure. Following histogram equalization of the image, DualTree Complex wavelet transformation (DTCWT) is used to extract the features. PCA (Principal component analysis) is then integrated to minimize the characteristics. Also, the last phase uses two classification techniques: probabilistic neural networks (PNNs) and k-means clustering. The

presented study is an extension and modification of earlier research on the diagnosis of brain illnesses; however, the research employs a bigger and more diverse database and gets a better classification rate with fewer characteristics. When diagnosing brain tumours using MRI, this method is quite helpful. Over 98.5% of PNN and 93% of K-means classifications were correctly classified [6].

A deep learning-based (DL) technique for the segmentation of brain tumours utilizing multiple MRI modalities is provided in this research study. This proposed hybrid CNN architecture makes consideration of a novel patch-based methodology that considers both contextual and local information in predicting the output label. The proposed network addresses the data imbalance flaw with a two-phase training method and over-fitting issue with a dropout regularizer combined with batch normalization. The proposed method comprises three steps: a pre-treatment step that normalizes and corrects the bias field in images; a post-processing phase that removes small false positives surrounding the skull section; and a feed-forward run via a CNN. The suggested approach is verified using the BRATS 2013 dataset, demonstrating improvements over the well-established approach with dice score, sensitivity, and specificity of 0.91, 0.86, and 0.86, for the whole tumour area [7].

The use of a CNN for brain MRI tumour identification is presented in this study. For the images, the Softmax Fully Connected layer had a classification accuracy of 98.67%. Furthermore, the CNN obtains 94.24% accuracy with the Decision Tree (DT) classifier and 97.34% accuracy with the Radial Basis Function (RBF) classifier. In addition to the accuracy criterion, the proposed model evaluates network performance using the benchmarks of Sensitivity, Specificity, and Precision. Network accuracy results for the photo testing show that CNN's Softmax classifier has the most efficient accuracy based on the classification findings. This is a revolutionary method that combines CNN with feature extraction techniques to identify tumours from brain imaging. The result of the suggested approach on the test data was 99.12%. The significance of the diagnosis given by the clinicians increased the accuracy of the doctor's diagnosis and patient treatment [8].

To highlight the inhomogeneities field effect caused by the MR slices and integrate them along with input image slices, the paper makes use of a high-pass filter image. Additionally, the fused slices are subjected to the median filter. Subsequently, an optimum threshold is used to cluster comparable pixels from the input slices in a 4-connected seed-generating method, which is applied depending on the intensity of these slices. The optimized two-layer SSAE (stacked sparse autoencoder) model is then fed the segmented slices. The model's hyperparameters are chosen following a great deal of experimentation. There are 200 secret units in tier one and 400 secret units in tier two. The Softmax layer is tested to forecast which photos will have tumours and which ones won't. The BRATS datasets from 2012, 2013, 2014, and 2015 are utilized to train and validate the implemented detection model. A variety of performance measures are used to evaluate the model that is being given, showing increased performance [9].

Tumors in the brain, lung, liver, breast, neck, etc. can be analyzed using imaging techniques including tomography, appealing reverb imagery (MRI), and ultrasonic imaging. In this specific study, appealing reverse imagery is used to investigate the mind's tumour. However, the massive volume of data generated by the MRI scanner at any given moment blocks the manual tumour vs non-tumour order. As the calculations for many photos are dependable, the technique has presented several difficulties. Increasing the planned order's survival rate is an obvious requirement. Because of the extraordinary spatial and fundamental fluctuations that accompany a local brain tumour, scheduling the tumour is an extremely difficult undertaking. In this study, CNNs are used to characterize a planned investigation into mental tumours. The completeness of the utilization of little holes is the composition type that matters the most. CNN's paper has an accuracy of 97.5 and less predictability [10].

There are techniques like MRI, CT scan, and X-ray that could be utilized to find brain tumours. Numerous studies have discovered that incorrect identification of the afflicted portion of brain tumours causes deaths in patients. The precise location of the brain tumour's afflicted region must be determined. Currently, the most difficult and developing field is bio-medical image processing. In this research, the tumours in MRI brain images are divided using MATLAB, and the SVM classifier (Support Vector Machine) is utilized to identify such kinds of tumours. The segmentation procedure is the major application for the provided algorithm. The procedure is carried out by breaking it up into three phases, which include the preprocessing, segmentation, and output stages. Every step has a certain purpose. As a result, the SVM classifier is used to identify the kind of brain tumour, and the threshold segmentation approach is used to segment cancer areas from the MRI brain picture [11].

Tools for processing medical photos and detecting malignancies have been actively developed by engineers. Tumor detection frequently makes use of the potent method known as medical picture segmentation. To improve and expand this tool's functionality, several researchers and doctors are operating on it. The goal of this research is to use a Matlab GUI interface to identify brain cancers from MRI images. To get the best results, this application may combine several segmentation, filter, and other image processing method combinations using the GUI. First, we apply a Prewitt horizontal edge-emphasizing filter on the picture. "Watershed pixels" are the next stage in the tumour detection process. The fact that all of the Matlab programs utilize the GUI called the "Matlab guide" is the most crucial aspect of this project. This makes it possible to combine several filter sets and use additional image processing methods to provide the best outcome that will identify brain cancers in their early stages [12].

Due to their similar colours, brain tumours and normal tissue are difficult to identify from one another. Therefore, to treat brain tumours, a more thorough analysis is needed. In this paper, three steps are included in the morphological identification of tumours using MATLAB image processing: pre-processing, processing, and post-processing. Firstly, the pre-processing stage involves converting the default RGB picture to a grayscale image and then using a Gaussian high-pass filter for noise reduction which comes first after receiving the MRI data. The median filter is used in the second stage of the pixel-enhancing system. The third phase is post-processing, where diverse outputs can be obtained using the Weiner filter, Regional Maxima, Gradient Magnitude, Entropy filter, and SDF (Standard Deviation Filter). This algorithm-driven post-processing method produces reports automatically, with very less wait time, and improves the efficiency of brain tumour diagnosis [13].

The offered research describes a thorough method for utilizing MATLAB to automatically identify brain tumours in MRI pictures in a unique and well-structured way for better accuracy. It highlights the difficulty of manual characterisation and the importance of accurate medical image processing in this particular situation. Three main steps make up the suggested methodology: segmentation, edge detection, and pre-processing. Here, pre-processing stage is the process of turning photos into grayscale and removing noise, whereas segmentation uses the watershed method to cluster images and find areas impacted by tumours. The main tool for carrying out

these procedures is MATLAB. The paragraph also highlights experimental results that show how the suggested strategy is more accurate than current approaches, paying specific emphasis on how grey-level modifications and specialized filters may improve the quality of MRI images. In the end, the technique provides a strong foundation to support physicians in the treatment and diagnosis planning of brain tumours [14].

An organized approach to brain tumour detection based on MR imaging data enhancement is presented in this study. This approach makes it simple to identify a patient using MR imaging data and permits substantial clinical experience for the diagnosis of brain cancers. In this research, the researchers have presented a MATLAB program for brain magnetic resonance imaging (MR) data to separate tumour pictures. Using the suggested MATLAB Coding, the tumour and MRI imaging data demonstrate the excellent accuracy of tumour identification. By adjusting the grey level (0 to 255) and adding more varied filters, these scripts improve the quality of MR images. The MRI dataset attests to the fact that the algorithm's findings are more suited for identifying brain tumours in typical output pictures. Therefore, this kind of clinical ground truth estimation method is available in this study. The outcomes are practically attained to the best of the researcher's ability [15].

The brain is the body's regulating centre that helps us to think and stay alive. It regulates several bodily processes, including memory, hearing, vision, personality, and problem-solving skills. The primary cause of brain tumours is the brain cells' abandoned development. As per multiple medical associations, brain tumours are the second most common cause of mortality for the general population globally. Hence, detection of a brain tumour early allows for the possibility of successful medical intervention. It has been established that, in comparison to Computed Tomography pictures, Magnetic Resonance Imaging images are more consistent and detailed. Brain tumours and neoplasms can be found utilizing various methods. The presented research paper discusses the best and most efficient algorithms reviewing several research publications as per their relevance. The majority of studies employ pre-processing brain pictures, segmenting them, extracting features, grouping, and detecting tumours [16].

The three types of brain tumours—glioma, meningioma, and pituitary gland tumours—as well as healthy brains devoid of tumours, are diagnosed using MRI images in the work that is being

presented. This makes it possible for doctors to accurately diagnose tumors in their early stages. 3264 Magnetic Resonance Imaging (MRI) brain scans, including pictures of healthy brains, meningiomas, gliomas, and pituitary gland tumours, were included in the dataset used in this study. This study looked at six machine-learning techniques for classifying brain tumours. Training accuracy for the proposed auto-encoder network and 2D CNN was determined to be 95.63% and 96.47%, respectively. The average recall scores of the auto-encoder and 2D CNN networks are 94% and 95%, respectively. Statistical tests (p-value<0.05) revealed a substantial difference between the average of both the methodologies presented in the work and many machine learning techniques [17].

This work proposes a system for classifying brain tissue from FAIR MR images into normal and pathological tissues. To pixel-level precision, tumours are segmented concurrently using the suggested regional classification technique. This study considers fractal, statistical, and texton histogram properties as region-based features. It is a very first study to address class imbalance at a micro level using the RMD-SMOTE (Random Majority Down-sampling-Synthetic Minority Over-sampling Technique). An RF-based regional classifier, selected for its outstanding generalization skills, is used in the proposed technique. We evaluate the strength of the implemented technique on the publicly available BRATS 2012 dataset. Considering accuracy and specificity at the 5% confidence interval, this method performs better than its SVM and AdaBoost counterparts. It surpasses three benchmark tumour classification algorithms in the Dice score aspect as well[18].

This implementation presents a deep learning-based approach for segmentation of a brain tumour into three sub-parts: the tumour's core, the tumour as a whole, and the tumour that is undergoing expansion. The three main modifications to the proposed design, a 3D convolutional neural network, is a heavy encoder, the use of dense blocks in place of skip connections and the use of self-ensembling in the network's decoder phase. Two methods were used to evaluate the network: a multitasking framework that segmented all tumour subregions at once, and a three-stage cascaded framework that segmented one tumour sub-part at a given time. Using proper patch extraction at the pre-processing stage allowed for the resolution of the class imbalance issue. Consideration of connected component analysis was done through the post-processing phase to decrease number of false positive predictions. Average Dice Scores for the total tumour, increasing tumour, and tumour core were obtained by this model, and those were 0.90, 0.78, and 0.82, respectively. The approach was useful based on all the related available data [19].

The patient's scan slices are the study's input, and the output is a subset of those slices that contain a tumour. A suggested method called the BBBGA (Bounding 3D Box Based Genetic Algorithm) makes use of a GA (Genetic Algorithm) to determine which parts of the brain are most different between the left and right hemispheres. This objective function is used to compare 100 randomly generated 3D boxes, each with a distinct size and location in the left hemisphere of the brain, to their matching 3D boxes in the right hemisphere. These 3D boxes are updated and relocated during the GA rounds in the direction of the brain tumour site, which is the area with the largest difference between the current two hemispheres. The dataset contains 88 abnormal patient records from the MRI Unit at the Al-Kadhimiya Teaching Hospital, Iraq. The accuracy of the BBBGA and 3D segmentation of the tumour was 90% and 95%, respectively [20].

METHODOLOGY

For physicians, analyzing the patient's 3D brain MRI volume takes a lot of time. Physicians can invest in fascinating sections more quickly and complete the outcomes more effectively with the aid of deep learning algorithms. Brain tumour segmentation divides the healthy brain from the malignant portion of the brain. Pre-processing, segmentation, optimization, and feature extraction are the four categories under which brain tumour segmentation is divided. In recent years, the significance of MRI-based segmentation has grown. The best resolution, safety, and dependability are provided by MRI. It doesn't cause radiation, has no negative side effects, and does not harm other bodily components. After processing the MRI, the tumour is segmented. We presented an automated CNN-based segmentation technique in this research. It has several layers for segmenting brain tumours and extracting features. For this, there are 75 LGG (Low-Grade Glioma) photos along with 210 HGG (High-Grade Glioma) photos, in the BraTS 2018 collection.

The applied approach not only has the brain tumour been identified in this investigation, but the tumour's location has been segmented as well. In this process, the first step in receiving medical care is figuring out where the patient's tumour is located in their body. Early brain tumour discovery can contribute to a lower death rate in the medical industry and change the lives of several folks. Of all the types, the most

occurring type of tumours are 'Gliomas'. It falls into one of two categories: LGG (low-grade glioma) and HGG (high-grade glioma). One can learn more about gliomas by using MRI images. The MRI sequence includes a T1-weighted image, T1-weighted with gadolinium-contrast enhancement (t1gd), T2-weighted image, and the FLAIR weighted image for sub-parts and features of a brain tumour for easy identification, making the process reliable and rapid, for detecting the level of the tumour.

MRI (Magnetic Resonance Imaging) for Brain

In the medical industry, MRI is one of the very advantageous and most preferred methods to create pictures of many human body components, including the brain, heart, etc. The concepts of nuclear magnetic resonance lend credence to it. In the medical profession, it's commonly utilized. The best resolution, safety, and dependability are provided by MRI. Since the brain contains delicate organs and tissues, we choose MRI to obtain thorough information about the human brain. Even after being exposed to magnetic fields repeatedly, MRI has high resolution and no negative effects. The Fig. 1. shown below shows a few examples of MRI images from different angles.
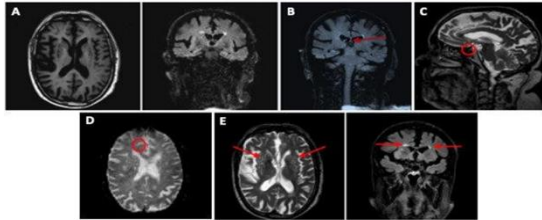

Fig. 1. Examples of MRI Images

MRI Sequences

An MRI produces images of a series of events that take place inside the machine. A variety of MRI (magnetic resonance imaging) sequence pictures are utilized while making diagnoses, such as FLAIR (fluid-attenuated inversion recovery) weighted MRI, T1-Weighted MRI, T2-Weighted MRI, and T1-weighted with Gadolinium Contrast Enhancement (t1gd). MRI pictures are divided into the following categories:

T1-weighted image

T1-weighted MRI images show poor signals in certain brain lesion areas (oedema). due to the high protein content of collagenous tissues and water. Compared to other scans, the T1-weighted pictures offer more anatomical detail. A T1-weighted MRI scan reveals that fresh blood arteries are bright, fat is bright, and water is dark. In contrast, it helps

monitor vascular alterations and is beneficial for breaking down the blood-brain barrier (BBB).

T2-weighted image

A T2-weighted MRI picture shows a high signal-to-water ratio. The T2-weighted picture displays a large signal intensity for CSF. A T2-weighted MRI scan reveals that fresh blood vessels are black, fat is dark, and water is light. We can distinguish the brain lesions from the normal brain using this sequence on the T1-weighted picture, but not from the CSF since the latter is excessively bright.

FLAIR image

While CSF is in a dark region, the image is comparable to the T2-weighted one. A grey-white distinction can be strengthened. Fluid-attenuated inversion recovery, or FLAIR, allows us to identify brain lesions, or edema, that are not visible in the T2-weighted sequence. It aids in distinguishing the hyper-intense region from the oedema. The medical industry makes the most use of fluid images. The MRI sequences are all displayed in the following Fig. 2.
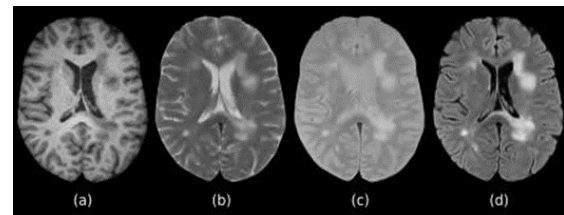

Fig. 2. FLAIR image sequences

Plane views of MRI

In comparison, MRI is characterized by several planes combined together. Similar to a system of Cartesian coordinates, the human's position is described in the planes. The coronal, sagittal, and planes are where the MRI is categorized in the plane system. The terms coronal, sagittal, and axial planes refer to the front, side, and top views of the body, respectively. We assess and examine the illness to some degree with the aid of these aircraft. As seen in Fig. 3., the sagittal plane, coronal plane, and transverse plane represent the three primary plane views of MRI of the human body.
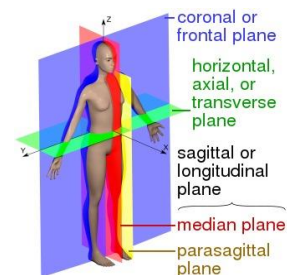

Fig. 3. Different planes for MRI viewing

Sagittal plane: The Sagittal plane is a sideways plane that divides left from right and runs from top to bottom. The body's side vision is provided via the sagittal plane. The human body's left or right side can be viewed.

Coronal plane: This provides the front-to-back view of the body-axis plane that divides the posterior from the anterior.

Transverse plane: The transverse plane, which divides the superior from the inferior—or, to call it different manner, the top (head) from the bottom (feet)—is an x-y-z parallel plane to the earth.

Fig. 4. displays the axial, coronal, and sagittal plane MRI head scans.
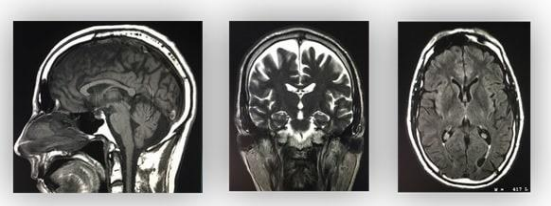
Fig. 4. MRI head scans in three planes

Brain Tumour Segmentation

Image Segmentation

For appropriately localizing the picture's features at the pixel level, then dividing it into segments, one class label is assigned to pixels with the same intensities, while another class label is applied to other pixels. More precise localization of the relevant area is possible using pixel-level segmentation. Classification and detection are easier tasks than segmentation. The bounding box is the only representation of the class in detection. In segmentation, the contour surrounding the segmented component comprises only the interesting region, as illustrated in Fig. 5., even when bounding boxes feature distinct pixels other than the interested class.
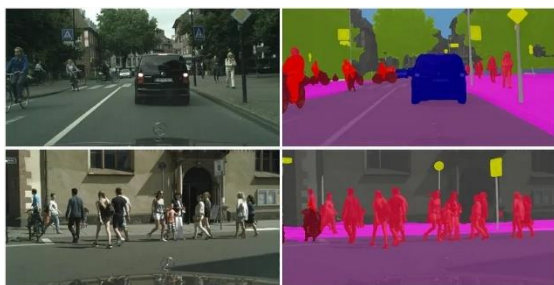

Fig. 5. Interested regions obtained through image segmentation

Label 0 serves as the backdrop in the binary picture segmentation, whereas Label 1 is mapped to area of

interest. Compared to multiclass segmentation, which involves classifying more classes, this segmentation task is simpler.

Different Segmentation Types:

The two most common forms of segmentation are as follows. Several designs are used to segment images. Semantic and instance segmentation are the two types of segmentation that are discussed briefly.

Semantic Segmentation

Semantic segmentation assigns a class label to items of the same type. A higher level of image knowledge is needed for this segmentation challenge. As a result, the procedure requires algorithms that can generate boundaries based on various intensities, contexts, textures, etc. and that operate well at the pixel level. In the implemented model, semantic segmentation is employed. This sort of segmentation uses an applied technique and has four different groups of tumours to segment.

2D vs 3D Brain tumour segmentation

2D Brain tumour segmentation

Every brain slice is segmented independently in two-dimensional brain tumour segmentation. By doing this, the tumorous and non-tumorous regions are distinguished. While 2D segmentation produces very efficient results and requires less training time, but use of it in real-time applications is still not recommended. As it takes a lot of work to analyze each individual brain picture slice, and then analyze and aggregate the entire volume. Analyzing the affected area of the brain becomes impossible. The most severe problems could arise from any error. Physicians will analyze the brain imaging using their domain expertise. Given the high likelihood of errors, 2D image segmentation is not recommended in this scenario for real-world applications. However, the 2D technique can be implemented easily, and combining different axial views can result in seeing the entire brain tumour portion.
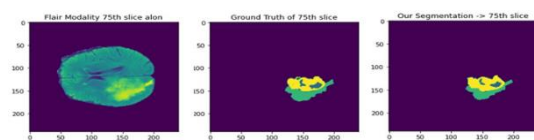

Fig. 6. Slicing in segmented images

In Fig. 6. on the extreme right-side, it displays a segmented portion present, that obtained by the implemented architecture. And, in the central region, the actual truth of the brain image is shown.

3D Brain tumor segmentation

Unlike 2D segmentation, which segments each slice independently, 3D brain tumor segmentation does not do so. In this case, the entire brain's volume is fed into the model, which outputs the entire segmented volume. This will assist in resolving the problems we encountered with the aforementioned segmentation strategies. The image allows for simultaneous observation and accurate identification of the entire volume.

Segmentation Architecture

In deep learning, several segmentation concepts are employed. A brief description is given of the most recent and practical architectures that are best suited for segmentation. The research has discussed the advantages of certain architectures over others and the rationale for the selection to use the U-NET architecture for segmentation of tumour in brain.

The U-NET Architecture

The U-shaped design of UNET architecture inspired its name. This architecture is specifically designed to address the segmentation of images in biomedicine. because it is difficult to access a lot of data in the medical field. Neural networks can take months to train to extract features from vast volumes of data.

It is more difficult to work with a tiny dataset than a large one. They created an architecture that facilitates working with little data after conducting extensive study. Similar to FCN, U-NET design has an encoding-decoding path design. Its contracting path extracts the image's high- and low-level characteristics by down sampling the image.

Convolutional layers having 3*3 filters, a non-linear activation function, and a max-pooling layer make up contracting route. The quantity of characteristics is the key to the contracting path. This combined functionality into a single bottleneck. Subsequently, features having concatenation of the similar shape contracting layers along with cropping are located using an expanding path with transpose convolution. 1*1 convolutions are employed at the last layer to divide the class. (As shown in Fig. 7.)
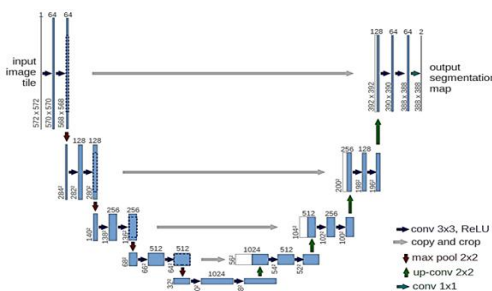

Fig. 7. Working of U-Net architecture

The greyscale input image comes after the two convolutions, each with sixty-four filters, in succession. After that, the image size was decreased by max-pooled. 1024 filter bottlenecks have all integrated features. The 'what' of the picture is this. The 'where' portion of the picture, which employs skipping connections and concatenates to find the wanted portion, comes after the bottleneck.

Segmentation Losses

An essential component of any kind of machine learning model is the loss function. The model's ability to fit the training set is indicated by the loss function. We always want to experience a very small loss. On training data, a zero loss value denotes 100% model correctness. Depending on the model, many kinds of loss functions exist. In every iteration, the model's parameters are modified based on the loss value. Classification and segmentation losses are not the same. The following are the main semantic segmentation losses that either positively or negatively aid the implemented model:

Dice Score Loss

To determine how similar two images are, the field of computer vision frequently uses the Dice coefficient.
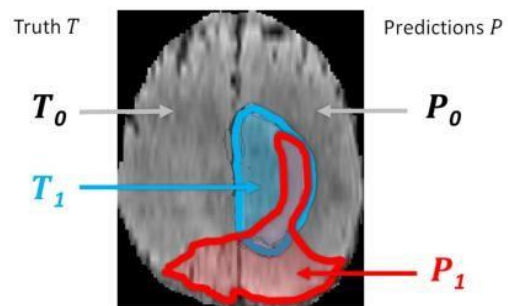

Fig. 8. False and True Regions in an Image

In Fig. 8. the region above represents the truth, where there is no tumour; T1 represents the ground truth, where the tumour is present and is represented in blue; Po represents the prediction, where the tumour is not present; and P1 represents the predicted tumour, which is depicted in red.

Sensitivity Specificity Loss

Sensitivity and Specificity are often considered parameters to assess the predictions for segmentation, much like the Dice Coefficient. The dataset in our application is incredibly unbalanced. W is considered to modify loss for comprehending the model and making precise judgments to go around that problem. Whereas TN is a real negative,

TP is a true positive. The definition of loss is given as:

$$SSL = w \times sensitivity + (1 - w) \times specificity$$

U-NET Model Architecture

U-NET architecture has been employed in the project's practical implementation. For the best results, use this architecture for segmenting biomedical images. When compared to other methods now in use for picture segmentation for biomedical applications, it is thought to be the best. It improves the outcomes without changing the image files' original information.

RESULTS

Segmentation Results:

There are 210 3D photos in the Brats 2018 dataset collection. The total number of 2D photos is 151200 as it will slice the 3D images and capture pictures from three axes. Due to their appropriateness for the dataset, all of the parameters and models were left the same. The data was then utilized to train the model to obtain proper results, yielding the following outcome:

Table 1. Results obtained after implementation

Training and Testing	Two class segmentation	Four class Segmentation	Four class segmentation post-hyper-parameter Tuning
Epochs	10	10	45
Training accuracy	0.972	0.726	0.7526
Training loss	0.0274	0.2474	0.2474
Testing accuracy	0.92224526007970188	0.6383521348237992	0.7266646613677342
Testing Loss	0.07775473992029826	0.3616478661696116	0.27333533962567647
Mean sensitivity for class 0	0.99879688042886612	0.9973130890962196	0.99944186080065988
Mean specificity for class 0	0.81575437802639499	0.7399030542635091	0.78557679360447544
Mean sensitivity for class 1	0.81575437802639499	0.3213817273098429	0.42280200482909755
Mean specificity for class 1	0.99879688042886612	0.9994933975562182	0.99979339025240288
Mean sensitivity for class 2	NULL	0.41349304918469726	0.6064759350159152
Mean specificity for class 2	NULL	0.9996057752590369	0.9993690548406183
Mean sensitivity for class 3	NULL	0.8404884744002085	0.82659523085818187
Mean specificity for class 3	NULL	0.9955309186827245	0.99859831583850012

The above table 1. displays the various parameters applied in the model testing, and these parameters are useful while considering the effectiveness of the results obtained by executing the whole model.

The effectiveness of the implemented project must also be tested by considering the number of epochs used to get the required results. So, the below-shown Fig. 9. and Fig. 10. below display the two curves of

model accuracy and model loss compared with epochs, respectively. Also, the negative images are shown in the below-mentioned Fig. 11. And Fig. 12. It displays the accurate image showcasing the appropriate region of the affected brain area. Hence, it results in a noble solution to detect brain tumours and makes the entire process seamless.
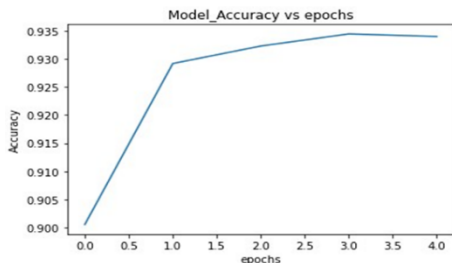

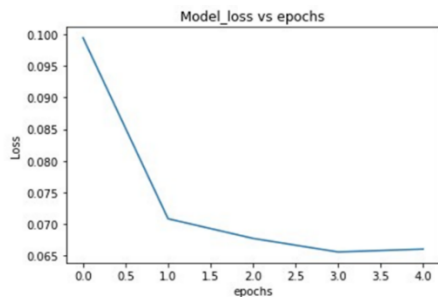Fig. 9. Graph showing Model Accuracy vs. Epochs

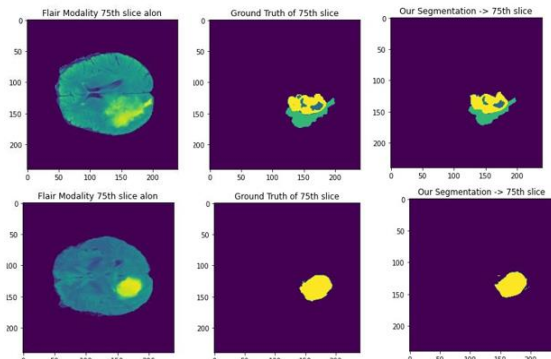Fig. 10. Graph showing Model Loss vs. Epochs

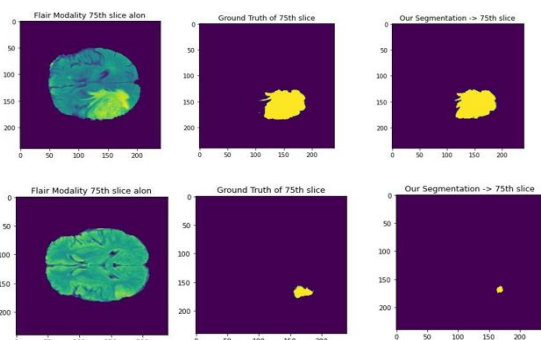

Fig. 11. Negative images having intense tumour

Fig. 12. Negative images showing lower intensity of brain tumour

Therefore, the proposed model manages to solve one of the biggest problems in the medical sector i.e. identifying the brain tumour and its threat to an individual's life. So, implementing this model with a robust hardware system can solve a major problem, and can save many lives.

FUTURE SCOPE

The overall research solves the major problem of brain tumour detection and threat analysis. However, the necessary updates required in the project execution include the involvement of real-time MRI machines and high-precision instruments. Implementing the model in these machines can save a lot of time, and doctors can serve multiple patients in less time. Further, the project can be extended to scan other kinds of tumours (e.g. breast tumours, lung cancer, etc.) in human bodies and can solve such multiple problems. Also, the accuracy and precision of the implemented model can be greatly refined with the evolution of various newer algorithms in the Artificial Intelligence domain. So, this novel project can contribute efficiently to the medical field and help doctors make use of technology to solve such intricate problems daily in less time.

CONCLUSION

As brain tumours cause severe threats to human life, the implemented research enabled the identification of all three types of brain tumours successfully without changing the images in other formats which are not used in the medical industry. Also, with an average accuracy of ninety-six per cent on the original dataset, the project can be implemented in the medical sector effectively. The inclusion of this novel approach can bring significant change and resolve multiple problems faced by doctors and patients. Seamless involvement of this model with highly advanced medical equipment can support doctors in saving time, improving tumour detection accuracy, and deciding the level of threat in a medical condition. So, the model proves to be a fit in real-life circumstances and provides reliable solutions on a day-to-day basis.

REFERENCES

[1] Goswami, Suchita, and Lalit Kumar P. Bhaiya. "Brain tumour detection using unsupervised learning based neural network." In *2013 International Conference on Communication Systems and Network Technologies*, pp. 573-577. IEEE, 2013.

[2] Thara, K. S., and Kaur Jasmine. "Brain tumour detection in MRI images using PNN and GRNN." In *2016 International Conference on Wireless Communications, Signal Processing and Networking (WiSPNET)*, pp. 1504-1510. IEEE, 2016.

[3] Selvy, P. Tamije, V. P. Dharani, and A. Indhuja. "Brain tumour detection using deep learning techniques." *Int. J. Sci. Res. Comput. Sci. Eng. Inf. Technol* 169 (2019): 175.

[4] Soltaninejad, Mohammadreza, Guang Yang, Tryphon Lambrou, Nigel Allinson, Timothy L. Jones, Thomas R. Barrick, Franklyn A. Howe, and Xujiong Ye. "Automated brain tumour detection and segmentation using superpixel-based extremely randomized trees in FLAIR MRI." *International journal of computer assisted radiology and surgery* 12 (2017): 183-203.

[5] Tchoketch Kebir, S., S. Mekaoui, and M. Bouhedda. "A fully automatic methodology for MRI brain tumour detection and segmentation." *The Imaging Science Journal* 67, no. 1 (2019): 42-62.

[6] Latha, M., and R. Surya. "Brain tumour detection using neural network classifier and kmeans clustering algorithm for classification and segmentation." *Brain* 1, no. 01 (2016): 27-32.

[7] Sajid, Sidra, Saddam Hussain, and Amna Sarwar. "Brain tumor detection and segmentation in MR images using deep learning." *Arabian Journal for Science and Engineering* 44 (2019): 9249-9261.

[8] Siar, Masoumeh, and Mohammad Teshnehlab. "Brain tumor detection using deep neural network and machine learning algorithm." In *2019 9th international conference on computer and knowledge engineering (ICCKE)*, pp. 363-368. IEEE, 2019.

[9] Amin, Javaria, Muhammad Sharif, Nadia Gul, Mudassar Raza, Muhammad Almas Anjum, Muhammad Wasif Nisar, and Syed Ahmad Chan Bukhari. "Brain tumor detection by using stacked autoencoders in deep learning." *Journal of medical systems* 44 (2020): 1-12.

[10] Kumar, Sanjay, Naresh Kumar, Inderpreet Kaur Rishabh, and Vivek Keshari. "Automated brain tumour detection using deep learning via convolution neural networks (CNN)." *Int. J. Cur. Res. Rev* 13, no. 02 (2021): 148.

[11] Kumar, D. Dhilip, S. Vandhana, K. Sakhthi Priya, and S. Jeneeth Subashini. "Brain tumour image segmentation using MATLAB." *vol* 1 (2015): 447-451.

[12] Hassan, Esmail, and Abobakr Aboshgifa. "Detecting brain tumour from MRI image using matlab gui programme." *International Journal of Computer Science & Engineering Survey (IJCSES)* 6, no. 6 (2015).

[13] Sahu, Yogesh Kumar, Chanki Pandey, Preesat Biswas, M. R. Khan, and Shanti Rathore. "Minimum time delay and more efficient image filtering brain tumour detection with the help of MATLAB." In *2020 International Conference on Communication and Signal Processing (ICCSP)*, pp. 1195-1199. IEEE, 2020.

[14] Gaonkar, Omkar Maruti, Nitesh Sandip Jadhav, Dishant Krishna Koli, and P. V. Bhosale. "Brain Tumour Diagnosis Using Matlab with Edge Detection." *Int. J. Res. Appl. Sci. Eng. Technol* 10, no. 5 (2022): 122-128.

[15] Champka, Shahnaz Ayub, Alok Kumar, and Rishabh Kumar Baudh. "Analysis of MRI Data for Brain Tumor Detection using MATLAB." In *Proceedings of the International Conference on Advances in Electronics, Electrical & Computational Intelligence (ICAEEC)*. 2019.

[16] Keerthana, A., B. Kavin Kumar, K. S. Akshaya, and S. Kamalraj. "Brain tumour detection using machine learning algorithm." In *Journal of Physics: Conference Series*, vol. 1937, no. 1, p. 012008. IOP Publishing, 2021.

[17] Saeedi, Soheila, Sorayya Rezayi, Hamidreza Keshavarz, and Sharareh R. Niakan Kalhori. "MRI-based brain tumor detection using convolutional deep learning methods and chosen machine learning techniques." *BMC Medical Informatics and Decision Making* 23, no. 1 (2023): 16.

[18] Rehman, Zaka Ur, Syed S. Naqvi, Tariq M. Khan, Muhammad A. Khan, and Tariq Bashir. "Fully automated multi-parametric brain tumour segmentation using superpixel based classification." *Expert systems with applications* 118 (2019): 598-613.

[19] Ghaffari, Mina, Arcot Sowmya, and Ruth Oliver. "Automated brain tumour segmentation using cascaded 3d densely-connected u-net." In *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries: 6th International Workshop, BrainLes 2020, Held in Conjunction with MICCAI 2020, Lima, Peru, October 4, 2020, Revised Selected Papers, Part I 6*, pp. 481-491. Springer International Publishing, 2021.

[20] Hasan, Ali M., Farid Meziane, and Mohammad Abd Kadhim. "Automated Segmentation of Tumours in MRI Brain Scans." In *BIOIMAGING*, pp. 55-62. 2016.