# Efficient Brain Tumour Prediction using 2D

**Anusha V[1], Chinmayee C K[2], Chigicherla Sai Priya[3], Harshitha G[4], Harshavardhana Doddamani[5]**

[1,2,3,4] Students, Dept of CSE, S J C Institute of Technology, Chickballapur
[5] Assistant Professor, Dept of CSE, S J C Institute of Technology, Chickballapur

**Abstract:** *It is difficult and important for the medical field to identify and segment brain tumours using MR images. Early detection and localization of brain tumours can prevent death and provide doctors the opportunity to choose effective treatment options. Deep learning techniques due to their ability, performance, and potential to support precise diagnosis, prognosis, and medical treatment technologies. attracted researchers in medical imaging. Procedures and methods: Using deep neural networks (DNN) and data augmentation techniques, this research proposes a novel framework for segmenting 2D brain tumours in MR images. The proposed method (ZNet) propagates the intrinsic affinities of a relatively limited number of expertly demarcated tumours, such as hundreds, by utilising the concepts of skip-connection, encoder and decoder topologies, and data amplification. Results: Our experimental findings demonstrated high mean values. The capacity of the ZNet model to locate and automatically segment brain tumours in MR images is demonstrated by masks in the testing dataset. We can confirm that the suggested ZNet architecture and deep learning techniques can recognise and separate tumours in MR images. In some computer vision applications, a high pixel accuracy rating can be deceiving. Alternative evaluation measures, on the other hand, like IoU (Intersection over Union) and dice, are more factual for semantic segmentation. This study provides a real-world illustration of how AI technologies in medical imaging can be used to automatically segregate tumours in MR images. Brain tumour region segmentation, deep learning, augmentation and neural networks are some of the index terms.*

## I. INTRODUCTION

The ability to distinguish between normal and diseased features requires judgement and has a high margin of error. Building interpretable models that are trained on existing medical pictures to automatically recognise patterns, produce labels, and diagnose new cases can be greatly aided by computational and artificial intelligence (AI) approaches. In general, AI models are meant to support, supplement, and improve human medical expertise rather than to completely replace it. Derived computational models can improve and hasten clinical practise and scientific research. The process of identifying, detecting, and labelling anatomical components, physiologically important regions, or the intrinsic network organisation of the brain is known as medical picture segmentation. Brain map segmentation is a key step in computer aided diagnosis and helps clinicians make decisions.

Three types of segmentation are categorised in the literature: automatic, semi-automatic, and manual segmentation. There are generally three primary models to localise the borders of brain areas as curves in 2D images or surfaces in 3D volumes, such as the regions of brain tumours These include deep learning techniques, atlas registration, and conventional machine learning techniques. In traditional machine learning picture segmentation, manual segmentation masks created by experts are used to train a classifier. Tools for label annotation are employed to specify the desired features, objects, or shapes. Machine learning methods are used to train and evaluate the model in order to find similar features and shapes in upcoming out-of-bag (fresh) datasets. For instance, the segmentation of the anatomical structure of the brain was modelled using a statistical learning approach, and a probabilistic brain atlas was created. The performance is also relatively when the line separating malignant and normal tissues is poor is unclear.

A semi-automatic segmentation technique called Multi-Atlas Segmentation (MAS) uses data from previous atlases. The single atlas technique gave rise to the MAS; however, it is seen to be unsuitable for medical segmentation because to the lack of prior knowledge, which results in poor performance and inferior accuracy. For segmenting novel images, multi atlases with more historical data are utilised as an alternative. In order to propagate the atlas labels into the space of the new image coordinates, for instance, pairwise registration could be utilised between each atlas image and the novel image.

Deep learning techniques for medical image analysis. Due to numerous papers demonstrating excellent results for identifying and predicting the target forms in the images, segmentation has attracted a lot of attention. There are other segmentation methods in the literature, but the completely convolutional the most successful techniques for segmenting medical images are believed to be neural network (FCN) and convolutional autoencoder algorithms. Each layer in a fully conventional network (FCN) generates a three-dimensional array of size hxwxc, where h and w stand for height and width, respectively, and c for channel number. The input image is regarded as the first layer, and succeeding layers are the results of convolving earlier layers. Convolution, pooling, and activation functions are the fundamental components of each layer. In order to extract features from photos or input samples while retaining the majority of the original data, autoencoder algorithms were used. The encoder and decoder are the two primary components of the autoencoder.

The encoder part converts the input images into smaller-dimensional intermediate representations, while the decoder part uses the intermediate representation to recreate the original input images. When using autoencoders, the loss function is determined in terms of how similar the input and reconstructed pictures are. Convolutional networks, random forests, and UNet are some of the alternate techniques used in several recent studies on MRI tumour segmentation. A hybrid strategy combining RESNET and Unet has been proposed. Brain tumour segmentation performed well by dice = 0.90. In order to segregate brain tumours, combined genetic algorithms (GA) with convolutional networks. Instead, then using the conventional trial-and-error method to construct the convolutional network, GA strives to get the ideal CNN structure. On the TCGA (The Cancer Genome Atlas) dataset, several studies were conducted by to segment brain tumours using Feature Pyramid Networks (FPNs), RESNET, and Unet. The presented validation results demonstrate that utilising RESNET, performance is at its best when dice = 0.93. In a recent study, Cascade Convolutional Neural Network (C-CNN), a deep learning technique, was used to create an efficient brain tumour segmentation system. Their method circumvents high computing time constraints, limits resource utilization, and lessens the overfitting issue by relying on a small quantity of data rather than the complete dataset. With dice = 0.92, this approach likewise produced results that were competitive. Another study changed the Unet framework by omitting the deconvolution block and adding two convolutional layers in its place.

## II. METHODOLOGY

### A. DATASET

The Cancer Genome Atlas Low-Grade. Glioma (TCGA - LGG) was used in this investigation. The purpose of the goal of the TCGA-LGG compilation is to create cancer images. During the course of treatment and follow-up at several places, the dataset from was examined by Budget and made available for computer analysis and medical image processing. Additionally, the FLAIR MRI pictures, which feature LGG enhanced tumor images, are the subject of our attention. 110 patients' FLAIR pictures were manually evaluated, annotated, and labelled by neuroradiology specialists. The shape border of the FLAIR abnormality (tumor) in pathological instances was defined by the experts for each image. The training dataset was represented by the original MRI and the manually labelled masks.3,929 image slices were obtained in total, 2,556 of which were classified as normal and 1,373 as abnormal (tumor).

### B. DATA PREPROCESSING

The training (3005 images), validation (393 images), and testing (432 images) subsets of the dataset were randomly chosen. Approximately 10 percentage of the original dataset is used for validation, 15 percentage is used for testing, and the rest pictures are used to train the model. In the original dataset, the images' resolution was Due to the original image's size of 256x256 and the lengthy processing and computing required, we downsized the data to 128x128 pixels. Imaging data augmentation has become a common pre-processing step in data science and AI applications. It is primarily used when 2 training data is scarce or when the volume of data is crucial to creating a better computer model. Data augmentation can also lessen the overfitting issue and improve model performance.

To execute the required picture augmentation for this study, we used Augmentations, a free and open-source Pythonpackage. Augmentations processes offered a comprehensive and all-encompassing data augmentation. Based onhorizontally flipping the input around the y-axis, Horizontal Flip was used to create new images from the originalphotos.

By flipping the input around the vertical x-axis, Augmentations Vertical Flip was used to create new images. The input was rotated randomly by 90 degrees using the RandomRotate90 function. To swap the rows and columns in the supplied image, transpose was used. Shift Scale Rotate was used to generate new images based on shifting, scaling, and rotating the original images through random affine transformations. Finally, all pixels from the input photos were transformed into floating-point elements with a range of 0 to 1. Data that has been enhanced using Augmentations' Python library.

### C. ZNET FRAMEWORK

Networks (AN) and the Unet method—to build a unique framework for MR image tumor segmentation in the suggested network architecture. The encoder-decoder design from the Unet technique and the AN's skip connections and concatenating tensors principles are used in the framework. The suggested ZNet method's full design is depicted. The design comprises of a decoder (synthetic up sampling) and an encoder (analytic down sampling) component. Each of the five encoder blocks in the encoder component has double convolutions that are combined with batch normalization, rectified activation function ReLU, and max pooling.

ConvTranspose2d We ultimately obtain the original image dimensions in the final decoder block, which is often used to increase a tensor at the end of each decoder block. The output block, which comes last, is made up of a single convolution and sigmoid activation function. Using the adaptive moment estimation (ADAM) optimizer, three channels with a resolution of 128x128 pixels, a batch size of 32, and the binary cross-entropy loss function, we trained the model over 200 iterations.

### D. EVALUATION METRICS

Pixel accuracy, mean intersection over union (IoU), and dice coefficient are some of the most often used metrics for assessing the effectiveness of segmenting medical MR images. However, pixel accuracy struggles when there is a class imbalance in the images because the dominant class will ignore the subordinate classes and produce surprising results. However, it has been demonstrated that dice and IoU are generally preferable options for semantic segmentation. Since DICE is twice as much as IoU to quantify the similarity between ground truth A and anticipated segmentation B, the IoU and Dice evaluation matrices are similar and positively associated. In addition, we evaluated the 1800508 VOL using for pixel accuracy, for the F1 score, Matthews Correlation Coefficient proposed approach.

### III. OUTCOMES

200 epochs of training on the TCGA-LGG dataset revealed a validation dice of 0.96 for segmenting and detecting. The MR scans of the brain tumor. Using the technology described each epoch took about two to three minutes. The data is typically split into two groups in data science applications: the training set and the testing set. In order to prevent overfitting during training and to guarantee that model evaluation is carried out using an unknown set of data, the training set is also divided into two parts: the model training set and model validation set. The proposed algorithm's training and validation performance as red and dark blue curves, respectively, while the model loss is represented by a light blue curve. The ZNet model can predict and segment the tumor in MR images with a dice value of roughly 0.92 and die loss of 0.08, according to an examination of the 432-testing dataset.
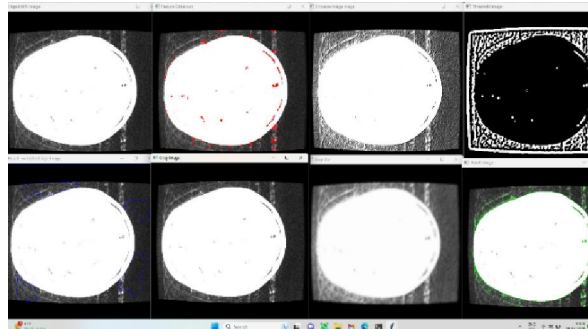


Figure 1:MR image tumour segmentation using the ZNet and UNet yields visual findings and comparisons.
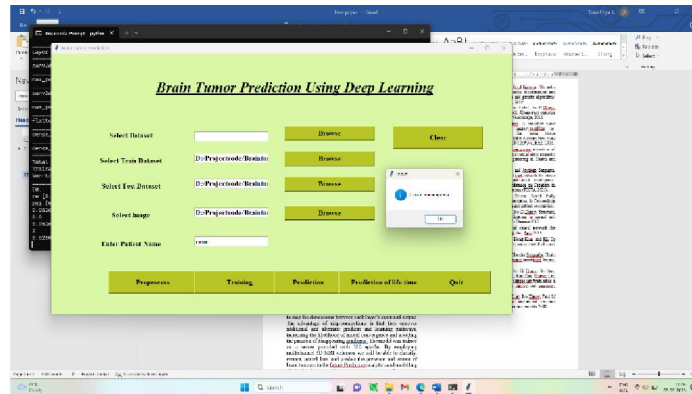
Figure 2: Login Page for training and testing and used for prediction



Figure 3: Training and Validation accuracy graph



Figure 4: Training and Validation Loss graph

## IV. CONCLUSION

In this study, we developed a novel method for segmenting MR pictures based on the neural network deep learning idea and data augmentation to make use of the available labelled images. The architecture is based on auto encoder-decoder, the skip connections theory, and residual neural networks, which necessitate merging the output of the previous layer with the next layer. Additionally, features maps are necessary to map the dimensions between each layer's input and output. The advantage of skip-connections is that they uncover additional and alternate gradient and learning pathways, increasing the likelihood of model convergence, and avoiding the paradox of disappearing gradients. The model was trained on a server provided with 200 epochs.

By employing multichannel 3D MRI volumes, we will be able to classify, extract, parcel late, and predict the presence and extent of brain tumors in the future. Predictive analytics and modelling of high dimensional neuroimaging hyper-volumes are difficult for a variety of reasons, including the difficulty of expressing higher-order data tensors, computing difficulties, and the optimization problem's inherent exponential growth in state space. An enormous amount of annotated ground facts is needed for the training of supervised learning algorithms like ZNet. It takes a lot of time and resources to gather testing and validation data on such a huge scale. Additionally, we are developing deep learning techniques to produce multimodal, high-dimensional, realistic neuroimaging data that includes ground truth labelling.

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