

A Deep Dive Into Brain Tumor Segmentation Using U-Net: Harnessing The Power Of Fully Convolutional Networks

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ABSTRACT

Brain cancer is a deadly illness that has a profoundly detrimental impact on the lives of those who are affected. Consequently, early brain tumour detection boosts patient survival rates and enhances the effectiveness of treatments. On the other hand, early brain tumour detection is a difficult undertaking and an unmet need. Magnetic Resonance Imaging (MRI) is a noninvasive imaging method, it is typically the first step in the diagnosis and segmentation of brain tumours. Thus, during the past several years, a lot of research has been done on creating reliable automated methods for detecting brain tumours. Segmenting an MRI brain tumour is crucial for automated brain tumour detection and subsequent analysis. This research article shall focus on developing a deep learning architecture for performing segmentation of tumor from the brain MRI. Also using the same architecture models will be developed to segment necrosis, edema, and enhancing tumor region from the MRI images. The fully convolutional architecture (U-Net) based models were trained, tested, and validated for performing segmentation. This shall assist the physician in planning further diagnosis and treatment process.

Keywords: brain cancer, tumor detection, magnetic resonance image, deep learning architecture, fully convolutional architecture, U-Net.

INTRODUCTION

The brain is a vital organ that has 100 billion neurons, or nerve cells. Brain tumours rank as the tenth leading cause of death in developed nations for both genders of adults and children. Brain tumours were the tenth most prevalent type of tumour among Indians in 2018 [1]. Brain cancer is currently the fourth most common and deadly disease in the world, but by 2030, it is expected to overtake skin cancer to take the second spot. According to the International Association of Cancer Registries (IARC), more than 28,000 instances of brain tumours are reported in India annually, and the disease is thought to be the cause of more than 24,000 deaths. In India, the number of instances of brain tumours is "steadily" increasing, with 20% of those cases occurring in youngsters. Brain tumours, often referred to as intracranial tumours, are composed of a heterogeneous population of malignant cells that originate in the brain's intracranial tissues and can vary in severity from benign to metastatic [2]. When cell division rates rise and multiply uncontrollably, brain tumours start. A brain tumour can grow in any part of the brain or skull, including the nasal cavity, base of the skull, brainstem sinuses, and protective lining of the brain. Brain tumours come in over 150 different varieties. Brain tumours can be broadly categorized as either malignant or noncancerous. The various cell types that make up the brain each have unique properties of their own. It is not possible to extrapolate outcomes from cancers in other organs to brain cancers. The primary cause of brain tumours is the distinct biology and microenvironment of the brain. The biology, management, prognosis, and risk factors of each type of tumour vary, making it challenging to characterize the brain tumour classification [3]. Three distinct tests and procedures are necessary to diagnose a brain tumour: imaging tests, neurological examinations, and biopsies. Magnetic Resonance Imaging is the most widely used and reliable technique for diagnosing brain tumours (MRI) [4]. It is possible to inject a dye into a vein during an MRI scan. Based on the results of the MRI scan, such as perfusion MRI, functional MRI, and magnetic resonance spectroscopy, experts evaluate the tumour and develop treatment strategies. Early diagnosis by medical professionals can lead to prompt

treatment, improving the patient's chance of survival. However, it might be difficult to identify malignancies in tumour locations since they often have confusing morphological characteristics. In order to help doctors diagnose cancer more precisely, computer-aided diagnostic (CAD) techniques have been available recently. The detection ratio of brain tumours has increased thanks to these cutting-edge brain imaging techniques. Significant advancements have lately taken place as a result of the need for intelligence in CAD systems; artificial intelligence (AI) is combined with CAD to lower recognition times and memory needs [5]. Furthermore, it facilitates the creation of a practical knowledge-based design system. When contrasting the new AI support with the conventional CAD system, it becomes evident that the new AI support works better when paired with CAD. The increasing use of Deep Learning (DL) in medical research and the expansion of big data analytics have enhanced the algorithms and accuracy of AI systems [6].

Brain MRI segmentation is a fundamental process that is crucial for many neurology applications, including functional imaging, operational planning, and quantitative analysis. Medical image segmentation is a challenging task due to various factors such as low contrast, poor spatial resolution, inconsistent object shapes, noise, partial volume effect, and other acquisition artefacts in the retrieved data [7]. Additionally, there aren't enough anatomical models to fully represent the potential deformations in each structure, even though magnetic resonance imaging (MRI) can accurately describe brain structures. A few straightforward strategies can be put into practice to address these restrictions. The diverse nature of tumours, including their extensive variability in size, form, location, and recurrence, poses a challenge in developing efficient segmentation guidelines. Despite these problems, the field has seen significant success thanks to ongoing advancements in computer technology and equipment.

The following categories of image segmentation systems have been established by numerous researchers: threshold-based, region-based, pixel classification, and model-based techniques [8]. The premise of threshold-based techniques is that all pixels falling within a given range are members of the same class. The pixel qualities at the boundary between two regions are assumed to change suddenly in boundary-based approaches. The premise of region-based techniques is that an area is made up of nearby pixels with comparable characteristics. Segmentation in pixel classification algorithms is based on feature space and pixel properties, which can include local texture, colour components, and grey level for each pixel in the image. When using model-based procedures, an object's shape, size, texture, orientation, and other a-priori knowledge are included into the model to create a specific anatomical structure. Certain hybrid approaches combine two or more of the previously listed techniques. This research focuses on developing fully convolutional neural network for segmentation of tumor and surrounding regions in brain MRI. The suggested methodology made use of the U-Net architecture. When the two routes are combined, U-net can learn both local and global characteristics and accomplish high segmentation task accuracy. U-net's flexibility in handling many input data formats, including multi-channel pictures, colour, and grayscale, is one of its advantages. In the experiments initially pre-processing techniques were employed for processing raw MRI images. Pre-processed MRI images are segmented using U-Net model and the encoder part of the model was designed using ResNet model which skip connections. ResNet is a Convolutional Neural Network (CNN) architecture that sets itself apart from other CNNs with a sequence of residual blocks (ResBlocks) with skip connections. The performance of the model in segmentation of tumor was compared with other U-Net architectures. Then a multiple models are developed to segment different areas of the tumor. The output of multiple models was combined to form a segmentation result.

RELATED WORK

There are a number of techniques for brain tumour segmentation that specifically create a parametric or non-parametric probabilistic model for the underlying data. These models typically comprise a previous model and a likelihood function that matches the observations. Tumours can be categorised as anomalies within normal tissue, subject to limitations on their structure and connection. Some methods make use of probabilistic atlases. Because brain tumours can vary in size, form, and location, the atlas needs to be calculated throughout the segmentation process. The atlases can be improved by using tumour growth models to assess the mass effect.

When using Markov Random Fields (MRF) to create smoother segmentations, the neighbourhood of the voxels offers helpful information [9]. After oversegmenting the image into supervoxels, Zhao et al. [10] also employed an MRF with a histogram-based likelihood function estimation to segment brain tumours. Menze et al. [10] noted that while generative models perform well in previously unseen data, it could be challenging to explicitly transform past knowledge into a suitable probabilistic model.

Alternative techniques referred to as "Deep Learning" address representation learning by automatically deriving from data a hierarchy of ever-more-complex features [11]. Consequently, the emphasis is on creating architectures rather than creating handcrafted features, which could call for specialized knowledge [12]. CNNs have been successful in a number of tasks, including medical image segmentation [13] and object recognition [14, 15]. A CNN has the benefit of being able to work with raw data and taking context into consideration because it operates over patches utilizing kernels. CNNs are also being explored in the field of brain tumour segmentation, according to recent researches presented in [16, 17].

The goal of brain tumour segmentation is to use MRI scans to automatically and precisely determine the location and size of brain tumours. While most of the current research focuses on using deep learning networks to segment

a region of interest (ROI) from an input image, classic machine learning techniques require handcrafted features to operate successfully. Even though deep learning has shown a great deal of success, these methods either depend on aggressive data augmentation approaches [19] or require vast amounts of annotated data [18]. One such system is MRNet [20]. The convolutional neural network is employed to identify anomalies connected to the knee.

When it came to classifying the three knee anomalies that were fed into the network, MRNet performed quite well. This network demonstrates how systems that can correctly identify health conditions from medical photos can be created using deep learning. The main function of the image classification system MRNet is to identify whether a given MRI picture has one of the three anomalies. The network employs logistic regression to ascertain which class the probability may belong to after computing this using an output probability.

One specific architecture meant for image categorization was called MRNet. Other network architectures, such as U-Net and V-Net, were created that could segment a ROI from an input two- or three-dimensional picture by applying comparable ideas to a convolutional neural network. Multiple convolutional layers in a convolutional neural network gradually extract the image's information using a range of kernels and pooling layers. When researchers looked into the possibility of applying deep learning architectures for advanced image segmentation, these networks were developed more actively.

LinkNet suggests a U-Net-like deep neural network design. Without significantly increasing the number of trainable/non-trainable parameters, the network facilitates learning [21]. LinkNet's lightning-fast speed, which was made possible by its lightweight architecture, was the foundation of its success. Similar to U-Net, LinkNet's architecture has at least 11.5 million parameters. Several encoder and decoder blocks gradually disassemble an image and reassemble the result through a sequence of final convolutional layers. The goal of LinkNet's architecture was to reduce the overall amount of parameters in the network. This made it possible to segment data in real time. Sample images showing the structure and position of the tumor is shown in Fig. 1

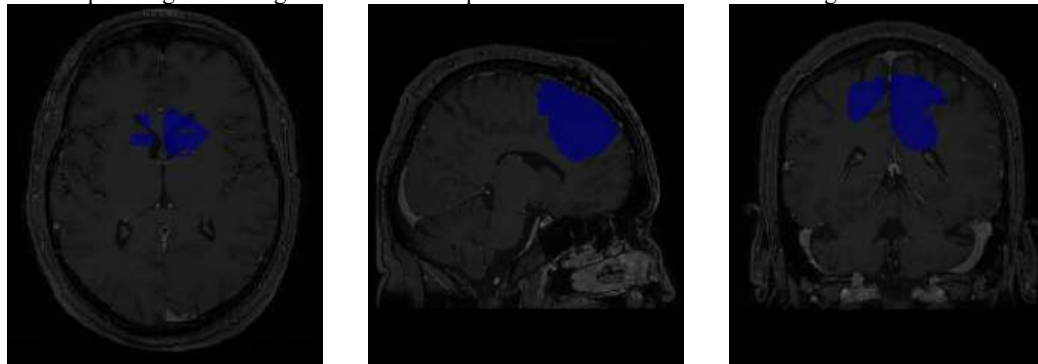


Fig. 1 Pre-operative MRI scan showing structure and location of their tumor

BACKGROUND CONCEPTS:

U-NET ARCHITECTURE

U-Net is a fully linked CNN that effectively separates images based on their semantic content. Such a U-Net deep neural network is suitable for a wide range of analytical applications. This is especially helpful in cases where the input data takes the form of images. Applications for this architecture include medical imaging, consumer movies and earth observation. An autoencoder network, which copies inputs to outputs, is the foundation of the U-Net design. By compressing the original image into a latent-space representation—basically, a compressed version of the images that shows which data points are nearest to one another—an autoencoder network may perform its function. An output is subsequently created by reconstructing the compressed data. An encoder and a decoder are the two pathways that make up an autoencoder network. While the decoder reconstructs the input data from its latent-space representation, the encoder encodes the data into a latent-space representation. Convolutional layers are employed by U-Net's convolutional autoencoder architecture to both encode and decode input images.

U-Net has two paths: a symmetric expanding path (decoder) and a contraction path (encoder), much like an autoencoder network. The U-Net encoder path, which is essentially a pipeline of convolutional and pooling layers, is responsible for capturing the image's context. Transposed convolutions are used in the decoder path to provide accurate localization. The U-Net only consists of stacks of convolutional and max-pooling layers; it lacks a fully linked feedforward layer, often known as a dense layer. While U-Net was initially created for images with a resolution of 572×572 , it may be readily adjusted to function with any image size. From the compressed input images, the network may extract more accurate features by using many stacked convolutional layers. The schematic view of U-NET model architecture is shown in Fig. 2.

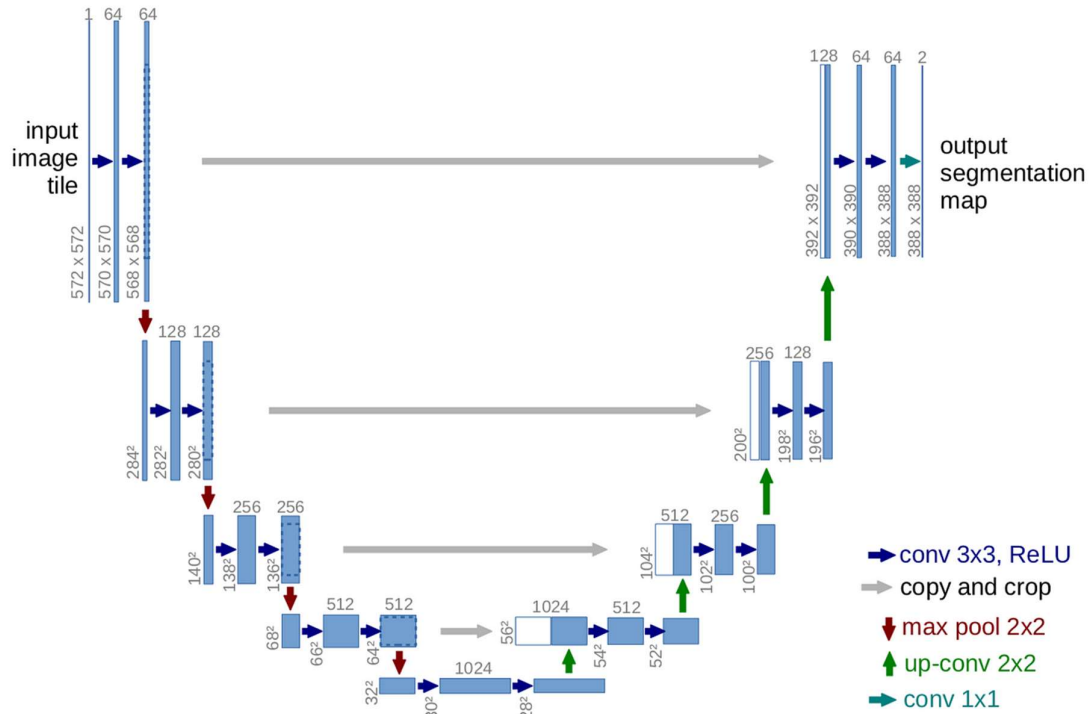


Fig. 2 Architecture of U-NET Model [22]

Multichannel feature maps are indicated by blue rectangles. It is stated above how many channels there are. Rectangles of white are used to indicate copied feature maps. The size of the feature map is displayed close to the bottom left corner. The direction of operation is shown by arrows. In order to close the gap between feature maps and the network's pathways (encoder & decoder), U-Net++, a relatively recent addition, altered the U-Net architecture to incorporate a number of layered dense skip routes [20]. It was also suggested that U-Net++ operate under deep oversight. In essence, the loss is now computed in addition to the conventional output layers at interim levels. This has been seen to assist in resolving the issue of disappearing gradients in loss backpropagation. For this network, a straightforward cost function was employed during training. The selection of binary cross-entropy loss, such as L_{BCE} , as the cost function was made because the network is only being trained to isolate the cancerous component of an input MR image. Since this loss function is a binary predictor with goal values (y_i) that can be either 1 or 0, it anticipates a sigmoid outcome ($\hat{y}_i$). Equation (1) defines L_{BCE} given the output size of N .

$$L_{BCE} = \frac{1}{N} \sum_{i=1}^N [y_i \cdot (\log \hat{y}_i) + (1 - y_i) \cdot (\log (1 - \hat{y}_i))] \quad \text{Eq. 1}$$

Metric callbacks were included to control the network's performance prior to each network beginning its training. In order to prevent the network's performance from deteriorating in the event that extreme values were added to the network's epoch range, Early Stopping and Model Checkpointing were employed. Intersection-over-union (IoU), precision, and recall were measured to track the network's performance. After extensive testing, the learning rate of 0.0001 was selected to train the model using the Adam optimizer.

PROPOSED SEGMENTATION MODEL – UNET with RESNET Encoder

The manual FLAIR abnormality segmentation masks and MR images found in the LGG Segmentation Dataset, which is accessible on the Kaggle competition platform, were employed. There are 1373 photos of brain tumours and 2556 images of no brain tumour in the dataset. This work utilizes U-net to partition brain tumours; in general, it may be thought of as an encoder followed by a decoder network. The first half of the architecture diagram is called the encoder, and it often constructed using a VGG/ResNet-style pre-trained classification network. Maxpool downsampling was used after convolution blocks to encode the input image into numerous feature representations at many levels. The decoder makes up the second half of the architecture. The encoder must conceptually project the discriminative features (lower resolution) it learnt onto the pixel space (higher resolution) in order to provide a dense classification. In the decoder, transpose convolution processes was implemented after upsampling and concatenation.

Increasing the number of deep layers in a model can deteriorate the forecast. Adding cross connections between the network's layers, which enable extensive segments to be bypassed if necessary, is a solution that has proven

to be highly successful. The loss surface that results from this resembles the picture on the right. The model may be trained with optimal weights to minimize loss much more easily. From its input, each ResBlock contains two connections: one that passes through a sequence of convolutions, batch normalization, and linear functions, while the other connection bypasses those steps. They are referred to as identity, skip, or cross connections. Both connections' tensor outputs are added together.

Every convolution operation uses 3*3 filters and the same amount of padding, therefore for every level of the contracting path and matching expanding path, the feature map's size stays constant. Boundary information is maintained and further convolutions can be added with the same amount of padding. The feature map from the contracting path does not need to be cropped in order to concatenate with the matching feature map of the expanding path because the feature size stays constant on a single level. Information is not lost when there is no cropping. There are local skip connections between convolutions on each level in addition to the long skip connections between each level of contracting and expanding routes. In addition to preventing gradient disappearance and explosion, skip connection aids in the creation of a smooth loss curve. It is extremely effective for semantic segmentation because of all these qualities. This specific design makes use of ResBlock from ResNet34. There are four downsampling and upsampling procedures over UNet's five layers. Upsampling and 2*2 convolution with half as many filters are combined to create expansion.

EXPERIMENTS & RESULTS

Brain MR images and manual FLAIR abnormality segmentation masks are included in the dataset. The Cancer Imaging Archive (TCIA) has provided the images. The images were collected from 110 individuals whose fluid-attenuated inversion recovery (FLAIR) sequencing and genomic cluster data are at least available, and who are part of The Cancer Genome Atlas (TCGA) lower-grade glioma collection.

The size of the images differed greatly amongst patients. The following operations made up the preprocessing of the image sequences:

- Cropping the image sizes to fit within a shared frame of reference.
 - Adaptive histogram equalization to normalize tissue intensities between cases based on the image histogram.
- The result of histogram equalization process is shown in Fig. 3

- Normalization of the whole data set using Z-score.

$$\min e^2 = E\{(f - f')^2\}$$

Eq. 1

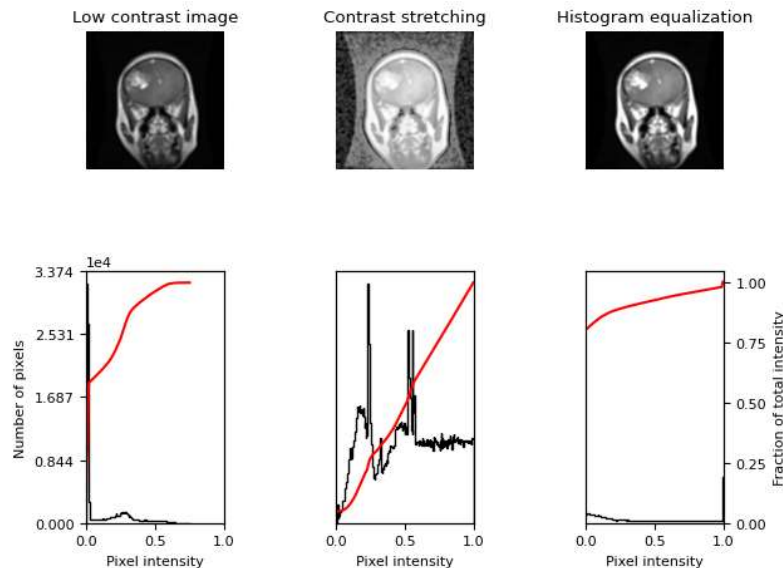


Fig. 3 Contrast enhancement using Histogram Equalization

A fully convolutional neural network with the U-Net architecture, which consists of four levels of blocks with two convolutional layers with ReLU activation function, one max pooling layer in the encoding part, and up-convolutional layers instead in the decoding part, was used to perform the primary segmentation step. Skip connections were used from the encoding levels to the equivalent layers in the decoding section in accordance with the U-Net architecture. During the training phase, they offer a shortcut for gradient flow in shallow layers. The results of the segmentation process is shown in Fig. 4 where the raw input image, binary mask (ground truth), binary mask (model predicted), raw image with ground truth highlighted, and raw image with model output highlighted were shown.

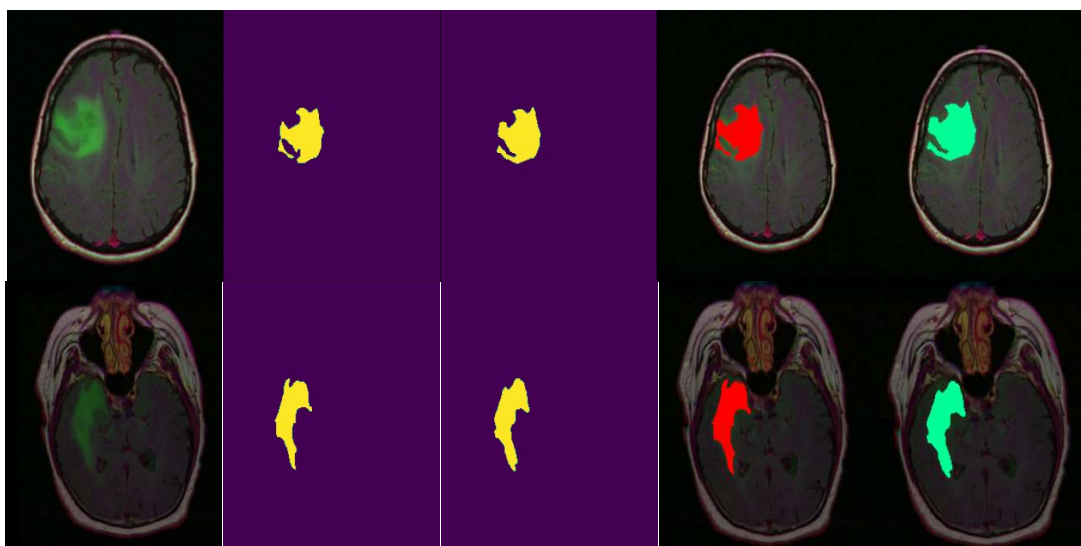


Fig. 4Results of U-Net – ResNet based model (raw image, ground truth, model output, MRI with ground truth (highlighted), MRI with model output (highlighted))

In another experiment using the same model architecture, three different segmentation models were used for segmentation of non-edema tumour area, enhancing tumour area, and entire tumour respectively. The final image was produced by merging these models' predictions. The dataset used for developing such model consists of 462 images; 335 are for training and 127 are for validation. The structure of the tumor region is presented in Fig. 5.

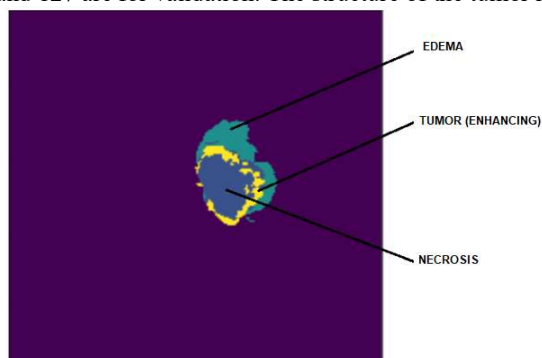


Fig. 5 Brain tumor with surrounding region

Upon closer inspection, the outcomes bear a striking resemblance to the original segmentation images. Images segmented by radiologists can be automatically segmented in a matter of seconds. For the training data, a 96% success rate and an 82% success rate were obtained. Upon analysis of the data, the Dice Coef metric yielded a success percentage of 88.2% for test data and 95.8% for the complete tumour. Success rates of 90.18% for test data and 97.1% for training were attained for the tumor-free region. Success rates of 87.9% for test data and 92.92% for training were obtained for the growing tumour area.



Fig. 6 Raw input MRI, binary, and model output

In the Fig. 6 the raw input image, corresponding binary mask, and combined output of the three different models corresponding to each region of tumor is presented.

Table 1. Performance evaluation (Dice coefficient) for three different models

Full tumor		Enhancing tumor		Tumor without edema	
Training	Testing	Training	Testing	Training	Testing

95.8%	88.2%	92.92%	87.9%	97.1%	90.18%
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The performance of the proposed U-Net + ResNet was compared with the performance of the UNet and its variants proposed in the other literature. Accurate results were obtained with an integrated neural network for medical image segmentation that leverages residual units and U-Net's advantages. With U-Net++ serving as the main network structure, the proposed architecture connects the encoder and decoder networks via redesigned skip pathways. Dense convolution blocks were used to transmit the feature map from the encoder network to the decoder network. With minimal training and validation loss, the model was able to attain better performance thanks to this network layout.

Table. 2 Comparison of UNet+ResNet with other UNet variants

Ref.No	Model	Full Tumor	Necrosis	Enhancing Tumor
[23]	U-Net	0.87	0.87	0.80
[24]	dResU-Net	0.86	0.83	0.82
-	U-Net+ResNet	0.88	0.88	0.90

CONCLUSION

This research offered a novel method for segmenting MR images that is based on the convolutional network deep learning idea. The model performance was boosted with a suitable pre-processing technique. The architecture is based on residual neural networks, which necessitates merging the output of the previous layer with the subsequent layer, skip-connections, and encoder-decoders based on ResNet architecture. In order to map the dimensions between each layer's input and output, features maps becomes essential. The advantage of skip-connections is that they identify additional and alternate pathways for the gradient and the learning process, increasing the likelihood of model convergence and avoiding the problem of disappearing gradients. After undergoing multiple training epochs, the model demonstrated dice accuracy of 0.96 in the training dataset and roughly 0.92 in the testing dataset. The model produced most accurate results (dice-coefficient – 88.2%, 87.9%, 90.18%) when used to segmentation of different tumor regions (tumor, enhancing tumor, edema).

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