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Enhanced Brain Tumor Detection and Segmentation in MRI Using Deep Transfer Learning

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Abstract*:* In the realm of medical image analysis, accurately segmenting brain tumours is crucial for precise diagnosis and treatment planning. Deep learning techniques, particularly convolutional neural networks (CNNs), have shown significant potential in automating this task. In this research paper, we propose a method that combines a "ResNet50 model with Transfer Learning" for tumour detection and a ResUnet model with a custom loss function for segmentation. To adapt the ResNet50 model to a new dataset, we leverage transfer learning techniques. This involves initializing the model's weights with pre-trained weights from a large-scale dataset such as Imagine. By harnessing the powerful feature extraction capabilities of ResNet50 and ResUnet, the model becomes adept at identifying and segmenting brain tumours from MRI images. This approach reduces training time and improves model accuracy, particularly when working with small datasets. We evaluate our proposed method using the "The Cancer Genome Atlas (TCGA)" dataset from The Cancer Imaging Archive (TCIA). To assess its performance, we compare it against other deep learning models such as DenseNet121, K-means clustering, and VGG16 for classification and segmentation tasks. Experimental results on the testing data demonstrate that our method outperforms other deep learning networks in terms of effectiveness and efficiency. Our research paper introduces a methodology that combines ResNet50 with transfer learning for tumor detection and ResUnet with a custom loss function for segmentation in brain MRI images. The results indicate that our approach is superior to alternative deep learning models, offering improved accuracy and efficiency in brain tumor segmentation tasks.

Keywords: low-grade gliomas (LGG), Magnetic Resonance Imaging (MRI), convolutional neural networks (CNNs)

1. Introduction

Gliomas, which arise from glial cells, are a prevalent type of brain tumor, accounting for approximately 40% to 50% of primary brain tumors. The World Health Organization (WHO) classifies gliomas into two categories based on their growth rate and likelihood of spreading: low-grade gliomas (LGG) and high-grade gliomas (HGG). HGG gliomas are more aggressive and malignant compared to LGG gliomas. Examples of LGG gliomas include Astrocytoma and Oligodendroglia, while Glioblastoma is the most common type of HGG glioma.

Magnetic Resonance Imaging (MRI) is a crucial diagnostic tool that enables doctors to visualize the shape, size, location, and activity of brain tumors. This information aids in treatment planning tailored to each patient. Advanced Abbreviations and Acronyms MRI techniques like diffusion-weighted imaging and perfusion-weighted imaging provide additional insights into the tumor's vascularization and cellular density, assisting in distinguishing between LGG and HGG gliomas. Timely and accurate diagnosis of gliomas is essential as it guides appropriate treatment selection, ultimately improving patient survival rates [1].

MRI plays a significant role in the diagnosis of gliomas. Standard MRI methods used for glioma diagnosis include T1-weighted MRI (T1-w), T2-weighted MRI (T2-w), T1-weighted MRI with gadolinium contrast enhancement (T1-c), and Fluid Attenuated Inversion Recovery (FLAIR). These imaging techniques provide valuable information about glioma features, location, and size, facilitating improved diagnosis and treatment planning by medical professionals.

Automated and precise segmentation of brain tumors and their sub- regions can greatly alleviate the manual labelling workload and time required by medical professionals. This approach offers a faster and more accurate alternative, enabling clinicians to diagnose and treat brain tumors with improved efficiency. However, several challenges must be addressed by researchers in this field.

Firstly, the variability in size, shape, and location of tumors poses a significant challenge for brain tumor segmentation. Achieving consistent and accurate identification and segmentation of tumor regions across different patients and images can be difficult.

Secondly, medical images, such as MRI scans, often contain noise and artefacts that can impact the accuracy of segmentation algorithms. Factors like patient motion, magnetic field in homogeneities, and imaging artifacts contribute to the presence of noise, making segmentation more challenging.

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Tumor heterogeneity is another crucial challenge in brain tumor segmentation. Tumors can exhibit complex and heterogeneous characteristics, making it challenging to precisely delineate tumor borders. Additionally, different sub-regions of a tumor may display varying degrees of contrast enhancement, edema, and necrosis, further complicating individual segmentation.

Addressing these difficulties is crucial to enhance the reliability and accuracy of brain tumor segmentation algorithms. Overcoming these challenges is essential for developing robust and precise segmentation approaches capable of handling the inherent variability and complexity of brain tumor images. Failure to address these challenges may result in inaccurate diagnoses and treatment planning, underscoring the ongoing need for research and development in this field. [1]

In MRI scans, the brain consists of white matter, gray matter, and cerebrospinal fluid, all of which can be observed. To detect brain tumors, various MRI modalities are employed, including T1, T1-contrast (T1C), T2, proton density (PD) contrast imaging, diffusion MRI (dMRI), and fluid attenuation inversion recovery (FLAIR) pulse sequences. These modalities offer a comprehensive analysis of brain tissue, enabling the identification of abnormal areas indicative of tumor presence, as well as active tumor tissue, necrosis, and edema. Glioblastomas, in particular, tend to infiltrate healthy surrounding tissue, resulting in blurred and indistinct tumor borders. However, by combining multiple MRI modalities, each tissue type's distinct characteristics can be discerned, enhancing the accuracy of tumor region identification [2].

Deep convolutional neural networks (CNNs) have shown impressive performance in medical image segmentation. In 2015, the introduction of ResNet brought a residual learning framework that enabled the training of significantly deeper networks compared to previous models. Residual networks with up to 152 layers have been evaluated on the ImageNet dataset demonstrating their depth capabilities while being less complex than VGG nets.

Prior studies have explored the use of small convolutional kernels for segmenting tumors in MRI images. This approach employed smaller filter kernels to create deeper CNNs and cascaded additional convolutional layers to achieve a similar receptive field as larger kernels. Another study introduced a complex architecture with parallel branches and two cascaded CNNs for brain tumor segmentation. The network training involved two phases, refining the last layer using samples closer to those observed in brain tumors for each class.

However, patch-based methods used in these studies have limitations such as redundancy caused by overlapping between small patches and challenges in training CNNs due to vanishing gradients. The problem of degradation arises as the network depth increases, leading to saturation in accuracy.

Overcoming these challenges is crucial to develop more efficient and effective approaches for brain tumor segmentation. Addressing issues related to redundancy and vanishing gradients can help improve the performance and training process of CNNs in this context [3][4][5].

In this paper, we introduce a novel approach for brain tumor segmentation utilizing residual networks (ResNets) with transfer learning. ResNets are a type of deep convolutional neural network known for their effectiveness in image segmentation tasks. They incorporate shortcut connections, where the output of a layer is added to its input, improving the training of deep networks. This simple modification overcomes limitations of previous techniques and enhances performance.

To train our ResNet model, we employ transfer learning. This technique leverages a model pre-trained on a large dataset, such as ImageNet, to enhance the performance of a model trained on a smaller dataset for a different task. In our case, we utilize a pre-trained ResNet model from ImageNet and fine-tune it on a dataset of brain MRI images. This transfer learning strategy improves the model's performance by leveraging the knowledge learned from the large dataset.

The structure of the paper is as follows: In Section 2, we present our proposed brain tumor segmentation algorithm based on Residual Network (ResNet) with transfer learning. The section provides a detailed description of the method. Section 3 presents the experimental results. Finally, in Section 4, we conclude the paper and discuss the findings.

2. Method

The ResNet50, originally trained on a large dataset for image recognition, is employed in this study for brain tumor detection using transfer learning. Transfer learning involves adapting the pre-trained network to the specific task at hand. In this case, the fully connected layers of ResNet50 are replaced with convolutional layers, which are then trained on a brain tumor dataset. Throughout the training process, the weights of the pre-trained layers remain unchanged, while the newly added layers are trained to identify brain tumors. By applying transfer learning with the ResNet50 model, benefits such as faster convergence and improved performance are achieved since the network has already learned relevant features for segmentation tasks.

In addition, the UNet architecture, introduced by Olag Ronneberger et al., is specifically designed for biomedical image segmentation. The architecture comprises two main components: the encoder and the decoder. The encoder consists of convolutional layers followed by pooling operations, enabling feature extraction from the image. On the other hand, the decoder employs transposed convolutions to facilitate localization. Both the encoder and the decoder are fully connected layers networks. The UNet architecture effectively segments biomedical images by utilizing the strengths of the encoder and decoder components [6].

Convolutional Neural Network Segmentation: ResNet architecture

Our proposed method utilizes a Residual Network (ResNet), which offers different variants such as ResNet-18,

ResNet-34, ResNet- 50, and more, where the number represents the number of layers. For our approach, we employ the ResNet50 model with transfer learning. Here are the details:

ResNet50 is a deep convolutional neural network model comprising 48 convolutional layers, along with 1 MaxPool layer and 1 Average Pool layer. This configuration results in approximately 3.8 x 10^9 floating-point operations.

While increasing the number of layers in deep convolutional neural networks generally improves accuracy, enhancing model performance is not as straightforward as merely adding more layers. Despite the development of techniques to mitigate issues like vanishing or exploding gradients, the problem of accuracy

saturation and rapid degradation persists even in deep neural networks with numerous layers. This issue cannot be attributed to overfitting and is observed as an increase in training error when additional layers are added to an appropriate deep model.

To address the problem of accuracy degradation, one approach is to incorporate identity layers into a shallower model. Identity layers are essentially layers that pass their input through to their output without modifying it significantly. Adding identity layers does not increase the model's complexity, and it should not lead to an increase in training error. In fact, in certain cases, incorporating identity layers can actually improve the training error. The inclusion of identity layers can help stabilize the training process and prevent overfitting.

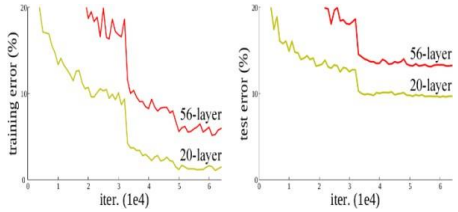


Figure 1 In the comparison between the shallower and deeper models, it can be observed from both the left and right sides that the deeper model consistently exhibits higher error rates, which is unexpected since the deeper model should not inherently perform worse.

To tackle the challenge of accuracy degradation in deep neural networks, a solution has been put forward in the form of a deep residual learning framework. This framework incorporates shortcut connections that function as identity mappings. These connections aim to counteract the problem of accuracy deterioration commonly observed in deep networks. By introducing these shortcut connections, the framework offers a way to mitigate the degradation issue and improve the performance of deep neural networks.

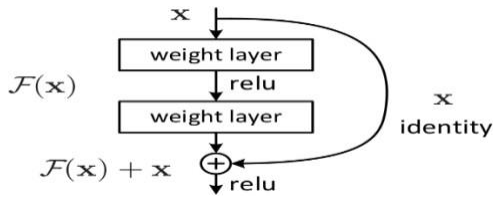


Fig 1 This is an illustration from the original ResNEt paper

To address the challenge of accuracy degradation in deep neural networks, a solution was proposed involving the training of layers to fit a residual mapping denoted as H(x). Additionally, a non- linear mapping F(x) is fitted using extra layers, such that F(x) = H(x) - x. This allows the original mapping to be expressed as

H(x) = F(x) + x, as illustrated in Figure 2.

One advantage of this approach is that it avoids the need to introduce additional parameters to the model. This helps to control computational time since shortcut identity mappings are utilized instead of incorporating extra layers with more parameters. By adopting this strategy, the problem of accuracy degradation in deep neural networks can be effectively tackled while maintaining computational efficiency.

Working on skipping connections in ResNets

To comprehend how ResNet addresses problems like vanishing and exploding gradients, it is essential to grasp the concept of skipping connections within the network. In traditional neural networks, the output of early layers is denoted as x_0, and subsequent layers perform computations based on this output.

$Z_1 = w_1x_0 + b_1$

$X_1 = \text{ReLU}(z_1)$

$Z_2 = w_2x_1 + b_2$

$X_2 = \text{ReLU}(z_2)$

By introducing a skip connection in a Residual Network, the calculations are carried out on the output of early layers as usual. However, in addition to this, the output is also bypassed through x_0 and summed with the main output before passing through the second activation function. In the case of ReLU activation, if the output z_2 is 0 and only the positive x_0 is fed into the ReLU activation, the resulting output will be equal to x_0.

$$X2 = \text{ReLU}(z2 + x0)$$

$$X2 = \text{ReLU}(0 + x0) = x0$$

By incorporating a skip connection that enables the direct passage of x_0 without undergoing computations in F(x), the operation can be represented as H(x), where x is added to the output of F(x). As the network's layer count increases, F(x) may diminish significantly or undergo alterations that hinder the network's capability to learn intricate mappings. By including x, the identity mapping of the input is embedded within F(x), offering the network a reference point for the function it needs to learn. It is important to recognize that the fundamental objective of a neural network is to uncover and comprehend a mapping.

$X \rightarrow Y$

It is possible that in some cases, the neural network may resort to utilizing identity mapping when a skip connection is introduced.

$X \rightarrow X$

The use of skip connections and residual blocks in deep neural networks allows the model to potentially bypass certain layers that may not contribute significantly to learning the problem at hand. During the backpropagation process, gradients of the loss function with respect to the weights are needed. However, to access the weights in earlier layers, gradients of the loss function with respect to the intermediate functions represented in the previous layers must also be calculated. When the final output is produced by the last activation function in the residual block and the cost J is immediately calculated, propagating the gradient back to the layers before the residual block requires calculating the gradient of the cost function with respect to x, the input to the residual block. Without the skip connection, the operation with all the intermediate steps required would be more complex and involve additional calculations. Using the chain rule, the full operation with all the intermediate steps to be performed without the skip connection looks like this [7] Deep Residual Learning for Image Recognition" by He et al. (2020).

$$\frac{\partial J}{\partial x}$$

$$\frac{\partial J}{\partial x_0} = \frac{\partial J}{\partial x_2}\frac{\partial x_2}{\partial z_2}\frac{\partial z_2}{\partial x_1}\frac{\partial x_1}{\partial z_1}\frac{\partial z_1}{\partial x_0}$$

By substituting the intermediate calculations with F(x), the process of computing gradients is now modified as follows:

When skip connections are incorporated into a neural network, an additional function H(x) = F(x) + x is introduced. During back propagation in networks with skip connections, the gradient of the cost function needs to be computed by differentiating through H(x) instead of solely through F(x) as in networks without skip connections. This is because the gradient must flow through the identity mapping established by the skip connection, which adds the input x to the output of F(x).

$$\frac{\partial J}{\partial x} = \frac{\partial J}{\partial H(x)} \frac{\partial H(x)}{\partial x}$$

By substituting F(x) + x with H(x) in the gradient calculation, we can simplify the expression. Since x has a derivative of 1 with respect to itself, the resulting expression becomes:

$$\frac{\partial J}{\partial x} = \frac{\partial J}{\partial H(x)} \left(\frac{\partial F(x)}{\partial x} + 1 \right) = \frac{\partial J}{\partial H(x)} \frac{\partial F(x)}{\partial x} + \frac{\partial J}{\partial H(x)}$$

The inclusion of skip connections in a neural network guarantees that the gradient of the cost function with respect to H(x) remains unaffected, even if the gradient of F(x) becomes exceedingly small due to multiple multiplications during back propagation through numerous layers. This characteristic allows the network to bypass certain gradient calculations during back propagation, thereby preventing the issue of vanishing or exploding gradients [8].

ResNet50 architecture

layer name	output size	18-layer	34-layer	50-layer	101-layer	152-layer
conv1	112×112	7×7, 64, stride 2				
		3×3 max pool, stride 2				
conv2_x	56×56	[3×3, 64; 3×3, 64] ×2	[3×3, 64; 3×3, 64] ×3	[1×1, 64; 3×3, 64; 1×1, 256] ×3	[1×1, 64; 3×3, 64; 1×1, 256] ×3	[1×1, 64; 3×3, 64; 1×1, 256] ×3
conv3_x	28×28	[3×3, 128; 3×3, 128] ×2	[3×3, 128; 3×3, 128] ×4	[1×1, 128; 3×3, 128; 1×1, 512] ×4	[1×1, 128; 3×3, 128; 1×1, 512] ×4	[1×1, 128; 3×3, 128; 1×1, 512] ×8
conv4_x	14×14	[3×3, 256; 3×3, 256] ×2	[3×3, 256; 3×3, 256] ×6	[1×1, 256; 3×3, 256; 1×1, 1024] ×6	[1×1, 256; 3×3, 256; 1×1, 1024] ×23	[1×1, 256; 3×3, 256; 1×1, 1024] ×36
conv5_x	7×7	[3×3, 512; 3×3, 512] ×2	[3×3, 512; 3×3, 512] ×3	[1×1, 512; 3×3, 512; 1×1, 2048] ×3	[1×1, 512; 3×3, 512; 1×1, 2048] ×3	[1×1, 512; 3×3, 512; 1×1, 2048] ×3
	1×1	average pool, 1000-d fc, softmax				
FLOPs		1.8×10^9	3.6×10^9	3.8×10^9	7.6×10^9	11.3×10^9

Our proposed method for brain tumor detection utilizes the ResNet50 architecture, as shown in Table 1. ResNet-50 is a convolutional neural network (CNN) design renowned for its ability to extract features at different abstraction levels, ranging from low-level to high-level features. This architecture, commonly employed for image classification tasks, consists of 50 layers. The ResNet50 architecture begins with a convolutional layer containing 64 filters of size 7x7, followed by a max pooling layer with a stride size of 2. This is followed by a block of three convolutional layers with filter sizes of 64, 64, and 256 respectively (sizes 1x1, 3x3, and 1x1). This block is repeated three times, resulting in a total of 9 layers.

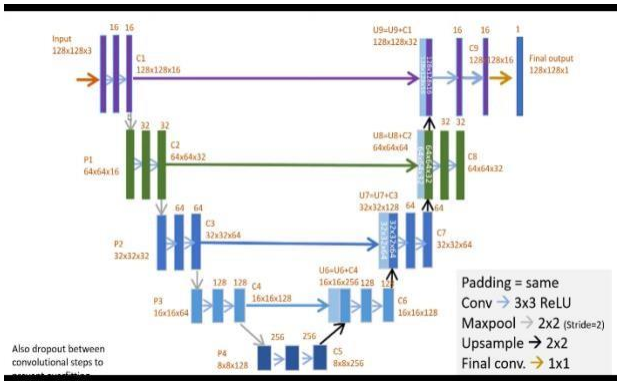
Subsequently, there is a block of four convolutional layers with filter sizes of 128, 128, and 512, repeated four times, resulting in a total of 12 layers. Following that, a block of six convolutional layers with filter sizes of 256, 256, and 1024 is repeated six times, totalling 18 layers. Finally, a block of three convolutional layers with filter sizes of 512, 512, and 2048 is repeated three times, comprising an additional 9 layers. The architecture concludes with an average pooling layer, followed by a fully connected layer with 1000 nodes, and a softmax function for classification purposes. Importantly, the ResNet50 architecture incorporates skip connections, allowing gradients to flow directly to earlier layers during back propagation. This mitigates the vanishing gradient problem and enables the network to learn more complex mappings.

Transfer Learning with Resnet50

By employing transfer learning with the ResNet-50 model, we leverage its pre-existing weights and adapt them to a new dataset specific to our tumor detection task. This approach offers several advantages, including reducing the amount of training data required and enhancing the model's accuracy. In our study, we utilized the pre-trained weights from the ImageNet dataset, which is a large-scale dataset containing millions of images and has demonstrated exceptional performance in various image recognition and classification tasks.

Pre-training the ResNet-50 model on the extensive ImageNet dataset equips the model with a robust foundation for feature extraction. The neural network has learned to capture a wide range of features from images, encompassing basic features such as edges and corners, as well as more complex features like object components and textures. These features are expected to be relevant in identifying brain tumors in MRI scans.

Furthermore, utilizing the pre-trained ResNet-50 model helps mitigate the issue of overfitting. Since the model has already learned meaningful features from the ImageNet dataset, it can effectively identify important features from the MRI images without overfitting. This aspect is particularly crucial in medical image analysis tasks where the dataset size is often limited, and overfitting poses a common challenge.



The ResUNet model is a modified version of the U-Net architecture that is well-suited for image segmentation tasks. It incorporates various layers, including convolutional layers, max-pooling layers, ReLU activation functions, concatenation layers, and up-sampling layers. The ResUNet architecture can be divided into three main sections: contraction, bottleneck, and expansion. The contraction section consists of four contraction blocks, where each block applies two 3x3 convolutional ReLU layers followed by a 2x2 max pooling operation. At each pooling layer, the number of feature maps is doubled.

The bottleneck layer comprises two 3x3 convolutional layers and a 2x2 up-convolution layer. This layer helps to compress the features while retaining the necessary information.

The expansion section is composed of several expansion blocks. Each block incorporates two 3x3 convolutional layers and a 2x2 upsampling layer, which reduces the number of feature channels by half. Additionally, the corresponding cropped feature map from the contracting path is concatenated with each block to aid in the reconstruction of detailed information.

Towards the end of the expansion section, a 1x1 convolutional layer is employed to adjust the number of feature maps to match the desired number of segments in the output.

Overall, the ResUNet model combines the strengths of contraction, bottleneck, and expansion sections to effectively perform image segmentation tasks by capturing and reconstructing detailed information.

The U-Net architecture employs the Tversky loss function for pixel-level image segmentation, enabling the identification of individual cells in the segmentation map. By applying softmax to each pixel, the segmentation problem is transformed into a classification problem, assigning each pixel to a specific class. The same approach is also utilized in the ResUNet architecture. When compared to U-Net, ResUNet demonstrates enhanced accuracy and performance in biomedical image segmentation, particularly in the context of brain tumor segmentation [9].

Implementation Details

Our implementation consists of two parts: 1) Detection using ResNet50 with transfer learning, and 2) tumor segmentation using ResUnet with a custom loss function. For the ResNet50 model, we selected the Adam optimizer and trained it for a total of 30 epochs based on previous experience [9]. The categorical cross entropy loss function was employed for this network [10]. By utilizing pre- trained weights from the ImageNet dataset, we expect to enhance both the efficiency and accuracy of the detection process.

In the case of the ResUnet model, we employed the Adam optimizer with a learning rate of 0.001 and trained it for a total of 60 epochs [11]. To perform tumor segmentation, we utilized a custom loss function based on Tversky loss, tailored to suit our specific requirements.

3. Experiment and Results

For result validation, we utilized The Cancer Genome Atlas (TCGA) dataset from The Cancer Imaging Archive (TCIA). In the case of ResNet50 with transfer learning, various metrics including accuracy, loss, confusion matrix, f1 score, recall, and precision" were employed for validation purposes. These metrics helped assess the performance and accuracy of the model.

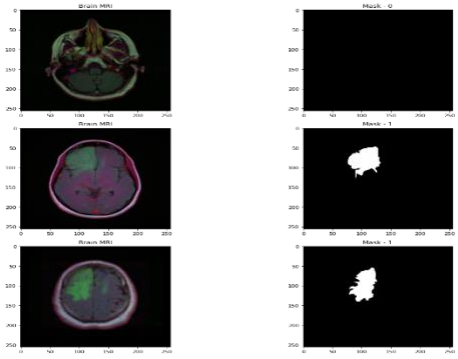


Fig 2 Brain MRI with Ground truth Tumour segmentation result

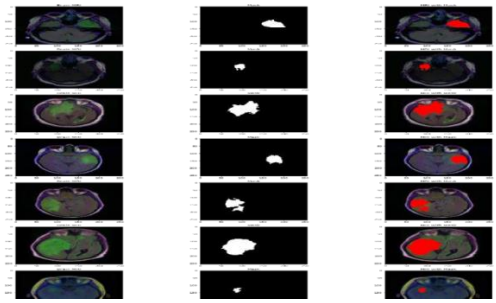
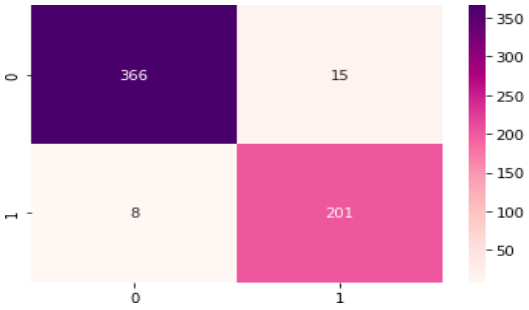


Fig 3 Brain MRI with tumor projected on the actual brain MRI for better representation



This is the confusion matrix for the resnet50 model for tumor detection.

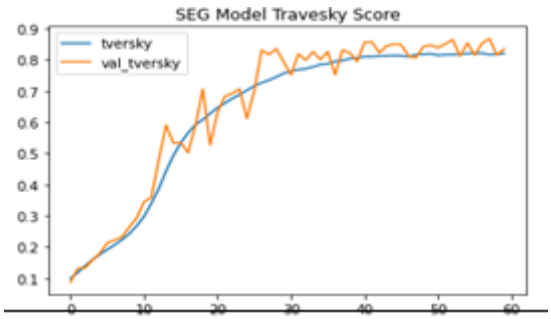


Fig 4 Segmentation model Tversky Score graph

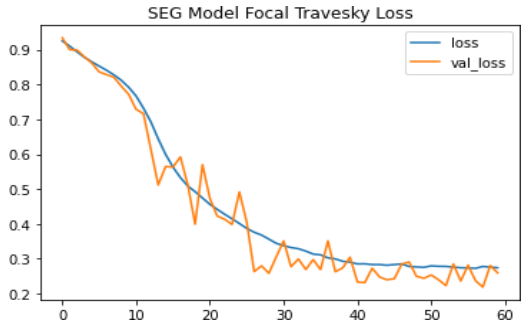


Fig 5 Segmentation model Tversky Loss graph

The graphs displayed represent the Tversky score and Tversky loss for the ResUnet model used in tumor segmentation. In Figure 10, we have presented the segmentation results achieved through our proposed method. To demonstrate the accuracy of the segmentation, we have showcased the predicted tumor mask and the actual tumor mask separately. Additionally, we have overlaid these masks onto their respective MRI images, with the original mask shown in red and the predicted mask shown in green, allowing for visual comparison and assessment.

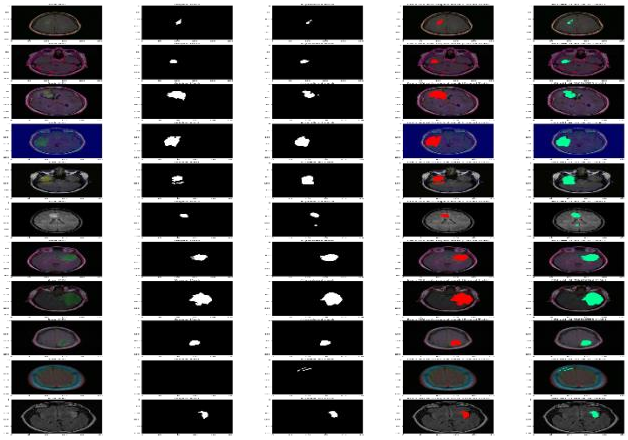


Fig 6 Final result, with predicted and actual tumor segmentation

We conducted a comparison of our results with several other popular methods for image detection and segmentation, including Densenet121, Vgg16, k-means clustering, and ResUnet (without our custom loss function). Our proposed method achieved an accuracy of 96% after training for 30 epochs. In comparison, Densenet121 achieved an accuracy of 95%, while Vgg16 achieved an accuracy of 94.08%. The ResNet50 model without transfer learning achieved an accuracy of 95.08%.

For the segmentation task using ResUnet, our proposed method resulted in a loss of 27.44%. In contrast, the ResUnet model without the custom loss function had a higher loss of 29.22%. Additionally, a simple U-net model produced a loss of 29.33%. These findings indicate that our proposed model outperformed the other methods in terms of accuracy, loss, and power efficiency.

4. Conclusion

In this research paper, we propose an approach for brain tumor detection and segmentation utilizing ResNet50 with transfer learning and ResU-Net with a custom loss function. Our approach incorporates multi-modal data during network training. The experimental results demonstrate the superiority of our approach compared to other deep networks. To elaborate, our approach begins by employing ResNet50 to extract features from MRI images. Subsequently, ResU-Net is utilized for tumor segmentation, and a custom loss function is employed to train ResU-Net. The custom loss function is specifically designed to enhance output stability and segmentation accuracy. The evaluation of our approach is conducted on a dataset of MRI images, demonstrating accurate tumor detection and segmentation. Notably, our approach outperforms other deep networks, such as U-Net and V-Net. Looking ahead, our future work involves integrating 3D U-Net, 3D ResU-Net, and 3D level set methods to further enhance the performance of our approach.

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Author contributions

Author Contributions: All authors contributed to the conception, design, and accuracy of the study. Together they developed the methodology, conducted the experiments, analyzed the data, and interpreted the results. In addition, they jointly contributed to drafting and revising the manuscript.

Conflicts of interest

The authors declare no conflicts of interest.

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