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RESEARCH ARTICLE

Brain Tumor Segmentation Using Generative Adversarial Networks

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ABSTRACT Deep learning has played a vital role in advancing medical research, particularly in brain tumor segmentation. Despite using numerous deep learning algorithms for this purpose, accurately and reliably segmenting brain tumors remains a significant challenge. Segmentation of precise tumors is essential for the effective treatment of brain diseases. While deep learning offers a range of algorithms for segmentation, they still face limitations when analyzing medical images due to the variations in tumor shape, size, and location. This study proposes a deep learning approach combining a Generative Adversarial Network (GAN) with transfer learning and auto-encoder techniques to enhance brain tumor segmentation. The GAN incorporates a generator and discriminator to generate superior segmentation outcomes. In the generator, we applied downsampling and upsampling for tumor segmentation. In addition, an auto-encoder is applied in which the encoder retains as much information as possible and then the decoder with those encodings reconstructs the image. The transfer learning technique is applied at the bottleneck using the DenseNet model. Combining auto-encoder techniques with transfer learning methodologies in GANs feature learning is enhanced, training time is reduced, and stability is increased. In this work, we enhanced the accuracy of brain tumor segmentation and even achieved better results for tumors having small sizes. We train and evaluate our proposed model using the publicly available BraTS 2021 dataset. The experimental result shows a dice score of 0.94 for the whole tumor, 0.86 for the tumor core, and 0.82 for the enhancing tumor. It is also shown that we achieve 2% to 4% higher accuracy than other methods.

INDEX TERMS Deep learning, GAN, auto-encoder, up sampling, down sampling, transfer learning, BraTS, DenseNet.

I. INTRODUCTION

Image segmentation is used to segment and classify different objects in an image. In image segmentation, we assign a label to a certain area in an image to get meaningful information. The procedure entails dividing an image into numerous segments and components to comprehend different important details contained within it. This plays a vital function in various applications like video monitoring, examination of medical visuals, enhanced reality, and self-driving cars, among other examples [1].

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Different techniques and algorithms have been developed for image segmentation for different problems like object detection, disease detection, video surveillance, etc. Early traditional techniques were developed for image segmentation like thresholding [2], histogram-based, region growing [3], watershed [4], clustering [5]. Then the technology advanced and some new methods were developed like sparsity-based [6], Markov random field [7], active contours [8] and graph cuts [9]. In recent years Deep Learning (DL) models have been developed with performance improvements and higher accuracy for image segmentation. These models include fully convolutional networks (CNN) [10], encoder-decoder-based models [11], multiscale and pyramid-based

models [12], recurrent neural network (RNN) based models [13] and generative adversarial network (GAN) training models [14] etc.

Medical imaging heavily relies on image segmentation, an essential element that enables healthcare practitioners to pinpoint and separate distinct elements within medical images. This process of dividing images into various regions of interest empowers researchers to gauge the dimensions of organs or anomalies, identify irregularities, and enhance comprehension of physiological mechanisms occurring within the human body. Within the realm of medical science, image segmentation holds particular significance in the domains of diagnosis, treatment preparation, and monitoring of therapies. With advancements in artificial intelligence and machine learning algorithms, computer-aided image segmentation has now become ubiquitous in medical imaging applications such as radiology and pathology. This technology also improves the speed and accuracy of diagnosis while reducing human error substantially.

Similarly, brain tumor disease is also one of the most dangerous diseases. It is important to detect brain tumor at early stage so it can be diagnose immediately. A brain tumor is shown in Figure 1. The diagnosis of brain-related diseases like Parkinson's disease, Alzheimer's disease, and brain tumor is very important in brain imaging. A report published by the American Cancer Society and National Cancer Institute brain cancer is the tenth most dangerous disease that causes death. In only America 18,090 deaths and 23,890 new cases were reported due to brain cancer in 2020 [15]. Therefore, early detection of brain tumors using the latest brain imaging techniques is very important so that it can be diagnosed at an early stage.

There are four types of brain tumors edema, necrosis, enhancing tumor, and non-enhancing tumor. For diagnosis and treatment, it is important to detect tumors accurately. Segmentation of brain tumors is performed for the accurate treatment planning of tumor-related disease. Due to its size, shape, and location, it is difficult to segment brain tumor [16]. Segmenting out the type of brain tumor from an image is also still a challenging task. For the better treatment of brain tumor, it is necessary to segment brain tumor and its type accurately.

Manual segmentation is still widely used for tumor segmentation as it is still more reliable but it is a tedious task. In the medical field automatic segmentation has played an important role that saves time and produces better results. From many years of development on automatic segmentation of brain tumors carried out with traditional machine learning algorithms. For automatic segmentation deep neural network achieved great success and is widely used for image segmentation in the medical field [17] but it still lacks in producing better segmentation results and limits the accuracy of the final output.

In contrast, deep learning methods depend on the availability of large-scale datasets for training and typically necessitate fewer preprocessing steps compared to traditional

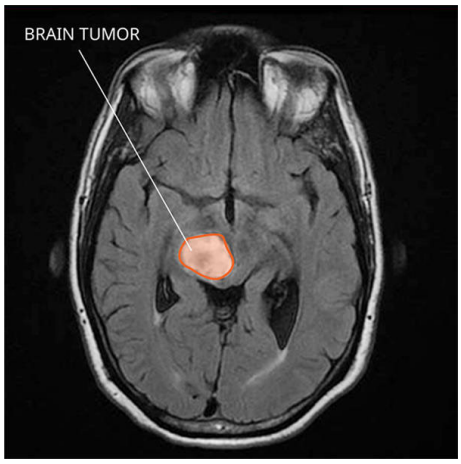


FIGURE 1. Brain tumor.

approaches. In recent years, convolutional neural networks (CNNs) have emerged as the predominant technique in the field of brain tumor segmentation [18]. Alom et al. [19] provides a detailed review of deep learning approaches that span across many application domains. Early studies [20], [21] identified deep learning as a promising approach for automating brain tumor segmentation. With deep learning, complex features are learned hierarchically from specific domain data, eliminating the requirement for feature engineering typical in other automated segmentation techniques. Therefore, the emphasis would be on designing network architectures and refining them specifically for the task at hand. Deep learning techniques have gained prominence due to their revolutionary performance in computer vision tasks. However, within the medical domain, there are typically insufficient training samples to effectively train deep models without encountering overfitting. Additionally, annotating ground truth for three-dimensional (3D) MRI scans is a time-consuming and specialized task typically handled by experts such as neurologists. Consequently, publicly accessible image datasets are scarce and often contain only a limited number of subjects.

In deep learning we have another technique named Generative Adversarial Network (GAN) that can be used for image segmentation to get better results [14]. Generative Adversarial Networks (GANs) have gained popularity in medical image analysis, including brain tumor segmentation. GANs consist of a generator network and a discriminator network. The generator network produces fake samples, while the discriminator network distinguishes between real and fake samples. Through training, the generator network learns to generate samples indistinguishable from real ones, while the discriminator network learns to correctly classify between the two [22], [23], [24], [25], [26].

In our proposed method, we focused on brain tumor segmentation. For this, we used GAN architecture having transfer learning with auto-encoder. In the generator part, we applied the transfer learning technique. In transfer learning we use already trained models for our own research

with some changing like adding extra layers, tweaks with the hyperparameters, etc. We also used auto-encoder with transfer learning so that we have minimum loss in data. The function of auto-encoder is when we are down sampling an image we will be losing some important information. With the use of an auto-encoder, we will be able to minimize the loss of this information. For training and testing, we used the publicly available BraTS 2021 dataset. This dataset contains images of brain tumor categorizing them as whole tumor, tumor core, and enhancing tumor. This is an edition of the BraTS dataset family and is the latest version. Our study shows that our model performed outclass for brain tumor segmentation.

The main contribution of our proposed work is described below:-

- GANs have demonstrated promising results for brain tumor segmentation by effectively handling variations in tumor size, shape, and location. By leveraging GANs in conjunction with transfer learning techniques, we show that it is possible to achieve higher accuracy rates in the segmentation of small tumors, even with limited training datasets.
- The integration of GANs with auto-encoders (VAEs) enhances the retention of tumor features with varying sizes, shapes, and locations. The encoder within the auto-encoder learns effective data encoding while down-sampling, preserving as much relevant information as possible. The decoder then reconstructs the full image from the encoding during upsampling, contributing to improved segmentation quality.
- Combining auto-encoder techniques with transfer learning methodologies in GANs results in superior performance compared to previous GAN models. This approach enhances feature learning, reduces training time, and increases model stability. Auto-encoders help in learning more effective data representations, while transfer learning facilitates efficient training on limited datasets, thereby achieving lower computational complexity.

The following is the structure of our paper: Section II describes the existing deep learning and GAN approaches that are already used by other researchers. Section III explains the methodology we have used in our research work. Section IV describes the experimental setup. Section V describes the results and discussion. Section VI gives a conclusion and future work followed by the references.

II. LITERATURE REVIEW

In recent years much work has been done for the segmentation of brain tumor using deep learning approaches. To show the importance of automatic segmentation of brain tumor the findings of this research need to be discussed here.

Rajendran et al. [27] used a Gray Level Co-occurrence Matrix (GLCM) feature extraction technique to eliminate unnecessary image details. Compared to the current state-of-the-art methods, the accuracy of brain tumor segmentation has been significantly enhanced using Convolutional Neural Networks (CNNs), widely utilized in biomedical image segmentation. By integrating outcomes from two separate segmentation networks, the proposed approach introduces a straightforward yet impactful combinatorial strategy that results in more precise and comprehensive estimations. Specifically, a U-Net and a Three-Dimensional Convolutional Neural Network (3D CNN) are employed to partition images into their constituent components. Subsequently, predictions are generated by leveraging two distinct models combined through various methodologies.

Jabbar et al. [28] introduced the Caps-VGGNet hybrid model, which combines the CapsNet and VGGNet models by incorporating VGGNet layers. This integrated model tackles the challenge of needing extensive datasets by autonomously extracting and categorizing features. The model's performance was evaluated using the Brats-2020 and Brats-2019 datasets, which feature high-resolution images of brain tumors. Comparative analysis with other traditional and hybrid models demonstrates that the proposed model achieved superior effectiveness, boasting higher accuracy, specificity, and sensitivity.

Karim et al. [29] examines the current landscape of brain tumor segmentation (BTS) through an exploration of emerging deep learning (DL) techniques applied to brain MRI analysis. The research provides a comprehensive comparison of recent DL methods, highlighting their effectiveness in addressing various types of tumors while mitigating challenges such as limited data availability and the need for robust validation. DL has significantly advanced BTS, with a primary emphasis on integrating robust DL models for brain MRI analysis. Despite outperforming traditional methods, DL encounters several challenges, particularly concerning the diversity of tumor types, insufficient datasets, and inadequate validation practices. Looking forward, DL-based BTS holds promising prospects for transforming the diagnosis and treatment of brain tumors.

The rise of automation represents a significant opportunity, aiming to enhance efficiency and afford medical professionals more time to dedicate to direct patient care. Traditional machine learning methods have traditionally relied on intensive feature engineering efforts. Vinod et al. [30] proposed a novel approach: an ensemble technique combining the U-Net model, a Convolutional Neural Network (CNN), and a Self-Organizing Feature Map (SOFM) for accurate segmentation of brain tumors using the BRATS 2020 dataset. Our assessment not only emphasizes segmentation accuracy but also leverages critical survival data from the dataset to predict patient survival rates.

Majib et al. [31] explore various traditional and hybrid machine learning models extensively constructed and analyzed to autonomously classify brain tumor images. Additionally, 16 distinct transfer learning models were evaluated to determine the optimal one for brain tumor classification using neural networks. Finally, employing state-of-the-art technologies, a stacked classifier VGG-SCNet (VGG Stacked

Classifier Network) was introduced that demonstrated superior performance compared to all other models developed in the study.

Ottom et al. [32] introduces an innovative framework for segmenting 2D brain tumors in MR images through the application of deep neural networks (DNN) and employing data augmentation techniques. The proposed method (Znet) utilizes skip connections, encoder-decoder architectures, and data amplification to extend the inherent characteristics observed in a smaller dataset of expert-delineated tumors such as those from hundreds of patients with low-grade glioma (LGG) to a much larger set comprising thousands of synthetic cases. The outcomes and visual representation of the DNN-generated tumor masks in the test dataset demonstrate the ZNet model's ability to accurately detect and segment brain tumors in MR images. This methodology can be extended to encompass 3D brain volumes, various pathologies, and a diverse array of imaging modalities.

Musallam et al. [33] introduces a three-step preprocessing method aimed at improving the quality of MRI images, coupled with a novel Deep Convolutional Neural Network (DCNN) architecture designed for accurate diagnosis of glioma, meningioma, and pituitary tumors. The architecture incorporates batch normalization to expedite training with higher learning rates and simplify the initialization of layer weights. It is characterized by a computationally efficient design, featuring a modest number of convolutional and max-pooling layers, as well as training iterations.

Lv et al. [34] presented three innovative applications that were investigated using parallel imaging in conjunction with the GAN model (PI-GAN) and transfer learning. Initially, the model was pre-trained using publicly available brain images from Calgary, and subsequently fine-tuned for 1) patients with tumors at our institution, 2) Various anatomical sites such as the knee and liver, and 3) Different k-space sampling masks with acceleration factors (AFs) of 2 and 6. Regarding the brain tumor dataset, transfer learning effectively addressed artifacts observed in PI-GAN, resulting in smoother brain edges. Transfer learning also demonstrated superior performance for knee and liver datasets compared to the PI-GAN model trained on its own dataset with fewer cases. Notably, convergence in the knee datasets was slower than in brain tumor datasets during the learning process. Transfer learning notably enhanced reconstruction performance for both AFs of 2 and 6, with better outcomes observed for the model with AF $= 2$.

Tokuoka et al. [35] proposed an inductive transfer learning (ITL) approach that utilizes annotation labels from source domain datasets to enhance tasks in target domain datasets through Cycle-GAN-based unsupervised domain adaptation (UDA). To demonstrate the effectiveness of the ITL approach, they applied brain tissue annotation labels from a source domain dataset of Magnetic Resonance Imaging (MRI) images to improve brain tumor segmentation on a target domain MRI dataset. The results show a significant enhancement in the accuracy of brain tumor segmentation. This ITL framework represents a significant advancement in medical image analysis, providing a foundational tool to enhance and facilitate various tasks using medical images.

Peiris et al. [36] utilized adversarial learning techniques to conduct brain tumor segmentation on MR images, specifically using the BraTS 2021 dataset. In their proposed methodology they used an architecture consisting of segmentation, critic, and Virtual Adversarial Training (VAT) networks. In segmentation up-sampling and down-sampling were performed. In critic fully convolutional adversarial network was constructed to predict the segmentation similar to ground truth. The VAT produces adversarial examples do that new patient data can also be predicted accurately. The result shows 90% accuracy on the whole tumor (WT), 85% on tumor core (TC), and 81% on enhanced tumor (ET).

Fawzi et al. [37] conducted a comprehensive examination of different approaches utilized for the segmentation of brain tumors. They compared machine learning, deep learning, and hybrid approaches for segmenting brain tumors in their review. They discovered via their research that hybrid and deep learning techniques are effective at segmenting brain tumors and producing superior outcomes, however, these techniques have computational and memory complexity issues.

Skandarani et al. [38] presented a review paper on applications of GAN in medical images. In their research, they used different GAN architectures like DCGAN, LSGAN, WGAN, StyleGAN, HingeGAN, etc on three different datasets SLiver07, ACDC and IDRID. They applied different GAN architectures on these datasets and found that GAN performed better on these medical image syntheses.

Ngo et al. [39] proposed a CNN architecture with a multi-task learning approach to identify and segment small tumors. In their study they mainly focused on enhancing tumor as they are very small in size as compared to other tumors. When sampling, they incorporate additional feature reconstruction work as a complement to retain key features. For their experiment they used BraTS 2018 dataset and achieved accuracy of 81% on ET, 89% on WT and 84% on TC.

Cirillo et al. [40] proposed a 3D GAN architecture called Vox2Vox for segmentation of brain tumor. Their architecture contains a generator and discriminator. The generator was built as a U-Net which consists of Input (I), Encoder (E), Bottleneck (B), Decoder (D), and Output (O). Images were an input, 3D convolutional layers with padding and Leaky Relu function as encoder, 3D convolutional layers with Leaky Relu function as a bottleneck, 3D transpose convolutional layers with Relu function as decoder and segmented prediction as output. The discriminator consists of Input (I), Encoder (E), and Output (O). In a discriminator image with its generator segmented prediction as input, an encoder is the same as the generator and outputs the quality segmented prediction generated by the generator. For their research they used BraTS 2018 dataset and achieved an accuracy of 90% on WT, 82% on TC, and 78% on ET.

Zhang et al. [41] proposed an architecture for the segmentation of brain tumor called AResU-Net. In their proposed methodology they embedded residual blocks to existing U-Net architecture. In the encoder, they used three residual blocks with a convolutional layer at the end with a dropout function. In the decoder, three up-sampling residual blocks are used. At last, they integrated the softmax layer for final segmentation. They performed their research on two datasets BraTS 2017 and BraTS 2018. On BraTS 2017 they achieved an accuracy of 89% on WT, 85% on TC, and 82% on ET whereas on BraTS 2018 dataset, they achieved an accuracy of 87% on WT, 81% on TC, and 77% on ET.

Nema et al. [42] proposed a model called RescueNet. In their proposed architecture they used both residual and mirroring concepts. It consists of an encoder and a decoder. In encoder it has convolutional layers with a normalization layer and ReLU activation function. Following this, a residual block, which includes a max pooling layer, is employed. In the decoder, it has a deconvolutional layer to up-sample the data. They performed their research on BraTS 2015 and BraTS 2017 datasets. They achieved accuracy of 94% on WT, 94% on TC and 87% on ET.

Chen et al. [43] introduced an enhanced version of Deep Convolutional Neural Network (DCNN) called Deep Convolutional Symmetric Neural Network (DCSNN) to segment brain tumors. The primary objective of the simple DCNN was to enhance the quality of feature extraction from an image. A symmetric mask was added to simple DCNN to extract more low-level features from an image. BraTS 2015 dataset was used by the researchers for their study. They achieved accuracy of 84% on WT, 68% on TC and 58% on ET.

Li et al. [44] suggested a method for segmenting brain tumors using an adversarial network, which consisted of a basic Generative Adversarial Network (GAN). The generator utilized a standard convolutional neural network with a feed-forward neural network, while the discriminator was also a conventional convolutional neural network that analyzed MR images alongside the segmented images produced by the generator. They used the BraTS 2017 dataset for their research work. They achieved accuracy of 88% on WT, 87% on TC and 77% on ET.

Pereira et al. [45] presented an adaptive feature segmentation method for segmenting brain tumor. The architecture contains a regular block of convolutional layers, residual connections, and pre-activation. Then they used recombination and recalibration of feature maps for segmentation purposes. They used BraTS 2013 and BraTS 2017 datasets for their experiment. On BraTS 2017 dataset the achieved accuracy of 88% on WT, 76% on TC and 69% on ET. Whereas on BraTS 2013 dataset 87% on WT, 83% on TC and 77% on ET.

Iqbal et al. [46] presented three distinct extended SegNet (deep convolution encoder-decoder architecture)-based enhanced network designs for intratumor segmentation: Interpolated Network, SkipNet, and SE-Net are listed in that order. Four sub-blocks were employed in each step of the decoder/encoder architecture, which was shared by all three structures. The training phase's stability and the disappearance or extension of convolutional gradients were both protected by the placement of a batch of normalisation layers adjacent to each convolution. However, this method has a limitation: if the model is trained with only a few ground truth samples, the segmentation quality may decrease. Nonetheless, this approach has the advantage of efficiently building a model quickly and with minimal memory usage by utilizing intermediary convolutional maps and interpolation techniques.

Cui et al. [47] introduced a deep convolutional neural network (DCNN) architecture that automatically divides 2D brain images into two distinct halves. They employed a pixel-wise fully convolutional network (FCN) to rapidly determine the tumor location in MR images, and then utilized a patch-wise CNN with smaller kernels and a deeper architecture to partition the limited tumor zone into sub-regions. Their hybrid CNN approach addressed the issue of unbalanced data. However, their method required time-consuming inference for processing the image patches during model training.

Chen et al. [43] presented a DCNN combined with prior knowledge to enhance the detection of brain tumor sub-compartments. They used a left-right similarity mask (LRSM) in the feature space to determine the placement weight of DCNN features. These features were then used to train the model to identify the asymmetrical position information of input images. This method improved the overall tumor segmentation by approximately 3.6% in terms of the dice similarity coefficient (DSC). It allowed the application of location weights to collect features using symmetric masks across multiple DCNN layers. However, it couldn't differentiate between the tumor core areas and the enlarged tumor region.

Xue et al. [48] proposed a complete adversarial network for segmenting brain tumors from MRI scan data. Their network consisted of a segmenter (generator) acting as an FCNN to produce segmentation label maps and a critic network (discriminator) with multi-scale L1 loss. The segmenter and critic networks were trained alternately in a min-max manner. Although this approach improved the learning of tumor characteristics, it required substantial processing resources for tumor labeling in MR images.

Myronenko [49] utilized an asymmetrical big encoder and decoder structure with a decoder to reconstruct dense segmentation masks. They addressed the issue of a small training dataset by adding a variational auto-encoder to the encoder's endpoint, and they reconstructed the input image together with segmentation to regularize the shared encoder at inference time. This model provided accurate intratumor segmentation without the need for ground truth labels or post-processing. However, it required substantial processing resources for tumor labeling in MR images.

Baid et al. [50] presented a fully autonomous segmentation of brain tumors using a novel 3D U-Net architecture

combined with weighted patch extraction. They proposed a weighted patch-based segmentation technique to address the class imbalance between tumor and non-tumorous patches. The architecture was trained using a unique set of feature maps and a 3D weighted patch-based methodology, enabling accurate segmentation of intra-tumor structures. They also employed a post-processing method called 3D-linked component analysis to improve tumor delineation. However, the method faced challenges in separating some tumor portions from MR images that included a small necrotic tumor cavity, and it required more training data to overcome inter-patient variances.

Zhou et al. [51] proposed a novel three-phase architecture for the automated segmentation of brain tumors from 3D MR images. They utilized a dense three-dimensional networking architecture to create reusable features and introduced a feature pyramid module to integrate multiscale contexts. Additionally, they implemented a supervisory 3D deep mechanism with auxiliary components to enhance the segmentation process.

Sun et al. [52] presented a method with multiple path 3D FCN model for segmenting brain tumors in a different research. Using 3D dilated convolution in each route, from multi-modal MR images, it extracts different receptive fields of feature maps and spatially integrates these features via skip connections. This paradigm makes it easier for this model to identify the limits of tumor areas. Nevertheless, the model needs a postprocessing phase since the difference in semantics between encoders and decoders and direct links between high-level and low-level characteristics would have unexpected results.

Ramzan et al. [53] suggested an efficient mapping of brain tissue segments to voxel-levels from MR volumes. In their approach, they used a 3D CNN that utilizes skip connection, residual learning concepts and dilated convolutions. By employing dilated convolutions to calculate spatial attributes at a high resolution, the computational cost was decreased. In this model, the spatial complexity was higher due to the usage of dilated convolution.

Hu et al. [54] proposed the integration of the multi-cascade convolutional neural network (MCCNN) with CRFs for the sub-region segmentation of brain tumors. In order to account for local label dependency and the usage of multi-scale features for coarse segmentation as the first stage of the segmentation process, which requires two phases, a multi-cascade network architecture was proposed. Second, by preserving the spatial contextual information of tumor edges and eliminating false positives, CRFs were used to improve segmentation findings. With minimal training data and computational complexity, the approach effectively segmented entire tumors using 2D patches taken from the Flair, T1c, and T2 modalities. The segmentation effectiveness for augmenting tumors and tumor cores, which are lower in size than entire tumors, might be impacted by this approach's sample imbalance problem.

In a more recent work, Zhou et al. [55] presented the 3D DCNN in combination with 3D atrous convolution filters (AFPNet) for intra-tumor segmentation. In addition to enhancing the learning characteristics of brain tumors, the combination of approaches intended to prevent spatial information loss brought on by the striding and pooling operations of conventional DCNNs. An atrous convolution feature pyramid was built by applying the 3D atrous convolution layers at various atrous speeds. Then, to carry out additional structural segmentation, a 3D fully connected CRF was used as the post-processing step. Notwithstanding the benefits, the method has certain drawbacks, such as the ineffective segmentation of microscopic lesion tissue. As a result, compared to total tumor segmentation, it has a comparatively poor segmentation rate for augmenting and core tumor areas. It also needs a post-processing step to improve segmentation even further.

Mahesh and Renjit [56] proposed the FJODCNN method, an automated segmentation and tumor severity level classification technique based on PSO for tumor segmentation and meta-classifiers for glioma severity analysis. There are three key steps in the model: Initially, using the PSO as a clustering technique, the core and edema areas were segmented. Following the extraction of the features from these areas, the features were then optimized by the fractional Jaya optimizer method before the classification was completed using the DCNN. With PSO-based segmentation, however, no qualitative or quantitative results were found.

One popular approach is to use machine learning algorithms such as convolutional neural networks (CNNs) to segment brain tumors. These algorithms use a large amount of labeled data to learn the features of brain tumors and then use this knowledge to segment new images. For example, the U-Net architecture is a widely used CNN for medical image segmentation that has shown promising results in segmenting brain tumors [57]. The U-Net architecture consists of a contracting path that captures context and a symmetric expanding path that enables precise localization.

VAE-GANs for brain tumor segmentation are presented in the work of Li et al. [58], where they proposed a VAE-GAN-based method for segmenting small gliomas. They used a dataset of 50 patients with low-grade gliomas and trained their model on patches of size $64 \times 64 \times 64$. Their results showed that the proposed method achieved better segmentation accuracy and generalization performance than other state-of-the-art methods.

Several studies have explored the use of GANs for brain tumor segmentation. For example, a recent study proposed a GAN-based approach for brain tumor segmentation that uses a 3D U-Net as the generator network and a 3D convolutional neural network (CNN) as the discriminator network [59], [60], [61]. The 3D U-Net is used to generate a segmentation mask for the input image, and the 3D CNN is used to

TABLE 1. Comparison of existing research.

Author	Techniques/Approaches	Dataset	Results/Accuracy
Peiris et al. (2022)	Employed adversarial learning methods to perform segmentation of brain tumors.	BraTS 2021	WT = 0.90 TC = 0.85 ET = 0.81
Fawzi et al. (2021)	Presented a critical review of a recent segmentation task using different techniques.	As it is a review paper no dataset was needed.	Deep learning and hybrid methods are efficient methods for brain tumor segmentation but still lacks computation and memory complexity.
Li et al. (2021)	Utilized a 3D GAN to segment brain tumors. Altered U-Net model with dense block.	BraTS 2017	WT = 0.90 TC = 0.78 ET = 0.68
Skandarani et al. (2021)	Performed a multi-GAN study to find the benefits of GAN in medical images.	Silver07, ACDC and IDRID	The results show that GANs are better for medical image synthesis.
Ngo et al. (2020)	CNN architecture with multi-task learning for extracting features like small tumor.	BraTS 2018	WT = 0.89 TC = 0.84 ET = 0.81
Domenico et al. (2020)	Proposed 3D volume to volume GAN called Vox2Vox.	BraTS 2020	WT = 0.90 TC = 0.82 ET = 0.78
Zhang et al. (2020)	Architecture called AResU-Net, which employs 2D attention and residual connections, to enable end-to-end processing.	BraTS 2017 and BraTS 2018	WT (2017) = 0.88 TC (2017) = 0.78 ET (2017) = 0.72 WT (2018) = 0.87 TC (2018) = 0.81 ET (2018) = 0.77
Nema et al. (2020)	An unpaired encoder-decoder network called RescueNet was proposed that uses mirroring and residual principles to segment the WT in brain MRI images.	BraTS 2015 and BraTS 2017	WT (2015) = 0.90 TC (2015) = 0.87 ET (2015) = 0.80 WT (2017) = 0.90 TC (2017) = 0.85 ET (2017) = 0.77
Chen et al. (2020)	Extended the DCNN segmentation method with symmetric masks and proposed a new method called the DCSNN segmentation method.	BraTS 2015	WT = 0.85 TC = 0.68 ET = 0.58
Li et al. (2017)	Adversarial approach in which the discriminator and generator are trained to produce artificial segmentation results.	BraTS 2017	WT = 0.87 TC = 0.72 ET = 0.68
Pereira et al. (2018)	Approach for segmentation using compression and linear expansion for the semantic segmentation.	BraTS 2013 and BraTS 2017	WT (2013) = 0.89 TC (2013) = 0.84 ET (2013) = 0.78 WT (2017) = 0.88 TC (2017) = 0.77 ET (2017) = 0.72

classify between real and generated segmentation masks. The two networks are trained simultaneously, with the objective of generating segmentation masks that are indistinguishable from real segmentation masks.

Here are some previous works and their study or results in given Table 1. In the table WT represents the whole tumor, TC represents the tumor core, and ET represents the enhancing tumor.

In our literature review, we explored research papers regarding deep learning and GAN in brain tumor segmentation. We found that traditional deep learning approaches are widely used but the problem with these traditional approaches is that they lack memory and computational complexities. We also found that the already work done is mainly focused on improving accuracy of overall tumors. Very few papers worked on small tumors, but they also lack higher accuracy. So, to overcome this issue a deep learning approach GAN can be used.

III. METHODOLOGY

In our research, we proposed another deep learning algorithm Generative Adversarial Network (GAN) with transfer learning and auto-encoder for better segmentation. GAN is used for transforming low-resolution images into high-resolution images. GAN uses a generator and discriminator to produce better segmentation results for a brain tumor. GAN architecture consists of fully connected dense layers for segmentation.

In this section, we will discuss our proposed model for brain tumor segmentation. Our proposed model is based on the GAN architecture that uses auto-encoder and transfer

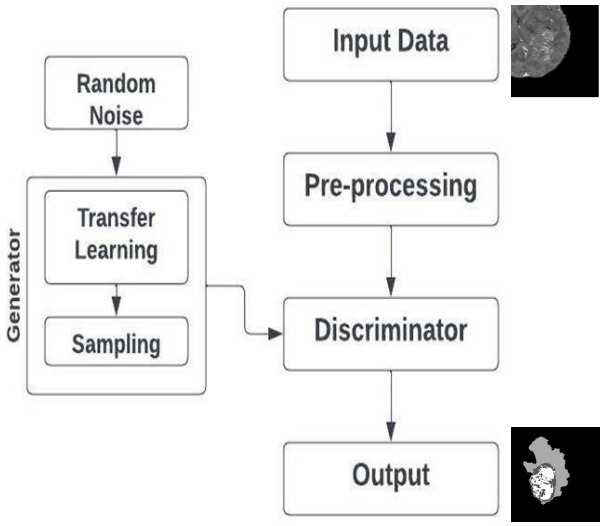


FIGURE 2. Flowchart of proposed model.

learning techniques for better performance. Figure 2 shows the flowchart of our proposed model.

Input Image: The model will get input from the BraTS 2021 dataset. This dataset contains images of WT, TC, and ET.

Pre-processing: The images will be cropped to the size that fits in the model and it will also reduce the memory issues that most deep learning architecture faces.

Generator: The generator with the help of some noise will create fake segmented images using the pre-trained model and give them as input to the discriminator. The generator will use transfer learning to produce segmented images.

Transfer Learning: This is a deep learning concept to uses the pre-trained models that already work for similar purposes. The DenseNet is the pre-trained model on the ImageNet dataset. This model produces better results in the segmentation process.

Discriminator: The discriminator will be first trained on the real images that are inputted from the dataset and then will take generated images from the generator. The discriminator will give the segmentation of brain tumor.

Output: Finally, the model will produce a segmentation of brain tumor.

Model Evaluation: Bases on Dice Similarity Coefficient (DSC).

The segmentation of brain tumors will be performed using a technique called Generative Adversarial Network (GAN). GAN is a deep learning model that uses a generator and a discriminator to maximize and minimize a certain object. Initially, the images in the provided dataset will undergo preprocessing to prepare them for training or testing. During the training process, the generator aims to maximize a particular feature in order to deceive the discriminator, which in turn tries to minimize the same feature to avoid being fooled. Then the discriminator will produce a segmented brain tumor as an output.

A. IMAGE PRE-PROCESSING

To fit within the CPU memory, each and every one of the brain MR pictures are sampled with a size of 128 × 128 × 128. The datasets are unaffected by this approach, which nevertheless preserves the majority of the image's content within the resize region while reducing the size and computing complexity of the image. By resizing the images to focus only on the region of interest (ROI) e.g., the brain in MRI scans, pre-processing can help reduce irrelevant background noise. Resizing focuses the model's attention on the critical areas of interest, potentially improving the training process. We mainly focus on the ROI which is the tumor part. To align with our proposed architecture and efficient execution we resized the data. To resolve this issue, we resized the data using the Keras resize library technique.

MRI scans for medical pictures are typically acquired using various scanners and acquisition techniques. Therefore, normalizing MRI intensity values is essential for balancing picture heterogeneity. Every input picture is normalized to have a mean of zero and a variance of one. Additionally, we collect each voxel's intensity between 5% and 95% from the MR picture.

B. GENERATOR

Input a 3D image with four channels: T1, T2, T1Gd, and T2 FLAIR. These channels refer to different types of MRI scans that capture images from various angles and perspectives. T1 shows fat in white and fluid in dark colors while T2 reverses this effect by making fat appear dark and fluid bright. Adding Gadolinium (T1Gd) further enhances contrast and can highlight areas of inflammation or abnormal tissue growth. Finally, the T2 FLAIR sequence helps identify water accumulation in regions where it shouldn't be present such as tumors or lesions.

Our model is inspired by the U-module. The U-module is based on an auto-encoder with the purpose of better parameter initialization of CNNs for medical image classification. The U-module is proven to retain the feature in the next layers of CNNs. In our paper, besides the main task of segmentation, we add a U-module to our model as an auxiliary task, which helps to force the model to preserve as much of the relevant and important information as possible. In detail, the operation of the U-Module [39] is described as the following formula:

$$\varphi : F \rightarrow Z \tag{1}$$

$$\rho : Z \rightarrow F \tag{2}$$

$$\varphi, \rho = \begin{pmatrix} argmin \parallel F - (\varphi^{o} \rho)F \parallel^{2} \\ \varphi, \rho \end{pmatrix} \tag{3}$$

where the φ and ρ transitions present the encoder and decoder of the U-module. The encoders compress the original feature map F into a smaller feature map Z. The decoder uses the upsampling layer and MF unit to recover the original feature map. The difference between the reconstructed map and the features map is minimized so the small feature map can represent the large feature map. This way, the most important

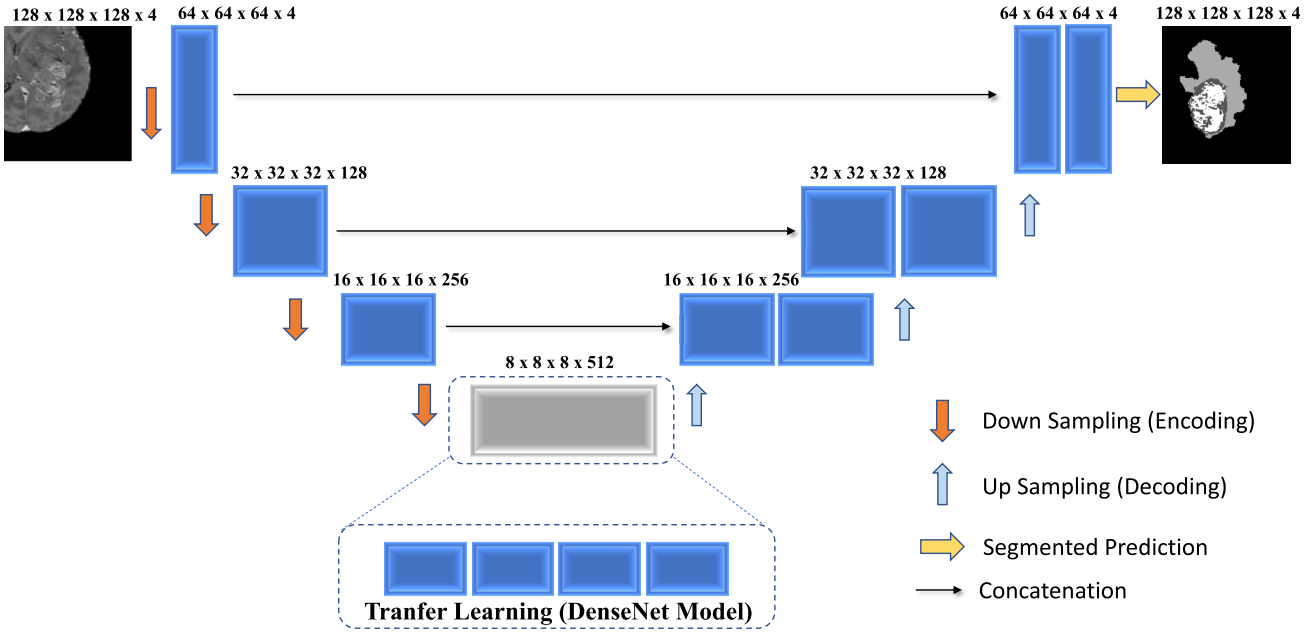


FIGURE 3. Overall architecture proposed model.

and relevant features of the previous layer will be retained in the next layer. In our model, we used two U-modules at the first and second encoder layers because those layers had the largest feature resolution to be kept. In addition to helping our model retain the properties of small tumors, the U-Module can also improve parameter initialization as its original purpose.

Figure 3 shows the complete architecture of the proposed generator.

1) AUTO-ENCODER

An auto-encoder is a type of neural network that is able to learn how to compress and then decompress data. In the context of tumor segmentation, this means that it can take in images of a patient's brain and then output an image with just the tumor highlighted. The encoder in the auto-encoder learns effective data codings while down sampling and tries to keep as much of the pertinent data as it can. The decoder takes the encoding and builds a whole picture from it while upsampling.

In the encoder, with the kernel size $4 \times 4 \times 4$, the same padding, and stride 2 there are 3D convolutional layers. These layers are followed by the ReLU activation function and batch normalization.

Normalization is mathematically defined as:

$$mean = \frac{1}{m}\sum_{i=0}^{n} x_i \tag{4}$$

$$variance = \frac{1}{m}\sum_{i=0}^{n}(x_i - mean)^2 \tag{5}$$

$$normalized = \frac{x_i - mean}{\sqrt{variance + \epsilon}} \tag{6}$$

ϵ is added in the denominator for numerical stability and is an arbitrarily small constant.

In the decoder, with the kernel size $4 \times 4 \times 4$ and stride 2, there are 3D transpose convolutional layers. These layers are followed by the ReLU activation function and batch normalization. Concatenation of each 3D convolution input with the corresponding encoder output layer.

2) DOWN SAMPLING

Downsampling operation that compresses the input images into low-resolution representations. This reduces computational complexity while preserving critical information about the location and arrangement of image features. Downsampling ensures that larger regions can be analyzed effectively without overloading computer memory or causing other issues.

At each step, we use an encoder which have a 3D convolutional layer with the kernel size of $4 \times 4 \times 4$, the same padding, and stride 2. This layer is then followed by Instance normalization and ReLu activation function. For regularization purpose, we set the dropout ratio to 0.2. This process is added to each encoder step. This will help the encoder to retain as much information as possible. The detailed architecture of downsampling in Figure 4.

3) TRANSFER LEARNING

Transfer Learning refers to the process by which a machine learning model leverages the knowledge it acquired from solving a specific problem to tackle another related problem.

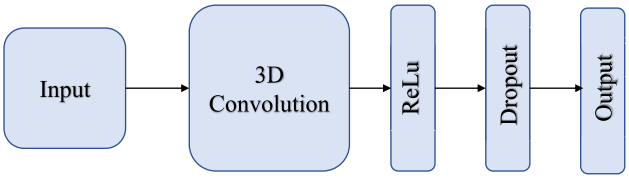


FIGURE 4. Down sampling architecture.

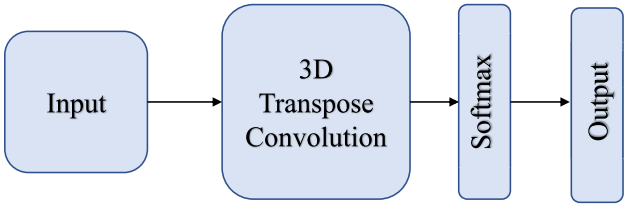


FIGURE 5. Up sampling architecture.

It involves transferring learned skills from one task to another. By utilizing a pre-trained model, it becomes possible to fine-tune it for a new task using fewer data and computational resources compared to training it from scratch. This technique has demonstrated remarkable effectiveness in various domains such as computer vision, natural language processing, and speech recognition. It enables models to quickly learn from limited labeled training data, address the challenge of overfitting on smaller datasets, and improve overall performance in real-world scenarios.

In this paper, the DenseNet model is employed. DenseNet is a convolutional neural network (CNN) specifically designed for transfer learning purposes. It allows pre-trained models to serve as a starting point for various tasks, including image classification, object detection, and segmentation. The key idea behind the DenseNet model is to establish connections among all layers within the network, enabling each layer to receive information from all preceding layers. This approach promotes effective feature reuse and facilitates fine-tuning even with smaller datasets.

In the bottleneck, we used the DenseNet architecture for the better performance of the algorithm. The DenseNet is trained on the ImageNet dataset which is a very huge dataset. This architecture is trained on this dataset. We set the trainable parameter to false so that we can freeze the layers of this model so that the weights cannot be updated with our algorithm. The model uses the input that is provided by the dataset with the activation function softmax.

This model is then followed by the max pooling and flatten layer. Then it is followed by the Dense layers and activation function softmax. It will produce the segmented result from an image and then will be given to the upsampling model.

4) UP SAMPLING

Upsampling in U-Net is a technique used to increase the resolution of an image or feature map by interpolating and/or copying information from lower-resolution layers. In U-Net specifically, the up-sampling step helps to recover spatial details that were lost during downsampling, allowing for more accurate segmentation of objects at different scales

At each step, we use a decoder which has a 3D transpose convolutional layer. This layer has a kernel size of $4 \times 4 \times 4$, applies the same padding, and has a stride of 2. Subsequently, Instance normalization and ReLu activation function are applied. Then this is followed by the concatenation process with the encoder layer. For regularization purposes, we set the dropout ratio to 0.2. This process is added to each decoder step. This will help the decoder to rebuild the segmented image with the encodings provided by the encoder. The detailed architecture of upsampling is shown in Figure 5.

At the end with the size of $128 \times 128 \times 128 \times 4$ having transpose convolutional with 4 filters, 2 strides, and $4 \times 4 \times 4$ kernel size followed by Softmax activation function give a prediction of the input image.

C. DISCRIMINATOR

We build the GAN model using a 3D convolutional neural network with a classification function as the discriminator. An image pair serving as both the original, unsegmented pictures and the corresponding, segmented images are inputted into the discriminator. These image pairings may be categorized into two groups based on the succession of segmented images. The first category is made up of a series of original images and segmented images that have been carefully labeled by specialists and correspond to the genuine value. The generator automatically labels segmented images in the second category, which corresponds to the produced value and is labelled as 0, in a cascade of original images. Figure 6 shows the architecture of the discriminator.

In the discriminator, there are five convolutional layers. Each convolutional layer contains two blocks of convolutions with the kernel size of $3 \times 3 \times 3$ and the Relu activation function. After the convolutions, a maximum pooling block with a sliding window of $2 \times 2 \times 2$ was applied reducing the feature maps. With the help of these pooling blocks, the features are reduced to half of the features. Additionally, the discriminator included three fully connected dense layers. In the first two layers, there are 4096 neurons and the last one has 2 neurons that correspond to the number of categories. These fully connected dense layers are followed by the Sigmoid activation function.

D. LOSS FUNCTION

As we had discussed earlier the GAN works with a generator and discriminator. The generator tries to fool the discriminator and the discriminator tries not to be fooled with the fake image generated by the generator. If generator wins then its discriminator loss and if the discriminator wins then its generator loss. So, there will be two loss functions for each generator and discriminator.

First, we have discriminator loss, L_D, is the sum of L_E error of discriminator, $D(x, y)$, the original image x and the gound-truth y with tensor one and L_E error of discriminator between

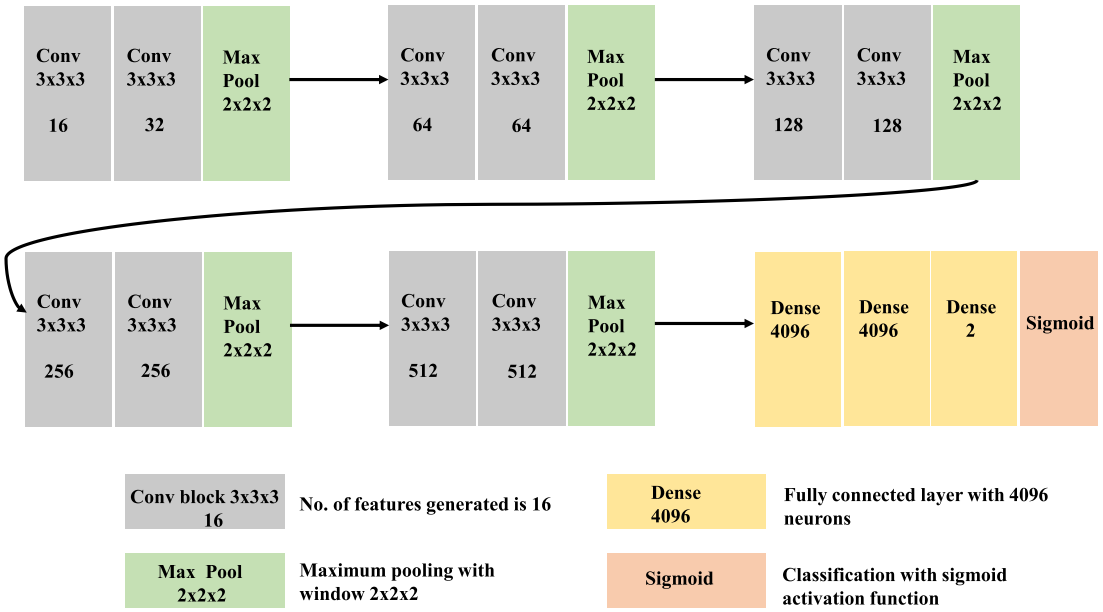


FIGURE 6. Architecture of proposed discriminator.

the original image and the respective segmentation prediction $\hat{y}$ generator by generator with tensor zero. Discriminator loss [40] is calculated using the following equation:

$$L_D = L_E[D(x, y), 1] + L_E[D(x, \hat{y}), 0] \tag{7}$$

Now generator loss, L_G, is the sum of L_E error of discriminator, $D(x, y)$, the original image x the respective segmentation prediction y generator by generator with tensor one and the generalized dice loss, $GDL(y, \hat{y})$, between the gound-truth and generator output multiplied by scaler $\alpha \geq 0$. Generator loss [40] is calculated using the following equation:

$$L_D = L_E[D(x, \hat{y}), 1] + \alpha GDL(y, \hat{y}) \tag{8}$$

From equation 11, it is concluded that if $\alpha = 0$, it will minimize only the unsupervised loss given by the discriminator.

IV. EXPERIMENTAL SETUP

This section will describe the experimental setup of our proposed research work.

A. DATASET

In the proposed work a well-known and publicly available images dataset BraTS 2021 has been used [62], [63], [64]. This dataset is the latest version of the BraTS challenge. In this dataset, there are 1251 MR images of shape $240 \times 240 \times 155$ for training, 219 images for validation, and 570 images for testing. These MR images are required for the segmentation of tumors in the brain. Table 2 shows the dataset samples distribution for training, validation, and testing with class labels.

In this dataset, the MR images are described as T1 weighted sequence (T1), T1-weighted post-contrast (T1Gd), T2-weighted sequence (T2), and T2-Fluid attenuated recovery (T2-FLAIR). From this description, four different sub-regions of tumor can be identified from MR images as Enhancing Tumor (ET), Non-Enhancing Tumor (NET), Necrotic Tumor (NCR), and Peritumoral Tumor (ED).

TABLE 2. Summary of distribution of BraTS 2021 data across training, validation, and testing.

Dataset	Training	Validation	Testing
BraTS 2021	1251	219	570

Then further these four sub-regions are clustered together to form tumor classes as Enhancing Tumor (ET), the combination of NET, ET, and NCR represents Tumor Core (TC), and the combination of ED with TC represents Whole Tumor (WT).

B. EXPERIMENTAL PARAMETERS

The proposed model is implemented in Python using the TensorFlow and Keras libraries. We employ the ADAM optimizer for training our technique. The segmentation network generator denoted as G, undergoes training for 100 epochs. 5×10^{-4} is the initial learning rate, and after 2000 iterations, it decreases by a factor of 0.5. On the other hand, the discriminator, denoted as D, is trained for 200 iterations, approximately equivalent to one epoch, with a mini-batch size of 1. Additionally, we train G for 100 iterations using the same mini-batch size. Since G contains pre-training parameters, it requires fewer training iterations compared to D. The training process involves alternating between training the discriminator and the generator. To evaluate the effectiveness of the algorithm, we reserve one subset as a validation set for each cross-validation, while the remaining subsets are used for training.

Algorithm 1 Training Process

for i_round in **number of training rounds do**
  for k_D steps **do**
    sampling a batch of images x_{pdata} as training data;
    generating prediction y_Pred for x with $G(x)$;
    updating Discriminator parameters θ_D from L_D;
  end for
  for k_G steps **do**

  end for
  sampling a batch of images $\acute{x}_{pdata}$ as training data;
  generating prediction $\acute{y}_Pred$ for $\acute{x}$ with $G(\acute{x})$ and compute $D(G(\acute{x}))$;
  updating Generator parameters θ_G from L_G;
end for

We always need a good framework while working with machine learning/ deep learning techniques. Keras is the most widely used deep learning framework that provides us more power to do experiments and to generate faster results. Tensorflow helps us to make machine learning models and to train them. Tensor flow is an endways open-source stage for CNN and ML(machine learning) [65].

C. MODEL EVALUATION METRICS

The overlap between prediction and ground truth is represented by the Dice Similarity Coefficient (DSC), which is frequently employed as an assessment criterion in medical picture segmentation [63]. The distinction between false positive (FP) and false negative (FN) detections is not taken into account by the generalized dice loss function. Due of the modest size of the foreground, the algorithm would typically allocate a voxel to the background when FPs and FNs are equally weighted. Due to the extreme class imbalance, FN detections must get heavier penalties than FP detections. The weight of FNs is enhanced using the DSC coefficient, which is a variation of the Tversky coefficient.

For evaluation of result metrics Dice Similarity Coefficient (DCS) is used for the accuracy measurement. Mathematically, it is defined as below:

$$DSC(X_p, X_g) = \frac{2 \mid X_p \cap X_g \mid}{\mid X_p \mid + \mid X_g \mid} = \frac{2TP}{FP + 2TP + FN} \quad (9)$$

where X_p refers to the segmentation predicted by the algorithm and X_g represents the actual ground truth. Whereas TP refers to the true positive, FP represents the false positive and FN represents the false negative.

D. HYPER PARAMETERS

Hyper-parameters are deep learning model parameters that are specified before training begins and are not learned during training. Hyper-parameters are used to manage the model's behavior and fine-tune its performance. In deep learning, several types of hyper-parameters can be adjusted to achieve accurate predictions, such as learning rate, hidden layers, optimizer, batch size, activation functions, and many more.

TABLE 3. Hyper-parameter values.

Model	Hyper parameters	Values
Generator	Optimizer	Adam
	Hidden Activation	ReLu
	Output Activation	Softmax
	Batch Size	128
	Image Size	$128 \times 128 \times 128$
	Kernel Size	$4 \times 4 \times 4$
	Stride	2
Discriminator	Optimizer	Adam
	Hidden Activation	ReLu
	Output Activation	Sigmoid
	Batch Size	128
	Image Size	$128 \times 128 \times 128$
	Kernel Size	$4 \times 4 \times 4$
	Stride	2
Whole Model	No. of Epochs	100

We used the Bayesian Optimization technique for hyper-parameters tuning. Bayesian optimization is a powerful technique used to optimize black-box functions that are expensive to evaluate. Bayesian optimization for hyper-parameter tuning is a probabilistic approach to finding the optimal hyper-parameters for a machine learning model. This method uses fewer evaluations and finds better hyper-parameters than a grid or random search. It can handle complex relationships between hyper-parameters and model performance.

In our proposed work, there are two separate models for the generator and discriminator. So we have different parameter settings. The hyper-parameters we used in our models are displayed in the Table 3.

V. RESULTS AND DISCUSSION

In this section, the proposed technique's results are discussed. To verify the performance of our method, we conduct two steps: training and testing. The training set accounts for approximately 80% of the total data, while the test set comprises approximately 20% after preprocessing the dataset. The test set and training set lists are generated independently of each other through random selection. After augmenting the training set with additional data, we utilize adversarial training to alternate between training the generative network and the discriminative network. Once the model achieves an optimal balance, we save the network parameters generated for subsequent segmentation experiments.

A. RESULTS OF PROPOSED MODEL IN TERMS OF ACCURACY

Our model is evaluated with the Dice Similarity Coefficient. We have achieved good accuracy with our proposed

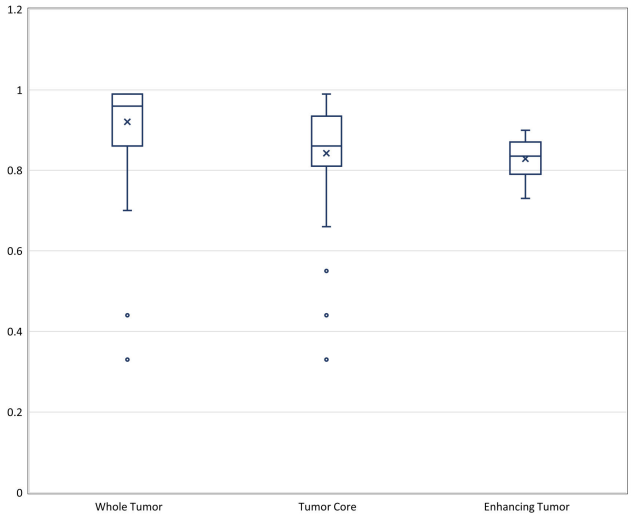


FIGURE 7. Accuracy graph.

TABLE 4. Dice score for three of the tumor categories.

Tumor	Dice Score	Sensitivity	Specificity
Whole	0.94	0.92	0.99
Core	0.86	0.86	0.98
Enhancing	0.82	0.83	0.98

generative adversarial networks framework. The main reason and difference between our and previous approaches is that we have used auto-encoder and transfer learning techniques in the generator. With the help of this approach, we are able to show better results for enhancing tumor.

Figure 7 illustrates the dice score, which represents the precision of our model's brain tumor segmentation for three distinct tumor categories. Figure 8 shows the segmented image of tumor.

After undergoing 100 epochs of training, our model achieved **0.94** score for the whole tumor, **0.86** score for the tumor core, and **0.82** score for enhancing tumor.

Table 4 shows the values for the dice similarity score, sensitivity, and specificity for the three of the tumor categories namely whole tumor, tumor core, and enhancing tumor.

The accurate segmentation of small tumors remains a challenging task due to their limited size and the subtle differences between tumor and non-tumor regions. Our approach leverages the synergistic combination of Transfer Learning (TL), Auto-Encoders (AEs), and Generative Adversarial Networks (GANs) to address these challenges effectively. Here, we provide a detailed explanation of how this performance is achieved:

1) TRANSFER LEARNING (TL)

Transfer learning allows the model to leverage pre-trained weights from large, annotated datasets, which significantly enhances its ability to generalize from limited training data. By using a pre-trained model as the starting point, the network benefits from learned features that are already well-suited for segmentation tasks. Fine-tuning the pre-trained model on our specific dataset ensures that these features are further refined to capture the nuances of small tumors. This approach reduces the risk of overfitting and improves the overall model performance.

2) AUTO-ENCODERS (AEs)

Auto-encoders play a crucial role in enhancing the feature learning process. In our method, the encoder part of the auto-encoder is responsible for compressing the input image into a lower-dimensional latent representation while preserving essential features. This compressed representation is particularly effective in highlighting the subtle characteristics of small tumors. The decoder then reconstructs the image from this latent representation, ensuring that the fine details of the tumor are retained. The encoder-decoder architecture aids in capturing complex patterns and enhancing the model's ability to distinguish between tumor and non-tumor regions, even for small-sized tumors.

3) GENERATIVE ADVERSARIAL NETWORKS (GANs)

GANs are employed to generate high-quality synthetic images that augment the training data, addressing the issue of limited datasets. The generator network produces realistic tumor images, while the discriminator network ensures that the generated images are indistinguishable from real ones. This adversarial training process not only enriches the training set but also forces the generator to learn and retain intricate details of small tumors. The enhanced dataset, combined with the discriminator's feedback, improves the model's robustness and accuracy in segmenting small tumors.

The combination of TL, AEs, and GANs contributes to the high Dice Similarity Coefficient (DSC) observed in our results. Specifically:

- TL initializes the model with robust, generalized features that are fine-tuned for our specific task.
- AEs ensure effective feature compression and reconstruction, focusing on retaining tumor-specific details.
- GANs enhance the diversity and quality of the training data, improving the model's ability to generalize and segment small tumors accurately.

Our experimental results demonstrate that this integrated approach significantly outperforms traditional methods in terms of accuracy, particularly for small tumors. The DSC values indicate that our method achieves precise segmentation by effectively capturing and utilizing the intricate features of small tumors, thereby validating our claims.

B. COMPARATIVE ANALYSIS OF THE PROPOSED MODEL

We compared the suggested GAN approach with many new brain tumour segmentation techniques using broad computational indicators. Since MRI images are made up of voxels, 2D and 3D segmentation techniques are often used. In these listed methods, Figure 9 shows the results of

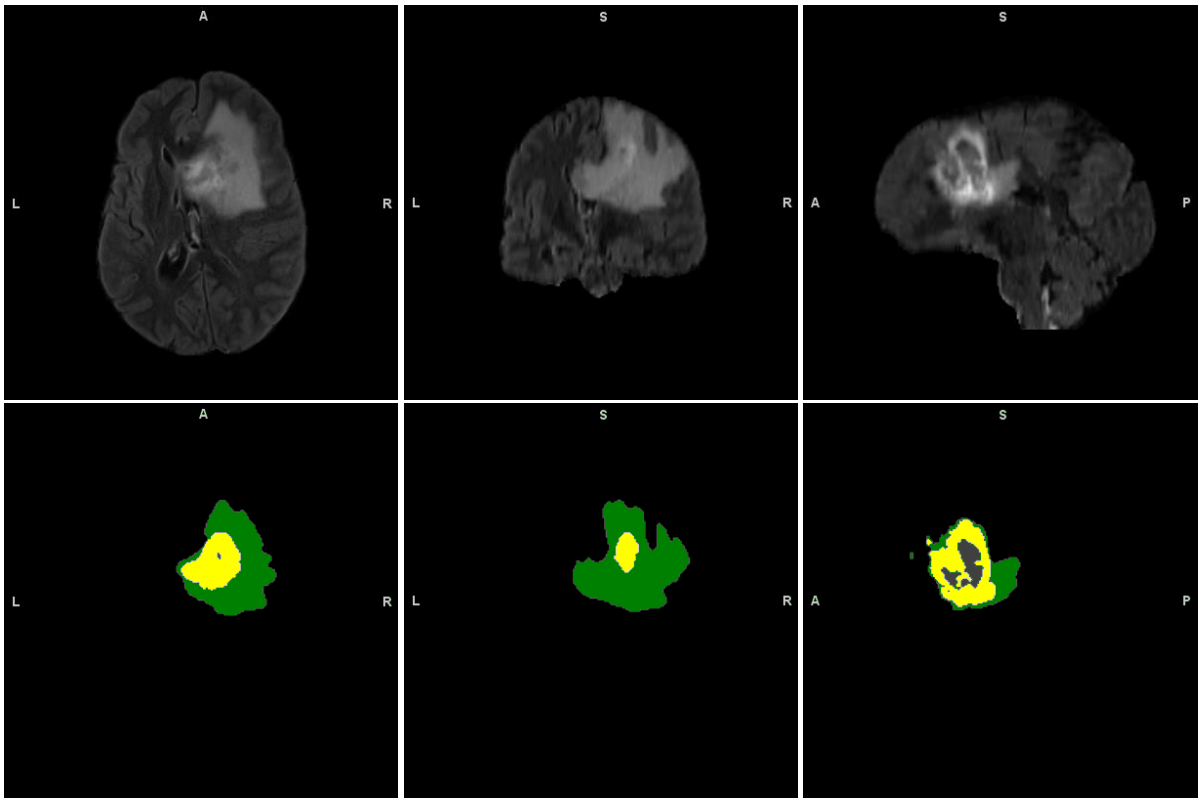


FIGURE 8. Validation phase results for the sample BraTS2021.

three different research works namely adversarial learning techniques for brain tumor segmentation [36], 3D GAN for brain tumor segmentation modified U-Net with dense block [66], CNN architecture with multitask learning for extracting features like small tumor [39], and 3D volume to volume GAN called Vox2Vox [40] are included.

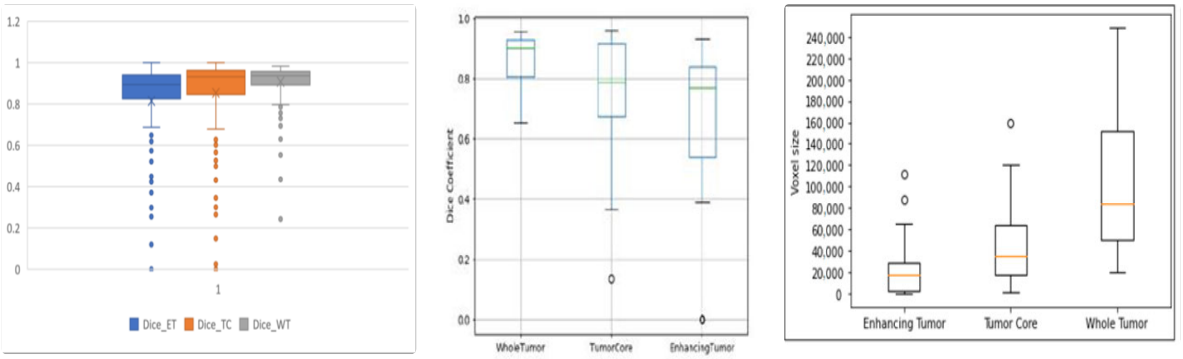
We compared our model with the most recent researches that used GAN architecture as well because our goal was to achieve better results for the enhancing tumor as they are in small size. We have achieved a dice score of **0.92** for the whole tumor, **0.86** for the tumor core, and **0.82** for enhancing the tumor. Our model contained GAN architecture with auto-encoder and transfer learning technique for brain tumor segmentation. Here presented the comparative study of four recent research work done by the other researchers with our model.

Our proposed model shows better results than the others because we used an auto-encoder and tranfer learning technique for brain tumor segmentation. In the generator part of GAN while downsampling the encoder retains as much information as possible and while upsampling the decoder uses that information to create the real image back. At the bottleneck, we used the transfer learning technique. In this technique, pre-trained model DenseNet is used. It produces better results while segmenting the enhancing tumor. The experimental result shows a dice score of 0.94 for the whole tumor, 0.86 for the tumor core, and 0.82 for the enhancing tumor. This presents well in comparison to other different techniques. Our proposed work presents a good result in the segmentation of brain tumor with variation in size, shape, and location. The results in table 5 show that our method has the highest accuracy in terms of segmentation. It is also showed that we achieve 2% to 4% higher accuracy.

By combining auto-encoder techniques with transfer learning methodologies in GANs, several synergistic effects occurred:

- Enhanced feature learning: Auto-encoders aid in learning more effective data representations, which improves the GAN's ability to generate high-quality outputs.
- Reduced training time: Transfer learning speeds up GAN training by starting from weights learned on other tasks or datasets.
- Increased stability: Both auto-encoders and transfer learning contributed to stabilizing the challenging training process of GANs, leading to a more consistent and reliable generation of outputs.

Overall, the incorporation of auto-encoder and transfer learning methodologies into GANs represents a strategic approach to overcome challenges and achieve superior outcomes in terms of output quality, training efficiency, and model robustness compared to earlier GAN models that lack these advancements.



Adversarial Learning Technique | 3D GAN | CNN Architecture

FIGURE 9. Comparison of three other architectures.

TABLE 5. Dice score for three of the tumor categories.

Methods	WT	TC	ET
Adversarial learning [36]	0.90	0.85	0.81
3D GAN [66]	0.90	0.78	0.68
CNN [39]	0.89	0.84	0.81
Vox2vox [40]	0.89	0.81	0.77
Proposed Model (Ours)	0.94	0.86	0.82

VI. CONCLUSION AND FUTURE WORK

Brain tumor segmentation is a significant field in medical research that utilizes deep learning techniques. Accurate tumor segmentation is crucial for the effective treatment of brain diseases. Although deep learning offers various algorithms for segmentation, it still faces challenges in providing precise analysis of medical images due to tumor characteristics such as structure, size, and location. With our approach, we found that GANs have shown promising results for brain tumor segmentation, with their ability to segment tumors with variations in size, shape, and location. With the help of GAN and transfer learning techniques, it shows that the segmentation of small tumors is possible with a higher accuracy rate. We found that GAN with auto-encoder shows promising results in retaining features of the tumor with different sizes, shapes, and locations. The encoder in the auto-encoder learns effective data encoding while downsampling and tries to keep as much of the pertinent data as it can. The decoder takes the encoding and builds a whole image from it while upsampling. GANs have been effectively employed in diverse medical image segmentation assignments, such as the segmentation of brain tumors. By incorporating auto-encoder and transfer learning methodologies, GANs yield superior outcomes compared to prior GAN models. We trained and tested our proposed model using the publicly available BraTS 2021 dataset. The evaluation of our work was based on the Dice Similarity Coefficient (DSC). The experimental results demonstrate a dice score of **0.94** for the whole tumor, **0.86** for the tumor core, and **0.82** for enhancing the tumor.

Through semi-supervised or poorly supervised deep learning techniques, we may attempt to address the issue of inadequate medical picture datasets in the next work and improve the model's segmentation accuracy and generalization capacity. We can attempt to apply the suggested approach to further multi-model medical pictures (such as ultrasound, CT, etc.).

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