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Residual Edge Attention in U-Net for Brain Tumour Segmentation

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Abstract - Identification and delineation of the tumour area in images of the brain constitute the crucial job of brain tumour segmentation in medical imaging. This task is crucial for diagnosis, treatment organizing, and keeping a track of brain tumours. Medical imaging methods like magnetic resonance imaging (MRI) or computed tomography scans are frequently used to divide brain tumours in real time. (CT). These imaging techniques provides high-resolution images for the brain that allows doctor to identify and locate tumours. There are several approaches to brain tumour segmentation, including manual segmentation by a radiologist, semi-automated segmentation using software tools that require some manual intervention, and fully automated segmentation using artificial intelligence (AI) algorithms. In this probing work, For segmenting brain tumours, we had anticipated Residual Edge Attention in U-Net design (ResEA-U-Net). Residual Edge Attention (ResEA) is a novel approach that enhances the performance of the U-Net architecture for brain tumour segmentation. The U-Net is often used in deep learning architecture for medical MRI brain image segmentation tasks, but it suffers from limited receptive field and feature reuse. To address this limitation, ResEA is expected to capture wide-range dependencies and enable network to focus on important regions of the image. The ResEA block contains of a residual block and an attention block that are connected in series. The residual block is created to improve the gradient flow and feature reuse, while the attention block focuses on important regions of the image by assigning higher weights to informative edges. The expected approach to evaluated on the BraTS data, which contain images of magnetic resonance of brain tumours. Experimental outcomes demonstrate that the ResEA-U-Net outperforms the baseline U-Net and other state-of-the-art methods. Overall, the suggested ResEA-U-Net architecture is a promising approach for brain tumour segmentation because it improves segmentation accuracy and lowers segmentation false positive rate, which can be essential for precise detection and therapy planning.

Keywords- MRI scanned images, Brain tumour segmentation, Residual Network, Edge Attention, U-Net Architecture, Data Augmentation, BraTS Dataset.

I. INTRODUCTION

Segmentation of brain tumour is identifying and splitting cancerous brain tissues from normal brain tissues in medical images, such as MRI scans. Brain tumour is a mass grow in cancerous or un-cancerous cells in the human brain. Neither the main brain tumour nor the secondary brain tumour can be caused by these cells, which can spread from other areas of the body to the brain [1]. There can be a variety of symptoms, depending on the type, size, and location of the tumour. Common symptoms include headaches, seizures, language or hearing difficulties, limb or leg numbness or stiffness, changes

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in eyesight, and psychological or behavioral problems. A biopsy may be required to establish the kind of tumour during the diagnosis of a brain tumour, which often involves imaging tests like MRIs or CT scans. [2]. Treatment for a brain tumour depends on the type, location, and size of tumour, as well as the patient's overall health. There are many treatments include surgery, radiation therapy, chemotherapy etc. It's important to note that not all brain tumours are cancerous, and not all require immediate treatment. However, any symptoms of a brain tumour should be evaluated by a healthcare professional to determine the appropriate course of action. There are various techniques used for brain tumour segmentation, including manual segmentation by a radiologist, thresholding, region growing, and machine learning-based approaches [1] [3]. One machine learning-based approach that has lately shown promising results and is growing favor is deep learning architectures.

Additionally, segmentation for brain tumours is a vital task in medical image analysis because it is crucial for the detection and treatment of brain tumours. The segmentation procedure involves separating the tumour region from the healthy brain tissue in medical images, such as MRI scans. For several reasons, accurate division of brain tumours is crucial. [4]. Firstly, it enables doctors to identify the area, dimension, and form of the tumour, which is important for planning surgical interventions and radiation therapy. Secondly, it allows for the tracking of tumour growth and response to treatment over time. Finally, it can assist in the development of new therapies and clinical trials.

The complexity and heterogeneity of modern brain tumours, as well as the wide range in picture clarity and sharpness, make segmentation a difficult task. Traditional segmentation techniques depend on arbitrary and time-consuming hand delineation by experienced doctors. [5]. Hence, In order to accomplish accurate and effective segmentation, automated segmentation methods have been created that make use of cutting-edge machine learning techniques like deep learning (DL) and convolutional neural networks (CNNs). Recent advancements in deep learning (DL) have led in development of new architectures such as U-Net, which has shown promising results in brain tumour segmentation [6]. These methods often require large, annotated datasets for training, which can be challenging to obtain. However, the area of research for brain tumour segmentation is developing quickly because of the expanding accessibility of medical imaging data, and it is expected to have a substantial effect on brain tumour diagnosis and therapy in the future.

Segmenting the brain tumour is an important stage in the diagnosis and planning of therapy for brain tumours. Deep learning algorithms have been the focus of current studies to boost the precision of brain tumour segmentation. [4] [6]. There are many glioma zones, including enhancing, non-enhancing, necrotic core, and peritumoural edema tumour core can also be accurately segmented using collection of 3D U-Net models.

To separate brain tumours, our study discusses Residual Edge Attention in U-Net design. A type of attention structure known as residual edge attention (ResEA) is a relatively new concept in medical picture segmentation study. For segmentation tasks, the commonly used U-Net design is used, but it has been modified. [7]. The U-Net technique contains a contracting path, in which it captures the context of the images, an expanding path, in which we perform the segmentation. The ResEA module is added to the expanding path, and it aims to filter the segmentation outcome by selectively attending to relevant features in the image. In segmentation of brain tumour, ResEA module can improve the accuracy of the segmentation by highlighting important edges and details in the tumour region. This is particularly important in cases where the tumour is small or has irregular shapes [8].

The ResEA module works by learning a bunch of attention weights that are used to weigh the feature maps at every layer of network. Attention weights are learned through a self-attention mechanism, which enables the network to selectively attend to important features [4] [7]. Overall, the field of study of medical Mri picture segmentation, including brain tumour for segmentation, has shown positive results with the inclusion of the ResEA module to U-Net methods and is anticipated to be an important area of research in the next years.

Moreover, we make use of Multi-mode Brain tumour picture segmentation Benchmark (BraTS) datasets. The regions of the brain that are affected by tumours have been identified in a compilation of medical pictures known as brain tumour segmentation datasets. These datasets are used to develop and evaluate algorithms for automatically detecting and segmenting brain tumours from medical images [9]. Among the most widely used datasets for segmenting brain tumours is the BraTS dataset, which consists of multimodal MRI scans of patients with brain tumours and manual annotations of the tumours. BraTS has become a benchmark dataset for evaluating brain tumour segmentation algorithms. This dataset contains MRI scans of 220 patients with gliomas, along with manual segmentations of the tumours.

There are other datasets like LGG/GBM (Low-Grade Glioma/ Glioblastoma Multiforme) Segmentation consists of MRI scanned images of patients with the low-grade gliomas and glioblastomas, along with manual segmentations of the tumours [6] [9]. HGG/GBM (High-Grade Glioma/ Glioblastoma Multiforme) Segmentation consists of brain MRI results of patients with gliomas and glioblastomas(high-grade), along

with manual segmentations of the tumours. MICCAI-BT (MICCAI Brain Tumour Segmentation) dataset consisting of multi-modal MRI scans of patients with brain tumours, along with manual segmentations of the tumours and ISLES (Ischemic Stroke Lesion Segmentation) dataset contains MRI scans of patients with ischemic stroke and includes manual segmentations of the stroke lesions. These datasets are important tools for academics and programmers developing algorithms for brain tumour automated segmentation and are used to compare the effectiveness of various segmentation techniques.

Despite these challenges, advances in medical imaging technology and machine learning techniques have made brain tumour division more accurate and efficient [10]. As research continues in this field, it is expected that brain tumour segmentation will become even more accurate and reliable, leading to improved diagnosis and treatment organizing for patients with brain tumours.

II. RELATED WORK

The segmentation of brain tumours is the topic of this study article. Brain tumours can be extremely dangerous and even fatal diseases. They are abnormal growths of cells within the brain that can disrupt normal brain function and cause a variety of symptoms, based on the tumour's size and position. Given the potential severity of brain tumours and the wide range of symptoms they can cause, it is crucial to identify and treat them as soon as feasible. Early intervention can lead to improved outcomes and a better chance of successful treatment [11]. Segmentation for brain tumour, as well as other imaging and diagnostic techniques, are important tools for identifying and treating brain tumours. One of the widely used deep learning methods is called U-Net design, and it is primarily used to divide biomedical MRI brain images. Convolutional neural network (CNN) design known as U-Net is frequently employed for image segmentation jobs. It was first presented by O Ronneberger in 2015. P Fischer, and U-Net with Convolutional Networks for Biomedical Image Segmentation by Brox Thomas.

Deep learning methods have recently come under the limelight to enhance the accuracy of brain tumour segmentation. These studies used a range of deep learning techniques, such as convolutional neural networks (CNNs), U-Net, and attention processes, to separate brain tumours from MRI images. The results have been promising, with many achieving high accuracy rates. One research suggested a reliable segmentation technique based on energy pre-fitting. [12]. Overall, these studies demonstrate the potential of deep learning methods for improving brain tumour segmentation accuracy.

U-Net's design is divided into two major sections. One route is a growth path, while the other is a contraction path. [13]. The high-level features of the input picture are extracted using numerous convolutional and max pooling layers that make up the contraction route. Up sampling and convolutional layers are used in the expansion route to restore the output's spatial precision. The U-Net architecture also incorporates skip connections, which allow information from the contraction path to be directly passed to the corresponding layers in the expansion path [14] This helps to maintain the original image's fine-grained features and increases the segmentation's precision. U-Net has been extensively used for biomedical image segmentation, but it has also been used for MRI segmentation of natural images and satellite data, among other kinds of image segmentation tasks. The U-Net design, which consists of an encoder and a decoder network, is a typical CNN layout for picture segmentation tasks. The decoder network up-samples the feature map to create a segmentation map, while the encoder network down-samples the incoming picture to extract high-level features. [15].

In the study of deep learning and computer vision, edge attention and the Residual network (ResNet) are both widely used methods. A deep neural network design known as a residual network employs shortcut links to assist the network in learning the residual function. Bypassing one or more levels with these short-cut links, the network can learn how to distinguish between their input and output. ResNet are very deep networks, with some architectures consisting of hundreds of layers. Edge attention, on the other hand, is a technique that focuses on important edges in a graph or image [16]. It involves assigning a weight or score to each edge in graph or image based on its importance. The weights or scores are then used to adjust the representation of the nodes or pixels in the graph or image.

This helps the network to focus on the most applicable parts of the input and improve its performance. Edge attention has been used in a variety of deep learning applications, including graph convolutional networks (GCNs), image segmentation, and object detection. Deep neural network creation can be enhanced by combining ResNet and edge attention. (DNN) [17]. Residual edge attention is a technique that can be used to improve the performance of convolutional neural networks (CNNs) on image segmentation tasks. In the context of segmenting brain tumours with the U-Net method, residual edge attention can be used to enhance the representation of important image features and suppress irrelevant features. To divide brain tumours, our research combines residual edge attention with a U-Net design. [18] By including a leftover link between the encoder and decoder networks and a collection of attention modules at the residual edge, the U-Net design typically includes leftover edge focus.

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The residual connection helps to preserve the fine-grained image details, the characteristics that are most pertinent to the segmentation job are selectively enhanced or suppressed by the attention modules. The attention modules typically consist of set of convolutional layers and SoftMax activation function, which produces an attention map that weighs the feature map at each spatial location [19]. The attention map can be used to selectively amplify or suppress the features, depending on their relevance to the segmentation task. In the circumstances of brain tumour segmentation, by improving the depiction of tumour boundaries and reducing the visibility of artefacts in the segmentation map, residual edge attention has been demonstrated to enhance segmentation performance [20]. This may result in segmentation findings that are more precise and therapeutically relevant.

Residual Edge Attention (ResEA) is a type of attention mechanism that can be incorporated into the U-Net technique for segmentation of brain tumour. A well-liked convolutional neural network (CNN) method for picture segmentation tasks is called U-Net. [22] [23]. The ResEA module is designed to enhance the feature representations of the U-Net by selectively highlighting informative regions in the feature maps. Utilizing the remaining links between the U-Net encoder and decoder components allows for this.

Specifically, the combination of the output from the encoder block and the input from the corresponding decoder block is accepted as input by a convolutional layer in the ResEA module. Output of the convolutional layer is then multiplied by a gating signal, which is generated by another convolutional layer applied to the same input. The gating signal serves as a mask to emphasize important features in the input while suppressing unimportant ones [24]. By incorporating the ResEA module into the U-Net architecture, the resulting network can better capture the fine details of brain tumour segmentation while also reducing the risk of overfitting. The ResEA module has been shown to improve the segmentation accuracy and robustness of the U-Net on various benchmark datasets.

On the whole topic Residual Edge Attention module can enhance the presentation of the U-Net technique for segmentation of brain tumour, by selectively highlighting informative regions and preserving contextual information. This helps increase in the accuracy and robustness of the segmented results or segmented output, which is crucial for clinical applications [25]. Due to its increased segmentation accuracy and decreased false positive rate, the ResEA-U-Net architecture is a potential way to segmenting brain tumours, which is crucial for accurate diagnosis and treatment planning.

III. DATA SETS

BraTS (Multimodal Brain Tumour Image Segmentation Benchmark) is a yearly worldwide challenge that examines cutting-edge techniques for classifying and segmenting brain tumour's using multi-model MRI scans. Each year a fresh dataset including MRI images of patients with brain tumours and their associated ground-truth labelling is made available for the competition. The main differences between the BraTS datasets are Data Size of BraTS dataset includes a larger number of patients [23] [24]. This makes the BraTS dataset more diverse and representative of the general population. Data Modalities of BraTS2020 dataset includes an additional MRI modality called diffusion-weighted imaging (DWI), which was not included in the other BraTS datasets. DWI provides information about the direction and movement of water molecules in brain tissue, which can be useful for detecting certain types of brain tumours and in comparison, to the other BraTS datasets, more particular ground-truth labels are included in some of the data labels for the cancer sub-regions including peritumoural edema, enhancing tumour, and non-enhancing tumour. This makes it possible to divide and categorise brain tumours with greater precision.

The BraTS 2020 dataset is an improved and more difficult standard against which to compare existing approaches to the segmentation and classification of brain tumours.

A. *BraTS 2020 Data Set*

In the area of medical image analysis, the BraTS dataset is a compilation of MRI scans of various stages of brain tumours. These images are used to capture different aspects of the brain tumour and gives complementary information for accurate division and diagnosis. BraTS2020 dataset is the latest version of the data and contains of a total of 369 multimodal MRI scans of brain tumours. Four distinct MRI image formats, including *T1*- weighted data, *T1's* weighted contrast-enhanced data - *T1c*, *T2* - weighted data, and Finally *FLAIR* - Fluid Attenuated Inversion, are included in each scan in the BraTS2020 dataset. In addition to the MRI images, each scan in the BraTS2020 dataset also includes a ground truth split cover that identifies the brain's tumour-bearing areas. These masks are manually annotated by experts and provide the gold standard for evaluating the performance of division algorithms. The two most prevalent kinds of brain tumours, low-grade and high-grade gliomas, are represented in the BraTS2020 collection. The dataset also includes scans from patients with multiple tumours and tumours in different locations in the brain.

The BraTS2020 dataset is widely used for studies involving the segmentation and identification of brain tumours, and it has been the subject of numerous international contests in the field of medical image processing. Researchers are urged to utilize

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the dataset, which can be downloaded for free from the BraTS (Brain Tumour Segmentation) website, to train and evaluate novel algorithms for brain tumour segmentation and diagnosis. Figure 1 shows the samples from BraTS2020 dataset.
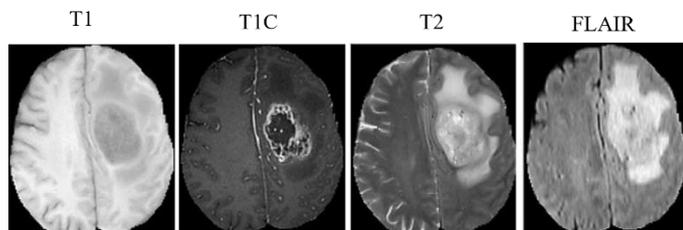
Figure 1: BraTS 2020 data set T1, T1c, T2 and Flair's MRI images.

B. BraTS 2019 Data Set

The BraTS2019 (Brain Tumour Segmentation) dataset is a publicly available medical imaging dataset that contains MRI (Magnetic Resonance Imaging) scans of brain tumours. Segmentation of brain tumours is the process of finding and delimiting tumours in medical pictures, and this dataset is intended to be used for training and assessing algorithms for this job.

Multi-modal MRI scans, such as *T1*-weighted data, *T1c*-weighted contrast-enhanced data, *T2*-weighted data, and *FLAIR* – Fluid Attenuated Inversion Recovery data pictures, are included in the BraTS2019 collection. Each voxel in an MRI image is assigned a label indicating whether it is part of the tumour core, peritumoural edema, or an enhancing tumour by use of a segmentation mask. There are 335 training instances and 125 validation examples included in the data. The BraTS2019 dataset contains a large and varied collection of high-quality MRI images with ground-truth segmentation masks, making it extensively utilised in the medical image analysis field for study and development of automated brain tumour segmentation methods. Few samples from BraTS 2019 has shown in Figure 2.
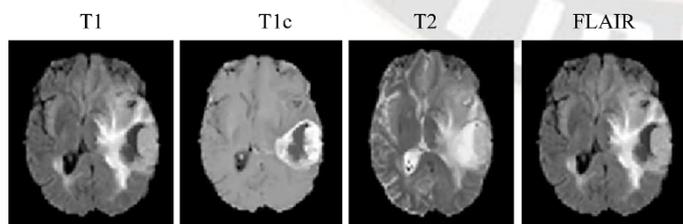
Figure 2: BraTS 2019 data set T1, T1c, T2 and Flair's MRI images.

C. BraTS 2015 Data Set

The BraTS (Segmentation for brain tumour) dataset is a collection of medical imaging data for the purpose of segmentation for brain tumour and classification. The BraTS 2015 specifically includes image of magnetic resonance (MRI) scanned images of the brain, which are collections from multiple medical centers around the world. The images were taken using four distinct MRI techniques: fluid attenuated inversion recovery (FLAIR), T1 is weighted, T1 with contrast enhancement (T1c), and T2 is weighted data like T1. The images from each modality were co-registered such that they all showed the same anatomical structure beforehand. Tumour and subregion designations, such as necrotic core and enhancing tumour, are included in the dataset with imaging data. Figure 3 shows samples from BraTS 2015 dataset. Clinical decision-making and treatment planning for patients may benefit from algorithms that can reliably segment brain tumours in MRI images, which is why this challenge was created. Many researchers in the field of medical imaging have utilized this dataset to test and refine their segmentation techniques.
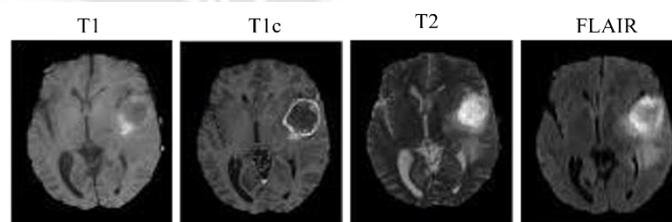
Figure 3: BraTS 2015 data set T1, T1c, T2 and Flair's MRI images.

D. BraTS 2013 Data Set

BraTS dataset (2013) is a publicly available dataset of brain MRI scans that has been used in several research studies on brain tumour division and classification. The BraTS2013 dataset specifically refers to the subset of the BraTS dataset that was released in 2013. The information is made up of pre-processed brain MRI images that are presented in four distinct weighting modalities: *T1*-weighted, *T1*-weighted with contrast enhancement is *T1c*, *T2*-weighted, and *FLAIR* (fluid-attenuated inversion recovery). The dataset includes MRI scans of both healthy brains and brains with different modalities of tumours, such as glioblastoma, astrocytoma, and oligodendroglioma. Figure 4 shows the samples from BraTS 2013 dataset.

The major goal of the dataset is to serve as a standard against which to evaluate algorithms for the automated segmentation of MRI images for the presence of brain tumours. This dataset has been widely utilized for developing and evaluating automated segmentation methods, which has helped improve research in the field of medical Mri image processing.
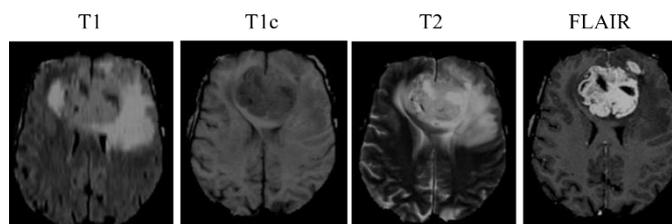
Figure 4: BraTS 2013 data set T1, T1c, T2 and Flair's MRI images.

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IV. DATA PRE-PROCESSING

The term "Data preprocessing" refers to any operation carried out on raw data to get it ready for further processing. It has always been a crucial first stage in the data mining process. Training machine learning models and artificial intelligence models, as well as performing inferences against them, have lately benefited from data preparation approaches. To make data mining, machine learning, and other data science processes more efficient, preprocessing is performed. For this reason, these methods are often used early in the machine learning and AI development pipeline.

The term "Data preparation" encompasses a wide range of processes, including: sampling (the selection of a representative subset from a large population of data), transformation (the manipulation of raw data to produce a single input), denoising (the removal of noise from data), imputation (the synthesis of statistically relevant data to replace missing values), normalization (the organization of data for more efficient access), and feature extraction (the selection of a relevant feature subset that is significant in a particular context).

These techniques may be used to both static data like files and databases, and dynamic data like streams.

A. Data Normalization

Normalization [11] is a process of scaling image intensities to a standardized range to improve the consistency of image features across different scans. This can help to reduce the impact of variations in imaging protocols and equipment, which can make it difficult to compare and analyse images.

Normalization can also help to enhance the performance of machine learning algorithms, which may be sensitive to variations in image intensity. Z-score normalization, which is used for image normalisation and standardization, involves taking the mean of each sample and dividing it by its standard deviation, resulting in an average and unit difference of zero in every MRI of the brain. In data normalization, the range of values is set to be uniform, often between 0 and 1. The normalization on image is applied as:

$$I_{norm} = I - \mu_i \sigma_i$$

In contrast, I_{norm} represents normalized input while I represent the original input picture. While "μ_i" denotes the average and "σ_i" stands for the input pictures standard deviation. In addition, owing to storage constraints, all MRI scans are downsized from their original 240x240x155 resolution to 128x128x128. All four kinds were piled on top of one another to make the most of the abundant data provided in the four sequences.

B. Data Augmentation

Data augmentation is an algorithm used in machine learning (ML) to artificially expand the dimension of a dataset by generating new examples from the existing ones [25]. This is especially useful in the case of medical imaging, where datasets are often small and difficult to obtain. When it comes to brain MRI scan images, there are several techniques that can be used for data augmentation.
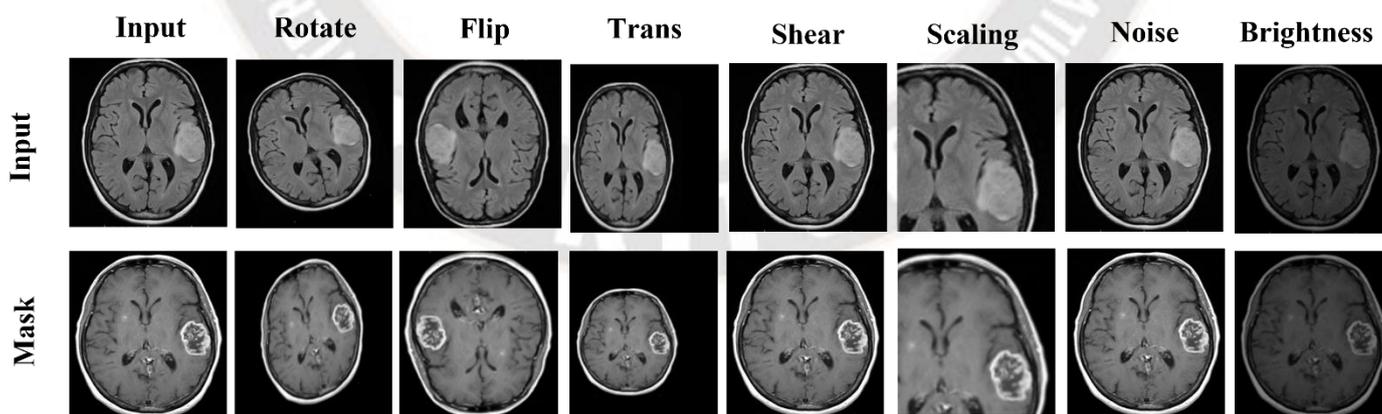
Figure 5: Augmented samples from different datasets.

Rotation: This involves rotating the image from a certain angle (e.g., 90 degrees) to create a new image.
Flip: To produce a mirror image, flip the image either horizontally or vertically.

Translation: It involves shifting the image horizontally or vertically, which can simulate different viewing angles or viewpoints.
Shear: It involves shifting one row or column of pixels in an image by a certain amount relative to the adjacent rows or

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columns.

Scaling: It refers to the process of resizing an image or other data, either by increasing or decreasing its size. Scaling can be used to simulate changes in the distance or size of objects in an image and can help improve the robustness of a model to variation in image size.

Noise: This involves adding noise to the image to create a new image.

Brightness: It refers to adjusting the overall brightness of an image or other data. This may assist make a model more resistant to changes in illumination by simulating different lighting scenarios.

The data augmentation approach should be implemented in a manner that respects the integrity of the picture and does not add any bias or artefacts that might influence the efficiency or accuracy of the model [26]. Additionally, it is recommended to apply data augmentation algorithms in a controlled way, testing the impact of different types and magnitudes of augmentation on the performance of model.

C.   Data Filtering

Filtering is an important technique used in data pre-processing for tumour segmentation in brain. To, increase the accuracy of the classification process, filtering may be used to clean up the data, lessen the number of distracting artifacts, and sharpen the pictures. [25] [26]. Here are some common filtering techniques used in tumour segmentation in brain:

Gaussian filtering: Gaussian filtering is a popular method for removing noise from MRI images. It entails applying a Gaussian filter to the image, which serves to maintain the image's edges while smoothing it out.

Median filtering: Median filtering is a nonlinear filtering technique that is particularly useful for removing salt-and-pepper noise from MRI images. It involves replacing each pixel in images with median value of its neighbouring pixels.

Anisotropic diffusion filtering: Anisotropic diffusion filtering is a technique that is particularly useful for preserving edges in MRI images while reducing noise. It involves diffusing the image over time using a diffusion coefficient that is dependent on the local gradient.

Wavelet filtering: Wavelet filtering is a multiresolution filtering technique that is particularly useful for analysing the frequency content of MRI images. It involves decomposing the image into a set of wavelet coefficients, filtering the coefficients, and then reconstructing the image.

Non-local means filtering: It is a technique that is particularly useful for reducing noise in MRI images while preserving fine details. It involves comparing patches of pixels in the image to find similar regions, and then averaging the values of those regions to produce the filtered image.

These filtering techniques can be applied in combination with other pre-processing techniques, such as normalization and segmentation initialization, to improve both the images' clarity and the segmentation algorithms' precision. It's crucial to carefully assess how various filtering methods affect segmentation performance and to tailor the filtering process to the application at hand.

However, in order to separate brain tumours using deep learning techniques, data pre-processing is a crucial stage. The quality of MRI scanned pictures may be improved and noise reduced by pre-processing methods, which in turn can increase the precision of division. [27]. One study proposed a pre-processing approach to work with deep learning methods for flexible and effective brain tumour segmentation. For the segmentation and classification of brain tumours, another research created a deep learning system that incorporates MRI picture pre-processing techniques. These works show the value of data pre-processing in increasing the precision and accuracy of deep learning-based tumour separation in the brain. Finally, pre-processing is a useful way for increasing the precision of tumour segmentation in the brain using deep learning techniques. Pre-processing methods are employed to improve the clarity of MRI scanned pictures and minimise noise, which can improve segmentation accuracy. For adaptable and efficient tumour segmentation in the brain using deep learning techniques, one research suggested using pre-processing techniques. [28]. According to the results of another research, using sophisticated algorithms and particular pre-processing steps greatly improves the tumour division efficiency for automated systems. These studies demonstrate that pre-processing is an essential step in improving in accuracy of segmentation for brain tumour using deep learning methods.

V. Methodology

Our proposed methodology is about Residual Edge Attention in U-Net for segmentation for brain tumour. In image division tasks, the U-Net architecture's accuracy may be improved with the help of Residual Edge Attention (ResEA). To help the model pick up on the finer details of a picture, ResEA zeroes on the residual connections between the encoder and the decoder in U-Net.

Convolutional neural networks (CNNs) may be made more effective in picture segmentation tasks by employing a method called Residual Edge Attention [29]. To do this, we augment the U-Net structure with residual connections and an attention mechanism. The U-Net architecture includes both an encoder and a decoder. A segmentation map is generated by the encoder using features extracted from the raw pictures by the decoder.

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The U-Net decoder is where the residual edge focus is implemented.

The suggested technique for applying residual edge attention in U-Net is to begin by building the network's encoder and decoder components using the standard U-Net design. Remaining links should be added to the network's encoder area. The output of one layer is combined with the output of another layer in a leftover link. This helps to preserve important features during the forward pass. Add an attention mechanism to the residual connections [30]. The attention mechanism involves calculating attention weights for each feature extractor map in the previous layer and then applying these weights to the corresponding feature maps in the current layer. This helps to focus the network's attention on the most important features. Combine the residual connections and attention mechanism to create the residual edge attention module. The U-Net decoder must include the residual edge attention module.

To solve the issue of data imbalance, loss functions is frequently utilized in tasks involving segmenting medical images. Nevertheless, it ignores another imbalance between easy and difficult instances that also negatively impacts a learning model's training process and solely addresses the problem of foreground and background imbalance. Use an appropriate loss function, such as dice loss or binary cross-entropy loss, to train the network.

$$Loss = \frac{Binary\ Cross - Entropy}{LogLoss}$$

To achieve this, flip the picture. The loss is raised by $\log(p(y))$, the log likelihood of y being green, for each green point $(y = 1)$. Each red area $(y = 0)$ will have an additional $\log(1 - p(y))$ added to it, where $p(y)$ is the log probability that the area is red.

To improve the network's generalizability, augment the training dataset with additional data by techniques such as rotation, cropping, and expansion [31]. Optimize the network's hyperparameters by evaluating its performance on a validation set.

Overall, residual edge attention is one of the powerful methods that includes introducing residual connections and an attention system to the decoder portion of the network in order to enhance the performance of U-Net in picture segmentation tasks.

A.   Process Overview

Residual Edge Attention (ResEA) is a method for segmenting images that is included into the U-structural Network design. The network may increase the feature representation and segmentation performance compared to a regular U-Net [32]. Features are extracted from raw pictures using a series of convolutional layers of the U-Net architecture, which may be summarized as the ResEA procedure as shown in figure 6.
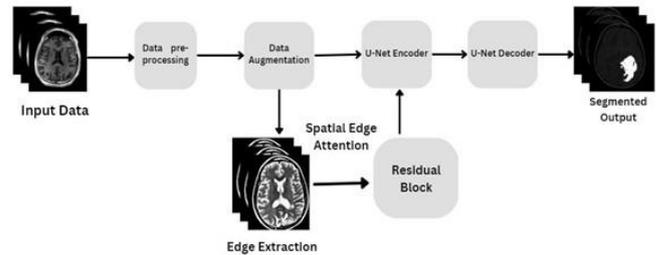
Fig 6: Block diagram of ResEA U-Net methodology for segmentation.

Encoding the input is down sampled through convolutional layers, this makes the feature channels more numerous but sacrifices spatial resolution. Encoding path consists of multiple layers, where every layer performs a convolution method then followed by an activation function called non-linear such as ReLU. Decoding path is the reverse of the encoding path, where the features are up sampled to the original resolution by convolutional layers (transposed). The last part uses skip links to join the traditional U-encoder Net's and decoder routes. In [33] REA, residual block connections are introduced among the encoder and decoder path. This enables the network to pass high-level features from encoder to decoder without any loss of information. In Edge Attention the residual connections are enhanced by an edge attention mechanism that selectively increases the flow of information. The edge attention mechanism takes the output from the residual connection and applies a convolution operation. This operation produces a set of attention maps, which are then used to weight the output from the residual connection.

The output from the edge attention mechanism is then used with the output obtained from the decoder and then produce the final

Segmented mask [34]. The fusion is performed using an element-wise addition operation. The U-Net design produces a segmented mask that makes educated guesses about where objects begin and end up in an input picture. In summary, the normal U-Net design is enhanced by the REA in U-Net, which adds residual links and an edge attention method. This increases segmentation efficiency and feature representation.

B.   Proposed Architecture

The Residual Edge Attention in U-Net architecture (ResEA U-Net arch.) is an adaptation of the standard U-Net design that adds support for attention to edges and residual connections. [35]. The encoder in this network is built from a sequence of convolutional layers with batch normalization, followed by a

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ReLU activation layer with max pooling. The detailed architecture has shown in figure 7.

Each convolutional block has a residual connection that allows for the gradient flow to be preserved during training. The mirror image of an encoder is decoder, with each convolutional block being replaced by a series of transposed convolutional layers, up-sampling layers, and concatenation with the corresponding encoder feature map [33] [35]. Edge attention is incorporated into the architecture by adding an attention module to each convolutional block.

The attention module imports feature maps from current convolutional block and the previous block and computes a weighting coefficient for each pixel based on similarity among the two of feature extraction maps. Final prediction is obtained by applying a 1x1(size) convoluting layer to output of the last and final decoder block, followed by a SoftMax activation function:

$$soft\max\left(x_i\right) = \frac{e^{x_i}}{\sum_{j=1}^{N} e^{x_j}}$$

$$e \approx 2.718$$

x = vector of raw outputs from the neural network.

The "i" is the entry of the $soft\max\left(x_i\right)$ output vector SoftMax(x) can be thought of as the forecast probability of test input belongs to class "i".

Residual Edge Attention in U-Net arch (ResEA U-Net arch) architecture is like the orthodox or traditional U-Net architecture, with the addition of residual connections and edge attention mechanisms [36]. The residual connections help to preserve gradient flow during training, while the edge attention mechanisms help to focus the model's attention on important edges in the input image.
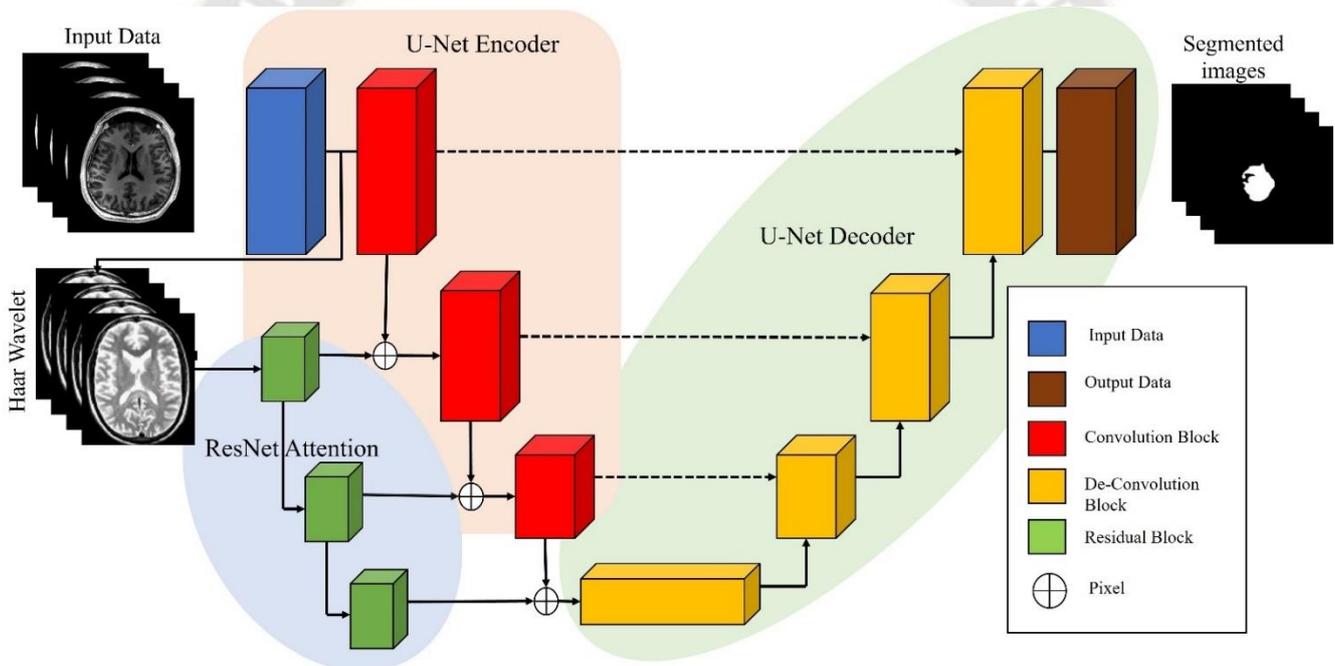
Fig 7: Proposed architecture of ResEA in U-Net

Similar to the 3D U-Net [37], the ResEA U-Net is composed of shrinking (encoder) and expanding (decoder) components linked together by skip connections. The network's depth is represented by the level, which is one of five in the bargaining sequence. The first four layers of the encoder part of the expected model include remaining blocks (Yellow blocks) for feature extraction. The suggested model takes a 128x128x128 stack of vowels of four distinct sorts as input to its encoder route (T1, T2, T1c, Flair). The maximum 3D pool size is 2, 2, 2, and the stride and dropout values are also both 2.

Three items plus a mapping are carried by each residual block. After the conv3D layers, both elements 1 and 2 use batch normalization and ReLU activation algorithms. This means it can't be activated by the ReLU function.

Before performing the ReLU function, the input and the shortcut are linked.

A residual block is one whose constituent blocks may be specified by an equation.

$$b = F\left(a, \{w_i\}\right) + a$$

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Where " *a* " is the input to the corresponding layers and " *b* " represents the output vector. The weights over the appropriate residual unit at the *i*-th layer are characterised by the function " $F\left(a,\{w_i\}\right)$ " which characterises the trained residual mapping that yields the same dimension of input " *a* " and function "F."

For training a model, a good loss function, such binary cross-entropy loss, is used. A deep learning model's efficiency and performance are not only determined by its architecture, but also by the loss function it employs. Around 61% of the tumourous area belongs to a full tumour, 24% via tumour core, and 15% through boosting tumour class [36] [37]. This is known as Brats' mystery, and it is a high-class imbalance challenge. So, selecting an appropriate loss function is vital to the success of the variant. This investigation use a mixture of focus loss and soft dice loss to cut down on testing of class imbalance issues.

The following equation may be used to think about multiclass focus loss in the context of the class imbalance issue.

$$L_{focal}\left(x,y\right) = \frac{1}{N}\sum_{n=1}^{N}\sum_{c=1}^{C}\left(1-x_{nc}\right)y_{nc}\log x_{nc}$$

Where "*x*" represents the projected result and "*y*" represents the actual result. Class is denoted by "*c*" while the total number of classes is denoted by "*n*".

The Edge-Enhanced Attention U-Net is a final suggested design for adding edge attention to a U-Net for brain tumour segmentation (EEAU-Net). The EEAU-Net design takes use of both spatial and channel-wise data by including an edge improvement module into the U-Net. Edge information is extracted using a Sobel filter, features from the edges are mapped to a lower dimensional space using a convolutional layer, and finally the features are rescaled to the [0, 1] range using a sigmoid function. Before sending the data to the decoder, the output of the edge enhancement module is multiplied, element by element, by the feature maps generated by the U-Net encoder.

In addition to the edge enhancement module, the encoding and decoding processes of EEAU-Net include attention modules. The attention modules capture the relationships between feature maps by computing attention scores that are used to weight the feature maps before passing them through a convolutional layer. Overall, the EEAU-Net architecture is designed to capture edge information and attention scores to improve the accuracy of brain tumour segmentation.

C. *Training and testing data manifestation*

BraTS (Multimodal Brain Tumour Imaging Segmentation Benchmark Dataset) is a publicly available benchmark dataset for brain tumour segmentation that was created using publicly available data. Magnet Resonance Imaging (MRI) scans of brain tumours are included, together with human annotations of the tumour locations.

We would usually divide the dataset into three sets: training sets, validation sets, and testing sets when using any BraTS dataset to train and evaluate a model for segmenting brain tumours. We split the data in two, with the training set receiving 70% and the test set receiving 30%.

As an added measure, we segmented the training data into training and validation sets, using 80% to 85% of the training data for training and 15% to 20% for validating. We used the ground truth of the manually annotated tumour locations to train the model using the training set. Throughout training, the trained model's performance may be monitored using the validation set, and any necessary adjustments can be made at the end of the process. Now, we assess the learned model's success on fresh data using the testing set. We would compare the predictions of the model for the tumour regions to the manual annotations for measuring the accuracy of the trained model. It's important to note that the BRATS collection contains data from various MRI techniques. (Weighted-T1, Weighted contrast-enhanced-T1c, Weighted-T2, and FLAIR), To train a model for brain tumour segmentation, it is typical to use a wide variety of kinds. In addition, some researchers have used data augmentation techniques to increase the capacity of their training datasets and hence improve the accuracy and performance of their trained models.

VI. RESULTS AND DISCUSSIONS

Residual Edge Attention mechanism aims for the improvement of U-Net architecture's segmentation performance by introducing a residual connection and an attention mechanism between adjacent convolutional layers. By connecting the residual block, it enables the network to analyze and learn the residual mapping between adjacent feature maps, which helps in preserving the fine details of the image. The attention mechanism selectively emphasizes informative regions of the feature maps and suppresses irrelevant regions.

Several studies have reported that Residual Edge Attention in U-Net for segmentation of brain tumour has achieved best results by using modern techniques and technology for the terms like accuracy of segmentation, dice similarity coefficient (DSC), as well as the DSC's sensitivity and precision. By contrasting the predicted segmentation masks with the actual segmentation masks, these measures assess the efficacy of the segmentation algorithm.

A. *Performance Metrics*

Performance metrics provides the quantitative findings in the form of three distinct tumour areas contain the various

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tumour structures. This is mostly because of real-world clinical applications. Tumour areas are described by enhance tumour refers to the area of the tumour that shows increased contrast enhancement on a MRI scan with gadolinium contrast. This area represents the region of the tumour that has the most active growth and is the most densely packed with tumour cells.

However, the center, non-enhancing part of the tumour is referred to as the core tumour. This section depicts the part of the tumour where the tumour cell density is reduced and where necrotic or dead tissue may be present. Finally, whole tumour refers to the combination of the enhance tumour and the core tumour. It represents the entire visible extent of the tumour on MRI.

$$\text{Dice (A, B)} = \frac{|A_1 \wedge B_1|}{(|A|+|B_1|)/2}$$

$$\text{Sensitivity (A, B)} = \frac{|A_1 \wedge B_1|}{|B_1|}$$

$$\text{Specificity (A, B)} = \frac{|A_0 \wedge B_0|}{|B_0|}$$

where A stands for model's forecasts and B for the actual names. Additionally, the subset of voxels B1 and B0 were forecast to be positive and negative for the tumour area, respectively. Likewise for A1 and B0. The BraTS Dataset techniques are included in this.

B. Performance evaluation

In this section, we discuss the performance of our proposed method on various datasets. To know the robustness of the proposed method, we planned to compare the results on four different datasets with existing state-of-the-art methods.

TABLE I. Performance evaluation on BraTS 2020 Dataset

Reference	Methods	Dice Score (%)		
		Whole Tumour	Core Tumour	Enhancing Tumour
R. R. Agravat [38]	3Dencoder-decoder FCNN	88.24	83.11	78.45
S. Grampurohit [39]	3D FCNN	88.74	70.04	71.42
Haozhe Jia [40]	H 2NF-Net	91.26	83.53	78.49
Theophraste Henry [41]	U-Net like	90.71	80.77	87.05
Carlos A. Silva [42]	DLA-Pool	89.16	78.85	72.46
Yixin Wang [43]	Modality-Pairing learning	92.49	89.80	86.30
Vikas Kumar Anand [44]	3D CNN Architecture	85.07	81.58	77.66
YU Liu [45]	SV NET	87.41	80.47	79.21
Fuhau Mu [45]	SF NET	87.84	81.45	80.49
Proposed	ResEA U-Net	94.56	90.17	88.72

Table I compares standard values of Dice Scores in Percentages (DSC) from various authors' WT, CT and for ET for segmentation of brain tumour using the BraTS 2020 Dataset to ResEA U-Net technique (proposed method). The ResEA U-Net technique we used has produced the greatest dice score outcomes for segmenting brain tumours.

Table II: Performance evaluation on BraTS 2019 Dataset.

Reference	Methods	Dice Score (%)		
		Whole Tumour	Core Tumour	Enhancing Tumour
Hamghalam et al.[49]	FCN	89.60	79.19	76.60
Jiang et al. [50]	Cascaded U-Net	90.91	86.40	80.20
Frey et al. [51]	U-Net	89.65	80.21	78.70
MD.Abdullah et al. [46]	Enhanced U-Net	95.12	87.17	94.22
NEIL MICALLEF[66]	Residual U-Net	84.34	75.12	64.28
S´ergio Pereira [42]	DLA-Pool	89.11	78.85	72.46
JIANXIN ZHANG [48]	AuGRes U-Net	89.40	86.54	83.17
Yading Yuan [47]	SA-Net	92.56	89.02	82.29
NEIL MICALLEF [66]	U-Net++	87.09	78.24	69.10
Minglin Chen [42]	AMPNet+TTA	87.18	78.85	72.85
Proposed	ResEA U-Net	96.29	91.45	89.72

In Table II, we can see the results of our method compared to some standard values of Dice Scores in percentages (DSC) from different author's WT, CT, and ET for segmentation of human brain using the BraTS 2019 Dataset. For segmentation of brain tumour, our suggested approach, the ResEA U-Net, has produced the best dice score outcomes for the WT, CT and ET.

Table III: Performance evaluation on BraTS 2015 Dataset.

Reference	Methods	Dice Score (%)		
		Whole Tumour	Core Tumour	Enhancing Tumour
Dong et al. [56]	U-Net CNN	86.14	86.71	65.91
Kamnitsasetal.[58]	3D-CNN+RF	84.25	66.23	63.78
Chen et al. [57]	Dual force CNN	85.12	70.24	63.91
Chenhong Zhou [59]	OM Net	86.25	71.19	64.74
Changxing Ding [59]	MC3	86.12	70.46	63.81
Fabian Isensee1 [60]	U-Net	85.50	74.74	64.08
Yi Ding [61]	FCN	81.23	65.78	52.45
Pereira et al. [63]	CNN (3x3) for deeper arch.	88.12	83.84	77.60

Dvora and Menze3 [64]	CNN and k-means using local structure	83.40	75.78	77.29
KAI HU [62]	MCCNN	82.56	70.99	68.15
Proposed	ResEA U-Net	93.72	89.94	86.62

From Table III, we can see the results of our method compared to some standard values of Dice Scores in percentages (DSC) from different author's WT, CT and ET for brain tumour segmentation using the BraTS 2015 Dataset. The ResEA U-Net technique we used has produced the greatest dice score outcomes for segmenting brain tumours.

Table IV: Performance evaluation on BraTS 2013 Dataset.

Reference	Methods	Dice Score (%)		
		Whole Tumour	*Core Tumour*	*Enhancing Tumour*
Zikic et al.[55]	CNN	83.70	73.65	69.72
Havaei et al.[54]	DNN	81.29	72.82	58.39
Zhao et al. [53]	FCNN model	70.26	62.46	64.25

Doyle et al. [52]	Hidden Markov fields	71.58	46.59	52.19
Mohammad Havaei [65]	kNN-CRF*	85.36	75.71	60.51
HugoLarochelle[65]	kNN*	81.52	68.53	65.95
Sérgio Pereira [42]	Input Cascade CNN*	84.72	72.33	62.11
Tustison et al.[67]	Random forest	87.15	78.17	74.10
P Bhagat et al.[69]	Map-reduce HMM	81.11	54.99	61.89
Hu K et al. [68]	Multi-Cascaded CNN	86.17	77.94	70.84
Proposed	ResEA U-Net	95.77	92.69	78.47

In the table IV, we can see the results of our method compared to some standard values of Dice Scores in percentages (DSC) from different author's WT, CT and ET using the BraTS 2013 Dataset to segment brain tumours. For brain tumour segmentation, our ResEA U-Net technique has shown the highest dice scores.
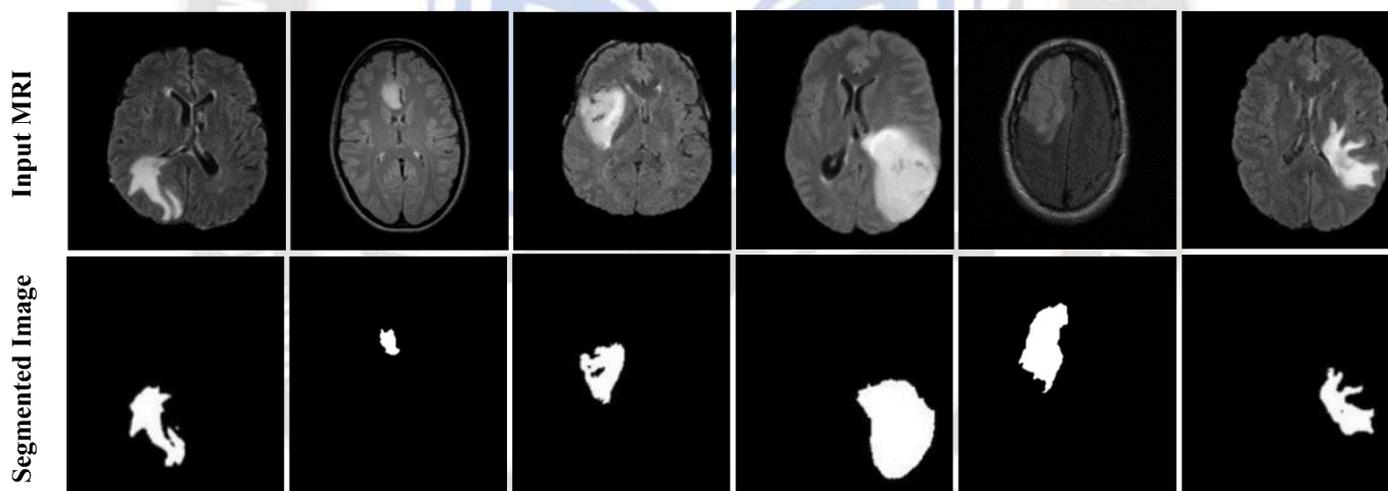
Figure 8: Segmented output mages

Figure 8 presents the human brain MRI images and the segmented output from our proposed method i.e., ResEA U-Net.

Segmented brain MRI output images refer to images that have been processed using a segmentation algorithm to identify and isolate specific regions of the brain.

The conclusion drawn from segmented brain tumour images depends on various factors, including the type, size, location, and stage of the tumour. Quantitative measurements from the segmentation method, such as tumours volume and tumours-to-brain volume ratio, can aid in prognosis and therapy selection.
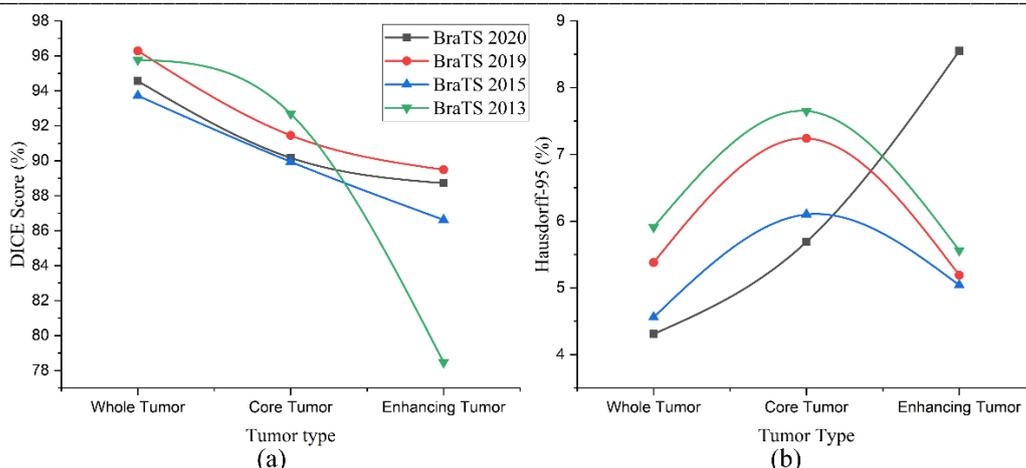
Figure 9: Plots of (a) DSC (%) and (b) Hausdroff (%)

Dice score and Hausdorff distance are two metrics used in image segmentation and analysis to evaluate the accuracy of a segmentation technique. The Sorensen-Dice coefficient (or Dice score) is a common metric used to evaluate the degree to which a segmentation's output resembles a given reference segmentation. To calculate it, we divide the sum of the two groups by their median size.

The Hausdorff distance is a measure of the farthest feasible separation between two sets of coordinates. In the context of image segmentation, it is typically used to quantify the largest difference between the segmentation result and the reference segmentation. The Hausdorff distance is calculated by finding the furthest point from one set to the other. The Hausdorff distance is useful for segmentation since it considers both false positives and false negatives. A smaller Hausdorff distance indicates more successful segmentation.

The Dice scores (DSC) and Hausdroff (H-95) values for WT, CT & ET of our proposed method i.e., ResEA U-Net for various data sets, BraTS 2020, BraTS 2019, BraTS 2015 & BraTS 2013 respectively were plotted and can be seen from figure 9(a) and 9(b). We achieved a better value than other benchmark value.

The figure 10 is the plot, which shows the sensitivity of our proposed algorithm on various benchmarking datasets with various types of tumours. There is a sharp inclination in WT,CT and ET from BraTS 2013 to BraTS 2015, then there is a small declination from BraTS 2015 to BraTS 2017. And finally, there is an inclination in WT, CT, and ET from BraTS 2019 to BraTS 2020. The highest accuracy obtained to our proposed model for all the metrics WT, CT and ET is for the 2020's BraTS dataset.

The specificity of the proposed ResEA U-Net algorithm has been tested on various benchmarking datasets and the plots were presented in figure 11. There is a sharp inclination in WT, CT and ET from BraTS 2013 to BraTS 2015, then there is a small declination from BraTS 2015 to BraTS 2017. And finally, there is an inclination in WT, CT, and ET from BraTS 2019 to BraTS 2020.
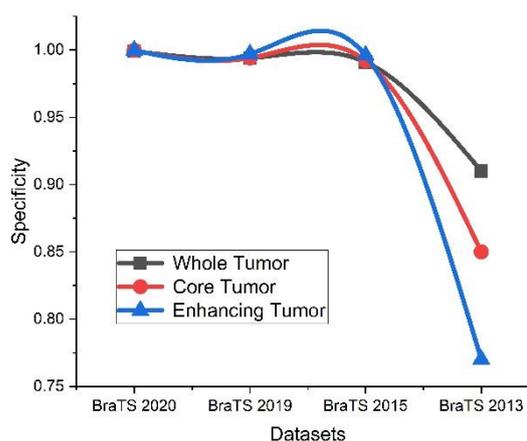
Figure 11: Specificity on different datasets.

Figure 10: Sensitivity plot.

Finally, the highest accuracy obtained to our proposed model for all the metrics WT, CT and ET is for the 2020's BraTS dataset.

VII. CONCLUSION

In conclusion, the Residual edge attention method in U-Net has shown promise in the segmentation of brain tumours. The model's training as a whole is enhanced by residual connections, which assist alleviate the issue of disappearing gradients. The edge attention technique improves segmentation results by emphasizing features close to the tumour's borders. Numerous analyses have demonstrated that the proposed method is more effective and efficient than baseline U-Net models for segmentation. The residual edge attention technique is easy to implement in existing deep learning systems and can be used to complete other segmentation tasks for medical pictures. To further assist clinical decision-making, nevertheless, it would be helpful to explore the model's interpretability and learn how it makes decisions. In overall, U-residual Net's edge attention method has shown a lot of promise for improving brain tumour segmentation, and it has also opened new research avenues in the field of medical image analysis.

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