EN3160 – Image Processing and Machine Vision

Project – Brain Tumor Segmentation from MRI Images

Index No: 200041E, 200285E

Team: Mahotas

Git Hub link:
https://github.com/askanuradha/Brain_Tumor_Segmentation_using_Deep_Learning/tree/main

---

Abstract

Brain tumor segmentation in magnetic resonance imaging (MRI) scans is a critical task in medical image analysis, as it plays a pivotal role in diagnosis and treatment planning. This paper presents a novel approach for brain tumor segmentation using a U-Net Convolutional Neural Network (CNN). The U-Net architecture is well-suited for semantic segmentation tasks due to its ability to capture fine-grained details and features within medical images.

Our proposed method begins with preprocessing the MRI scans to enhance contrast and reduce noise, improving the quality of input data. We then employ a U-Net CNN that consists of an encoder and decoder network, with skip connections to preserve spatial information. The network is trained on a large dataset of annotated MRI scans, which includes various tumor types, sizes, and locations.

During the training process, we employ data augmentation techniques to improve model generalization and prevent overfitting. The proposed U-Net CNN learns to segment brain tumors accurately by iteratively adjusting its parameters, and the model's performance is evaluated using various evaluation metrics, including Dice coefficient, dice coefficient loss, soft dice loss, intersection over union, specificity, f1 score and sensitivity.

Our experiments demonstrate that the U-Net CNN achieves state-of-the-art results in brain tumor segmentation, outperforming traditional methods and other deep learning architectures. The high accuracy and consistency of the proposed approach make it a valuable tool for radiologists and clinicians in the field of neuroimaging, aiding in the precise localization and characterization of brain tumors.

Furthermore, the U-Net CNN's ability to provide detailed tumor segmentations can facilitate treatment planning and monitoring, potentially improving patient outcomes. In conclusion, this study highlights the potential of U-Net CNNs as a powerful tool for brain tumor segmentation in MRI scans, offering promising prospects for the field of medical imaging and healthcare.

Introduction

Glioma, a type of brain tumor, represents a serious medical condition with potentially fatal consequences if not detected and treated in its early stages. The malignancy of gliomas is exacerbated by their propensity to infiltrate neighboring brain regions. According to the World Health Organization (WHO), an alarming statistic looms over the United States, with an estimated 23,820 adults and 5,270 children expected to receive a brain tumor diagnosis this year. The successful treatment of brain tumors hinges on various factors, including the patient's age, tumor type, and its precise location within the brain. Often, the insidious growth and diffusion of these tumors into adjacent healthy brain tissue complicate diagnosis and therapeutic interventions. Hence, it becomes imperative to develop accurate segmentation techniques for brain tumors, particularly in their early stages, to improve patient survival rates.

This research endeavors to classify gliomas into three significant categories: peritumoral edema, necrotic & non-enhancing tumors, and enhancing tumors. Delineating these categories is instrumental in tailoring effective treatments for patients. Magnetic Resonance Imaging (MRI) has emerged as a primary diagnostic tool for capturing detailed images of brain tumors. By configuring MRI scanners to capture different modalities, such as T1-weighted (T1), T1-Post contrast-enhanced (T1ce), T2-weighted (T2), and T2-weighted fluid-attenuated inversion recovery (Flair), medical professionals can gain critical insights into the nature of the tumors. T1 images excel in tumor-brain tissue segmentation, while T1ce images enhance the visibility of tumor boundaries. T2 images reveal edema (fluid) around the tumor, and Flair images are adept at identifying edema regions within the cerebrospinal fluid. The availability of three-dimensional views (Sagittal, Axial, and Coronal) facilitates comprehensive tumor examination by medical experts. Each tumor type exhibits distinct characteristics, with enhancing tumors predominantly displaying hyper-intensity in T1-weighted images, and non-enhancing and necrotic tumors, both core tumors, appearing hypo-intense in T1-weighted images. Peritumoral edema, often associated with meningiomas, can extend from nearby tumors.

Accurate segmentation of brain tumors in MRI images is an intricate challenge, primarily due to the intricate structure and varied appearances of tumors. Tumor borders tend to be indistinct, and their diffusion into neighboring brain regions further complicates differentiation from healthy tissue. Consequently, manual delineation of tumor boundaries in MRI images is time-consuming and susceptible to errors. Automatic brain tumor segmentation, powered by machine learning techniques, presents a promising solution to these issues, offering rapid and reliable diagnoses by precisely identifying tumor types and locations. Early tumor detection and treatment can be pivotal in curing patients.

In recent years, deep neural networks, particularly Convolutional Neural Networks (CNNs), have gained prominence in the field of image segmentation. CNNs excel in feature extraction and learning from images, offering remarkable accuracy. Numerous researchers have harnessed the power of CNNs to automate brain tumor segmentation in MRI images. This study aims to investigate popular CNN architecture called U-Net.

The U-Net architecture is a popular convolutional neural network (CNN) structure designed for semantic image segmentation tasks, where the goal is to classify each pixel in an image into specific classes or segments. It was originally introduced for biomedical image analysis, particularly for cell and tissue segmentation in microscopy images, but it has since found applications in various fields, including medical imaging, satellite image analysis, and more.

Segmentation of brain tumors using MRI image is shown in Figure 1.

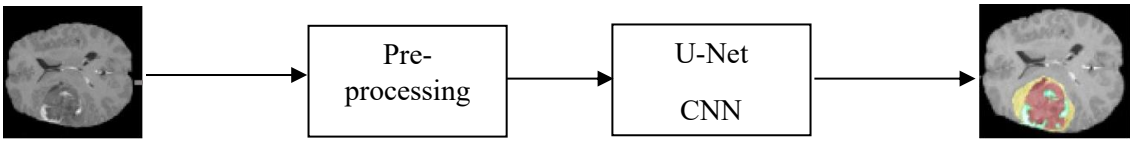


Figure 1

Related works

In the realm of brain tumor segmentation from MRI images, the task is inherently complex due to variations in intensity, shape, location, and boundaries of brain tissue across individuals. Consequently, various advanced approaches have been introduced to automate this process, with deep learning methods proving particularly effective.

Pereira (2016): Pereira presented a deep neural network architecture designed to handle these complexities. The architecture employs small 3x3 convolution filters to maintain a longer depth, allowing for the extraction of more features from input images. Comprising three convolution blocks with a depth of 11 layers, it includes six convolutional layers with 3x3 filters, two max-pooling layers, and three fully connected layers. Prior to training, preprocessing steps are undertaken to normalize intensity across all images and filter out noise by calculating standard deviations and mean intensity values across all training images. The proposed model achieved commendable accuracy rates, with 88% for whole tumor segmentation, 83% for core tumor, and 77% for active tumor segmentation in the BraTS dataset.

Urban (2014): Urban introduced an innovative three-dimensional convolutional neural network (3D CNN) for the segmentation of brain tumors in multi-modality MRI images. This approach, though computationally intensive, offers a valuable advantage in the form of 3D visualization, which enhances radiologists' understanding of tumor development. The architecture incorporates 3x3x3 convolution filters, batch normalization layers, ReLU activation functions, and 3D max-pooling layers. Input data are stacked into a 4D volume, representing the height, width, image channels, and the number of modalities. The model demonstrated substantial segmentation accuracy, achieving 87% accuracy for whole tumor, 77% for core tumor, and 73% for active tumor region in the BraTS dataset.

Salma Xsun (2019): Salma Xsun introduced a SegNet-based approach for the automated segmentation of brain tumors, training each MRI modality separately and combining their outputs during post-processing. Preprocessing steps involve normalization and bias field correction to eliminate unwanted artifacts, enhancing segmentation performance. SegNet is employed for separate training on the four distinct MRI modalities. The architecture is characterized by an encoder-decoder structure, featuring 13 convolutional layers with 3x3 filters, batch normalization, ReLU activation, and max-pooling layers with 2x2 filters in both the encoder and decoder. The resulting segmented features from the decoder are directed to softmax layers, classifying each pixel within its specific class. The segmentation technique achieved remarkable accuracy, with 85% for whole tumor, 81% for core tumor, and 79% for enhancing tumor in the BraTS dataset.

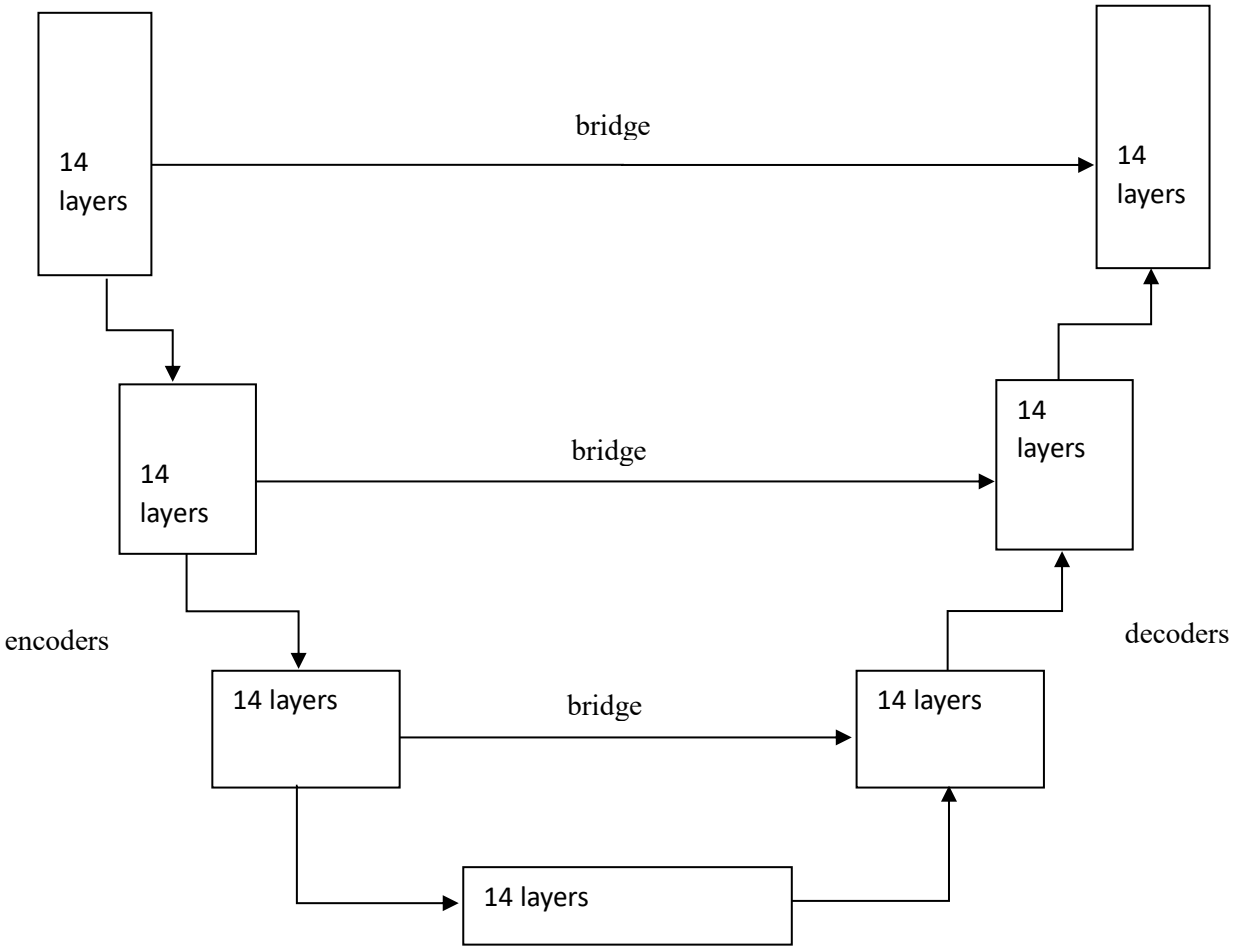
Hussain Shave (2017): Hussain Shave proposed a cascaded two-pathway CNN model, extracting both large 37x37 and smaller 19x19 patches concurrently. To mitigate overfitting concerns stemming from the model's high number of learnable parameters, the architecture incorporates maxout and dropout layers. The model comprises six convolutional layers with diverse filter sizes, facilitating the learning of features of varying sizes. ReLU activation functions are employed, and the output of the first CNN is cascaded with the input

of the second CNN for end-to-end training. Preprocessing involves applying the 3D slicer toolkit to MRI images for bias field correction, enhancing segmentation performance. This approach yielded significant segmentation accuracy, achieving 80% for complete tumor, 67% for core tumor, and 85% for enhancing tumor in the BraTS dataset.

These deep learning-based approaches have made substantial contributions to the field of brain tumor segmentation within MRI images, providing effective solutions to address the intricate nature of brain tumors and the need for accurate, automated segmentation techniques.

Proposed approach

Here we proposed to use the U – Net architecture for the image segmentation. The following figure shows the U - Net architecture. This CNN architecture consists of encoders, decoders and skip connections.



Encoder-Decoder Structure: The U-Net architecture is characterized by an encoder-decoder structure. The encoder part extracts feature from the input image through a series of convolutional layers and pooling operations, gradually reducing spatial dimensions while increasing the number of feature maps.

Skip Connections: One of the key innovations in U-Net is the inclusion of skip connections. These connections directly connect layers from the encoder to corresponding layers in the decoder. They help in preserving high-resolution spatial information, which is crucial for accurate segmentation. Skip connections enable the network to combine both local and global features, improving segmentation accuracy.

Training and Implementation details

After a thorough analysis of the dataset, it was observed that the axial plane images exhibit enhanced visibility of tumor boundaries and diffusion into other regions of the brain. This characteristic contributes significantly to improved tumor segmentation. Consequently, the 3D MRI scans were transformed into 154 2D slices along the axial plane. The intensity values of these images were pre-processed through normalization. The dataset comprises 1251 T1ce, T1, T2 and flair images extracted slice by slice from HGG patients. A sample of MRI image obtained by different MDR modality is shown in Figure 2.

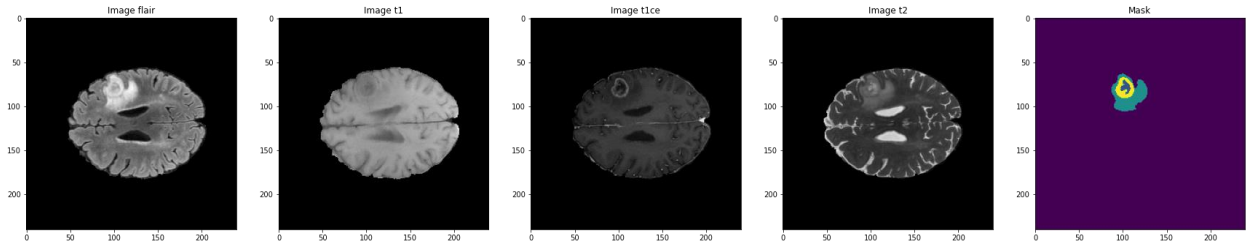


Figure 2

For model development, 80% of the dataset was allocated for training, while the remaining 20% was set aside for testing. The Data Distribution as follows:

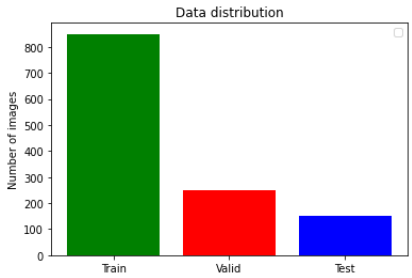


Figure 3

The CNN models were trained on a single CPU by accelerating it by a GPU P100, utilizing consistent training parameters for comparative performance evaluation. The training process employed by using the adam optimizer. Specifically, the training parameters were configured as follows: learning rate = 0.001, beta_1 = 0.9, beta_2 = 0.999, and epsilon = 1e-07. which are the default parameters for the Adam optimizer. The model was trained for 10 epochs. The mini-batch size was set to 16, and the model's architecture, as well as the data dimensions, were defined with an input shape of (128, 128, 2) to suit the data's characteristics. The training process used various evaluation metrics, such as accuracy, Mean IoU, precision, recall, AUC, f1_score, specificity, sensitivity, IoU, dice coefficient, and dice coefficient loss for performance analysis.

Early stopping was introduced to prevent overfitting. Larger epoch values minimize errors and result in improved segmentation outcomes. A mini-batch of 16 was chosen, as it is suitable for training on a single CPU, and increasing the mini-batch size could enhance results but would require higher memory resources.

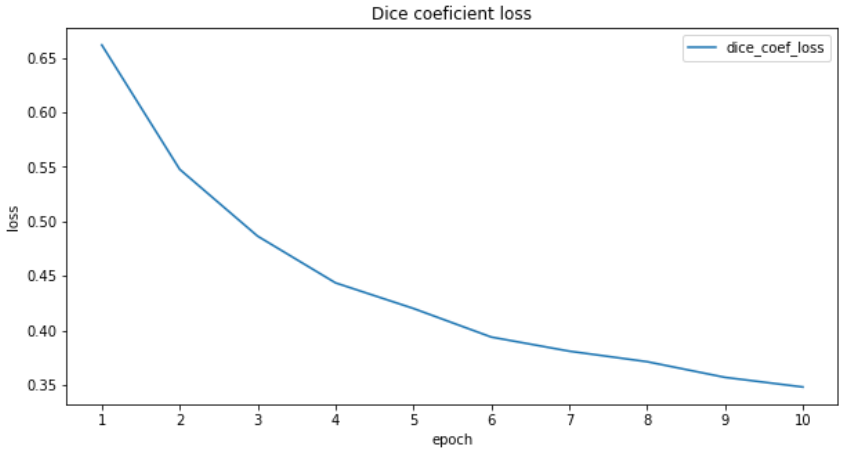
Results and Discussion

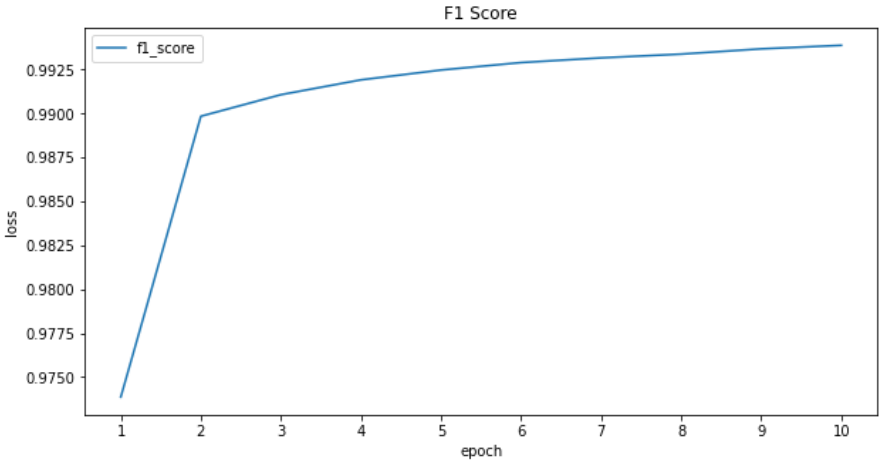
The study examines the efficacy of the implemented U-Net architecture in terms of segmenting different regions, including enhancing tumors (green), necrotic and non-enhancing tumors (red), peritumoral edema (yellow), and other structures (gray). The model takes neurons as input in the initial layer and processes them through multiple hidden layers. These neurons are categorized into four distinct classes in the output layer.

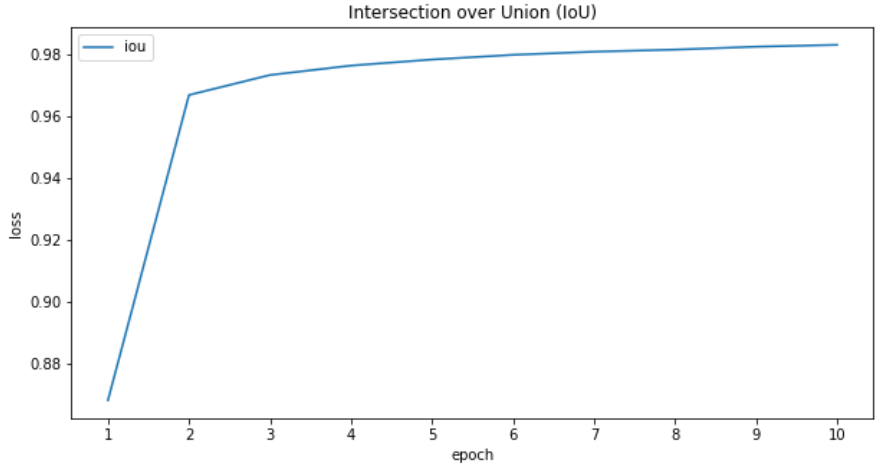
In order to assess the model's segmentation performance, various metrics such as loss, accuracy, mean IoU, precision, recall, AUC, F1-score, and more are taken into account. The values of these metrics are recorded at each epoch as follows:

	loss	accuracy	mean_io_u	precision	recall	AUC	f1_score	specificity	sensitivity	iou	dice_coef
0	0.114881434	0.982131064	0.375526875	0.992868662	0.961686373	0.997997761	0.973868847	0.997108519	0.964466035	0.86818558	0.338196367
1	0.032290403	0.990087748	0.375526935	0.994019449	0.984813213	0.999518275	0.989851713	0.997378588	0.987395108	0.966779232	0.452255309
2	0.02642189	0.991411567	0.375526965	0.994693995	0.986835718	0.999592483	0.991078615	0.997579753	0.989296496	0.973235846	0.513501525
3	0.023656702	0.992341936	0.375527054	0.99519515	0.988121152	0.999625623	0.991923273	0.997740865	0.990534246	0.976275921	0.556362569
4	0.021607431	0.992920578	0.375526965	0.995583415	0.988904655	0.999679089	0.992482603	0.997867048	0.99129045	0.97824049	0.579846978
5	0.020135766	0.99338913	0.375526965	0.995841265	0.989548087	0.999702275	0.992906928	0.99794668	0.991909027	0.979749024	0.606085718
6	0.019193999	0.99367851	0.375526905	0.996002734	0.989939153	0.999712765	0.993175685	0.997999966	0.992292762	0.980767906	0.619008362
7	0.018579394	0.993903518	0.375530869	0.996155739	0.990224898	0.99971211	0.993388891	0.998050392	0.992572248	0.981437683	0.628671885
8	0.017556213	0.99421829	0.375536203	0.996401548	0.990604103	0.999734104	0.993688345	0.998127222	0.992939353	0.982380092	0.643040717
9	0.016855467	0.994440794	0.375553519	0.996548891	0.990845799	0.999750316	0.993888676	0.998177409	0.993186176	0.982977629	0.651890218

The graphical representation of some of above parameters as follows:







The following results are taken from the testing data.

```
F1-Score: 0.9587984085083008
Sensitivity: 0.9576299786567688
Specificity: 0.9866868853569031
IOU: 0.9173577427864075
Dice-Coefficient: 0.2788873612880707
Dice-Coefficient loss: 0.7211126089096069
Soft-Dice loss: 0.7218898236751556
```

In summary, the U-Net model has proven to be a highly effective and dependable tool for accurately identifying and mapping brain tumors. It offers improved precision in diagnosing brain tumors, planning treatment, and monitoring the effectiveness of therapies. This has significant implications for the field of medical imaging and the treatment of brain cancer.

Our research not only contributes to the ongoing development of medical imaging but also has a profound impact on the lives of brain tumor patients. By providing more accurate and reliable tumor segmentation, the U-Net model has the potential to revolutionize how we approach the management of brain tumors. This could lead to better treatment outcomes, reduced treatment-related challenges, and an overall improvement in the quality of life for those living with this condition.

As technology in machine learning and medical imaging continues to advance, our findings highlight the substantial potential of the U-Net model in reshaping how we diagnose and treat brain tumors. Further research and its integration into clinical practice may usher in an era of more precise and effective medical care, benefiting both healthcare professionals and patients.

References

1. *Pereira, S´ergio and Pinto, Adriano and Alves, Victor and Silva, Carlos A. (2016) "Brain tumor segmentation using convolutional neural networks in MRI images." IEEE transactions on medical imaging35(5): 1240–1251.*
2. *Urban, Gregor and Bendszus, M and Hamprecht, F and Kleesiek, J (2014),"Multi-modal brain tumor segmentation using deep convolutional neural networks", MICCAI BraTS (Brain Tumor Segmentation) Challenge. Proceedings, winning contribution31: 35.*
3. *Alqazzaz, Salma and Sun, Xianfang and Yang, Xin and Nokes. (2019) "Automated brain tumor segmentation on multi-modal MR image using SegNet." Len,Computational Visual Media1: 11.*
4. *Hussain, Saddam and Anwar, Syed Muhammad and Majid, Muhammad. (2017) "Brain tumor segmentation using cascaded deep convolutional neural network." 2017 39th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC)1998: 2001.*