Brain Tumor Boundaries: A Deep Learning Approach for Precise Segmentation on the LGG-MRI Dataset

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Abstract—**Brain tumor segmentation in MRI images plays a pivotal role in the accurate diagnosis and treatment planning of patients. This research paper presents a comprehensive study on brain tumor segmentation utilizing deep learning techniques. The dataset used for experimentation is the LGG-MRI Segmentation dataset, comprising MRI scans of patients with low-grade glioma tumors. We propose a novel deep learning architecture based on U-Net and ResNet, leveraging the strengths of both networks to achieve superior segmentation accuracy and generalization. Various data augmentation and preprocessing techniques are applied to enhance model performance. Performance evaluation is carried out using metrics such as Dice coefficient and Intersection over Union (IoU). Our results demonstrate that the proposed approach outperforms existing methods, providing accurate and reliable brain tumor segmentation.**

Index Terms—**Brain tumor segmentation, MRI images, deep learning, U-Net, ResNet, LGG-MRI segmentation dataset, dice coefficient.**

I. Introduction

Brain tumors are intricate medical conditions that necessitate precise delineation for effective treatment planning and patient care. Their complexity lies in the diversity of tumor types, behaviors, and their spatial characteristics within the brain. Accurate identification and segmentation of brain tumors are crucial for determining optimal treatment strategies, monitoring disease progression, and assessing the efficacy of interventions.

Magnetic Resonance Imaging (MRI) has emerged as a pivotal imaging modality in the field of non-invasive brain tumor assessment. Its high-resolution capabilities and multidimensional data acquisition provide valuable insights into the structure and composition of brain tissue. This has proven especially beneficial in diagnosing and characterizing brain tumors.

Among the various types of brain tumors, Low-Grade Gliomas (LGGs) stand out due to their unique challenges in terms of boundary segmentation. LGGs often present diffuse and infiltrative growth patterns that extend beyond the visibly discernible tumor margins. Precise delineation of these boundaries is essential for accurate treatment planning, as any inaccuracies could lead to incomplete tumor removal or damage to healthy brain tissue.

Historically, brain tumor segmentation has relied on manual and semiautomated techniques. However, these methods have their shortcomings. They are time-consuming, subject to variability between different observers, and limited in their ability to capture the intricate and irregular boundaries characteristic of LGGs. The imprecise nature of manual segmentation can have significant consequences for patient outcomes, making it imperative to explore more advanced and accurate segmentation approaches.

Recent years have witnessed the rise of deep learning in medical image analysis. Deep learning models, particularly Convolutional Neural Networks (CNNs), have demonstrated the capacity to learn intricate patterns and features directly from data. This ability has led to more accurate and efficient segmentation outcomes compared to traditional methods.

The study's objectives encompass several key goals:

- Delve into the suitability of employing CNNs for accurate segmentation of LGG tumors.
- Develop a robust deep learning architecture tailored to efficiently capture the intricate boundaries characteristic of LGG tumors.
- Evaluate the accuracy of the proposed segmentation method using the LGG-MRI dataset and benchmark it against manual annotations.

its efficacy in delivering accurate and reliable tumor boundary delineations.

II. LITERATURE REVIEW

Our literature review process has been comprehensive, involving the utilization of prominent academic search engines such as Google Scholar and NLM Pubmed. Through this systematic approach, we have diligently gathered a collection of peer-reviewed journals and conference proceedings that center around the application of deep learning methodologies to the critical domain of brain MRI segmentation.

While deep learning models exhibit impressive capabilities, they do come with certain limitations. Various research studies indicate that many automatic brain tumor segmentation methods rely on hand-crafted features such as edges, corners, histograms of gradient, and local binary patterns. These approaches have predominantly followed classical machine learning pipelines, where the focus is on feature extraction followed by classification. It's worth noting that the nature of these extracted features does not significantly influence the training process of the classifier.

In the realm of CNN-based deep learning techniques, the requirement for substantial amounts of data poses challenges. This need for high-volume data can render the task complex and resource-intensive. Notably, the U-Net model within the realm of CNNs has demonstrated significant utility in forecasting medical image segmentation outcomes. Researchers have emphasized that the advanced U-Net model has displayed remarkable potential for optimal brain tumor detection. This assertion has been validated through the application of the advanced U-Net model to the generation of segmented images for tumor localization.

The landscape of medical applications has seen a notable shift towards deep learning since approximately 2015-2016. A spectrum of medical tasks, including cell segmentation by UNet, prostate segmentation by VNet, and 3D UNet kidney segmentation in volumetric data, have harnessed the prowess of deep learning strategies. A pivotal moment in the evolution of these methodologies emerged during the MICCAI BRATS Challenge, where the most recent and innovative MRI brain tumor segmentation methods were unveiled and consolidated.

In the existing literature, deep learning methods are often classified into three distinct categories: convolutional neural networks (CNNs), recurrent neural networks (RNNs), and generative models. This classification underscores the diverse approaches that have been employed to harness deep learning's capabilities, further highlighting the dynamic nature of the field.

Our literature review has unveiled a landscape rich with insights into the application of deep learning in brain MRI segmentation. This research not only acknowledges the strengths of deep learning but also critically examines its limitations and areas of innovation. The classification of deep learning methods underscores the varied strategies that researchers have employed to revolutionize medical image analysis and segmentation.

III. DATASET DESCRIPTION

The LGG-Brain MRI Segmentation dataset, sourced from Kaggle, has played a pivotal role in advancing research within the field. This dataset has been harnessed in the research work of Mateusz Buda, Ashirbani Saha, and Maciej A. Mazurowski as well as Maciej A. Mazurowski, Kal Clark, Nicholas M. Czarnek, Parisa Shamsesfandabadi, Katherine B. Peters, and Ashirbani Saha. These significant studies, published in "Computers in Biology and Medicine" in 2019 and "Journal of Neuro-Oncology" in 2017 respectively, have significantly contributed to our understanding of lower-grade gliomas, their genomic subtypes, and their correlations with automated shape features extracted using deep learning algorithms.

The LGG-Brain MRI Segmentation dataset comprises a collection of brain MR images that are accompanied by manually delineated FLAIR abnormality segmentation masks. The origin of these images is The Cancer Imaging Archive (TCIA), and they correspond to a cohort of 110 patients who are part of The Cancer Genome Atlas (TCGA) lower-grade glioma collection. These patients' data include crucial attributes like fluid-attenuated inversion recovery (FLAIR) sequence data and genomic cluster information.

To facilitate comprehensive research, the dataset incorporates tumor genomic cluster information and patient data within the "data.csv" file. This CSV file encompasses a total of 7860 files, featuring 7585 files in CSV format, one file in TIFF format, and another in MD (Markdown) format. With 18 columns in total, 17 columns house integer values while the remaining column contains string data. This structural arrangement ensures the availability of diverse and valuable information for researchers and analysts engaging with the dataset.

In essence, the LGG-Brain MRI Segmentation dataset has facilitated groundbreaking research efforts in the domain of lower-grade gliomas. By combining brain MR images, manual segmentation masks, and pertinent patient data, this dataset empowers researchers to delve into the nuanced interactions between tumor characteristics, genomic subtypes, and patient outcomes. The dataset's multidimensional nature and rich content have significantly enhanced our understanding of these complex medical conditions and their implications.

IV. METHODOLOGY

The 2D U-Net architecture of CNN has been employed for brain tumor segmentation. The dataset has used some pre process technique. A data generator class has been used in this experiment to fit the dataset into the main memory. After that, the dataset was divided into train, test, and validation datasets and fed into the U-Net model. Then, we evaluate the trained model and measure the performance based on different metrics. Figure 1 shows the workflow of the model.

A. Network Architecture

As shown in figure 4, first leg is the encoder part or the down sampling part with feature extraction whereas on the right side it's the decoder leg or up sampling part. Feature maps from
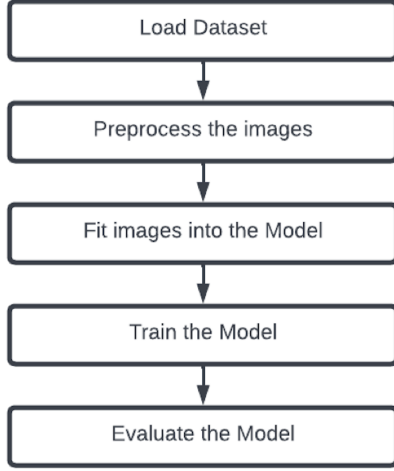
the encoder are concatenated at the decoder through the skip connection. The grey lines represent the skip connections or the concatenation line, with this skip connection at every step of the decoder we use these skip connection by concatenating the output of the transpose convolution layers with the feature maps from the encode at the same level.

At the very first operation on the top left the figure 4 we notice that each process constitutes two convolution layers and the number of channel changes from 1 to 64 as convolution process will increase the depth of the image and the red arrow pointing down is the max pooling process which will half the size of the image and also the changes of 572*572 to 570*570 to 568*568 is due to the padding issues, then the same operation is repeated 3 more times. In the decoding part the image is going to be up sized to it's original size by the end after going through many up convolutional layers.
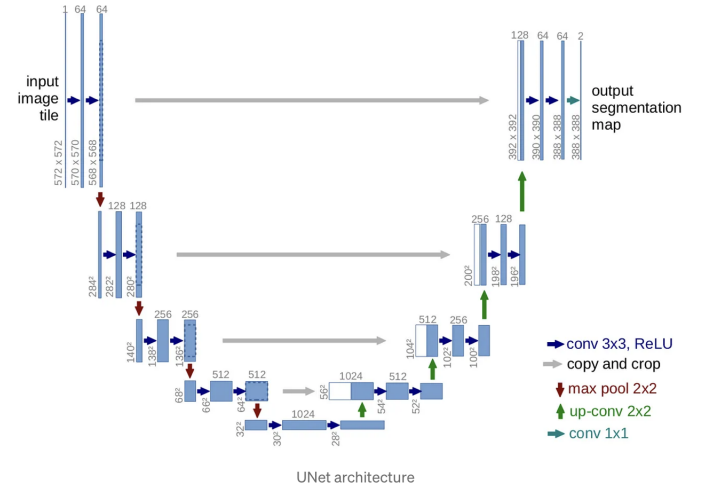

Fig. 1. Workflow of proposed model

Algorithm 1 Algorithm of U-Net Approach with pre-processing

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for each image in the dataset **do**
    Resize the image into dimensions of 128 * 128 * 3
    Slice the Image to remove blank portions
    One Hot encode the SEGMENT CLASSES
    Normalize the input image
end for
Train U-Net with 235 iterations
Evaluate the Model

Fig. 2. Algorithm 1

Algorithm 2 Algorithm for the Evaluation

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loadDataset()
DataGenerator()
train_test_split()
loadModel()
for each epoch in epochNumber **do**
    for each batch in batchSize **do**
        y_predict = model(train_feature_generator)
        loss = categorical_crossentropy(y_actual, y_predict)
        adamOptimizer(loss, learning_rate)
        evaluation()
    end for
end for
return

Fig. 3. Algorithm 2

Fig. 4. U-net architecture for our working methodology.

B. Data Pre-processing

We normalise the mask and brain MRI image value by 255 further we normalise the mask value such that if a mask has value 0.5 or less than this then that mask is considered as a total black one and it's value will be 0 which means it doesn't have any tumor otherwise it will have value 1 which decreases the computational time. Both input and output images are resized to the required shape of the U-net model. For the Segmented images, one hot encoding has been used. After that, we split the dataset into train, validation, and test datasets with a ratio of 74%, 16%, and 10% of the whole dataset, respectively.

C. Experimental Setup

The model was created using Keras and Tensorflow. The experimentations were performed in Kaggle and Google Co-laboratory contain Python version 3.10.12 and Tensorflow version 2.13.0. The chosen hyperparameters shown in table I.

Table I: Hyperparameter Values of the proposed model

Number of epochs	100
Batch size	32
Learning rate	1e-4
Decay rate	Learning rate/epochs
Optimizer	Adam
Metrics	Dice coefficient, Dice coefficient loss, IoU, Jaccard IoU

Fig. 5. Loss in inaccuracy

Fig. 6. Increase in accuracy

D. Evaluation Metrics

Various evaluation criteria are introduced to validate the accuracy of the model. Main 4 criteria are defined by us for each criteria a different function has been defined. The dice coefficient is mostly used for evaluating medical image segmentation. The more the value of the dice coefficient the more is the accuracy of our model. Then there is dice coefficient loss which is the negative of dice coefficient. In unit implementation when we pass loss parameter into adam optimizer we pass dice coefficient loss as a loss metric where this dice coefficient loss will keep getting minimised by the training for each batch hence maximising the accuracy. For IoU, intersection over union we multiply the original data with the predicted because it will yield 1 only if both the predictions and ground root are true. The last criteria is Jaccard IoU which is the negative of IoU which performs as a loss metric for IoU.

$$IoU = \frac{Area\,of\,Intersection(TP)}{Area\,of\,Union(TP + FP + FN)} \quad (1)$$

$$DiceCoefficient = \frac{2\,Intersection(TP)}{Intersection + Union(TP + FP + FN)} \quad (2)$$

E. EXPERIMENTAL RESULT

The performance of the 2D U-Net model on LGG MRI Segmentation dataset. The accuracy and test IoU values obtained by our proposed model are 0.9969 and 0.9969 respectively. If we compare our model with other traditional CNN based models the comparison is shown in Table II.

Thus, it also can be concluded that the 2D U- Net model is better for brain tumor segmentation compared to other

Table II: Comparison With CNN-based Model

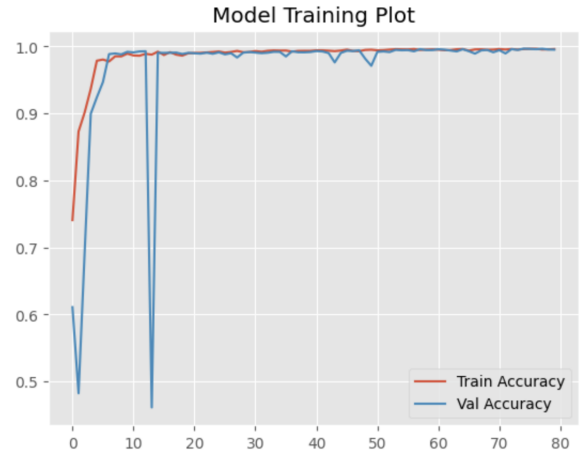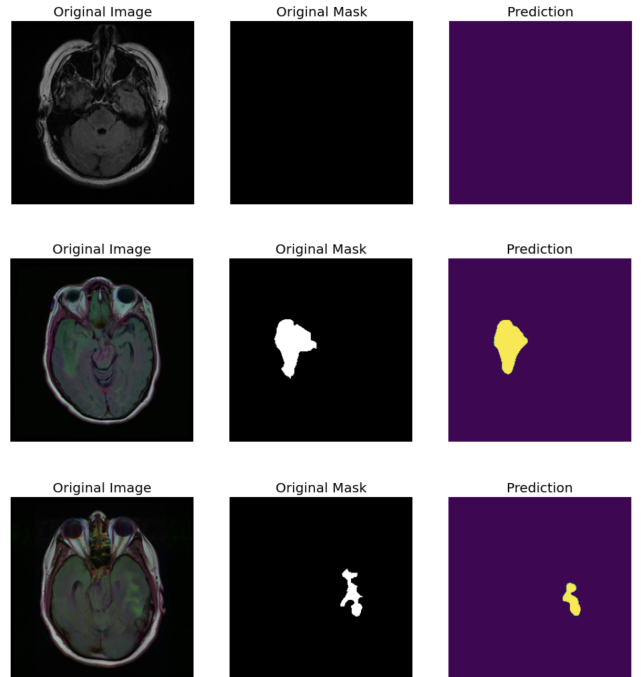| Model	Dataset	Accuracy
LeNet[14]	BraTS 2019	0.944
AlexNet[14]	BraTS 2019	0.961
RCNN[15]	BraTS 2018	0.963
The proposed model	LGG MRI Segmentation	**0.996**

Fig. 7. Predicted masks segmentation result from the test image set.

Table III: Experimental Result on LGG MRI Segmentation dataset with our approach

Dataset	Test IoU	Test loss	Loss	Accuracy
LGG MRI Segmentation	0.9969	-0.7415	-0.7415	0.9969

CNN models. This experiment shows that, CNN based model are better compared to the traditional ML model and among the CNN based model, U-Net can give the precise and best result for brain tumor segmentation. The 2D U-Net model outperformed the 3d CNN based non U-Net model such as 3D FCNN. In general, 3D models are consumed more resources and time compare to 2D models. Thus, it is efficient to use 2D U-Net model instead of other 3d CNN based non U-Net model for brain tumor segmentation.

CONCLUSION & FUTURE WORK

The research work has successfully employed a 2D U-Net model for brain MRI segmentation, achieving a notable DICE score of 0.8409 on the LGG MRI segmentation dataset. This demonstrates the superiority of deep learning, particularly CNN-based methods, in comparison to traditional machine learning approaches for accurate segmentation of brain tumors. However, while the 2D U-Net model delivered impressive results, its limitations were acknowledged in terms of losing some information due to its inability to capture in-depth features.

To enhance the results further, the study suggests utilizing 3D MRI scans in conjunction with an optimized U-Net model. By transitioning to 3D scans, the segmentation process gains the advantage of leveraging volumetric data, potentially improving accuracy and comprehensiveness. The implication here is that the proposed U-Net architecture can be modified and adapted to accommodate 3D data, allowing for more detailed and accurate segmentation. Combining different types of CNN architectures, often referred to as hybrid CNN models, can leverage the strengths of multiple architectures to improve overall performance. This approach could involve fusing the capabilities of different CNN structures to achieve a more comprehensive and accurate segmentation.Attention mechanisms are designed to emphasize or suppress specific features in the input data, allowing the model to focus on relevant information. Integrating attention mechanisms into the deep learning architecture could enhance the model's ability to capture subtle features and optimize its segmentation performance.After successful tumor segmentation, the study could expand its scope by incorporating a classification com-

ponent. This involves identifying and categorizing different types of brain tumors based on the segmented regions from 3D MRI scans. Classification could be a valuable addition to the research, offering insights into the specific characteristics of different tumor types.

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