BRAIN TUMOR SEGMENTATION USING IMPROVED U-NET

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ABSTRACT

Brain tumor segmentation from magnetic resonance imaging (MRI) scans is a vital task in medical image analysis. To develop an accurate and robust brain tumor segmentation model, this project takes advantage of deep learning and the Tenforflow and keras framework. The project encompasses a series of steps, from data acquisition to model deployment, aiming to assist healthcare professionals in the diagnosis and treatment of brain tumors.
The project's foundation rests on acquiring a diverse dataset of brain MRI scans, which are carefully annotated with tumor masks. For model development, the architecture is implemented using tenforflow and keras, allowing us to leverage its powerful tensor operations and GPU support for accelerated training. To ensure the model's generalization to unseen data, rigorous validation is conducted on the validation dataset. Fine-tuning of hyper parameters is performed to enhance the model's performance, balancing factors like precision and recall. The model's ultimate evaluation takes place on the test dataset, where it is assessed for its real-world performance in tumor segmentation. The developed model, trained on carefully annotated MRI scans, promises to contribute significantly to brain tumor diagnosis and treatment.

Keyword : - *Brain tumor segmentation , Tenforflow , Keras , and U-net .*

1. INTRODUCTION

Medical imaging has seen a dramatic transformation in recent years thanks to the integration of machine learning and deep learning algorithms. These advancements have significantly enhanced the process of tumor and disease segmentation, identification, and survival prediction. They also play a crucial role in aiding physicians in the early detection of brain malignancies, thereby improving prognostic outcomes. Gliomas, which commonly afflict adults and are believed to originate from glial cells and infiltrate neighboring tissues, constitute the primary type of brain tumor. Within the category of gliomas, there exist subtypes such as high-grade glioblastoma (HGG) and low-grade glioblastoma (LGG). While magnetic resonance imaging (MRI) modalities have traditionally undergone manual examination by radiologists to derive quantitative data, the segmentation of 3D modalities proves to be challenging due to variations and errors. This challenge is further compounded when tumors exhibit variability in size, shape, and location. [1].
TensorFlow, a popular deep learning framework, provides the necessary tools for building and training neural networks efficiently. The U-Net architecture consists of an encoder-decoder networkS with skip connections, enabling precise localization of tumors while preserving spatial information. By training the model on labeled brain imaging data, U-Net learns to segment tumor regions from healthy brain tissue with high accuracy. This

segmentation is crucial for various medical applications, including diagnosis, treatment planning, and monitoring of brain tumor progression[2].

1.1 U-net

The U-Net architecture, first introduced by Ronneberger et al. in 2015, has gained popularity in medical image segmentation tasks due to its ability to effectively capture spatial information and handle limited training data. It consists of a contracting path to capture context and a symmetric expanding path to enable precise localization. Brain tumor segmentation using U-Net is a crucial task in medical image analysis, particularly in the field of neuro-imaging. The aim of brain tumor segmentation is to accurately identify and delineate regions of interest within brain images that correspond to tumor tissue. This process plays a vital role in medical diagnosis, treatment planning, and monitoring of brain tumor patients.

1.2 Tenforflow and Keras

In the context of TensorFlow and Keras, brain tumor segmentation using U-Net involves implementing and training a U-Net model on a dataset of brain MRI images with corresponding ground truth segmentations. The model is trained to learn the mapping between input MRI images and their corresponding tumor segmentations, enabling it to accurately delineate tumor regions in unseen images.

2. EXISTING SYSTEM

Dimililera et al. (2016) provided a comprehensive understanding of brain tumors, delineating them as abnormal cell growth within the brain, classified into benign and malignant types, with primary tumors originating within the brain and secondary tumors spreading to other body parts. Given MRI's high resolution and image quality, it serves as the preferred imaging modality. Accurate segmentation of MRI brain images is crucial for radiotherapy planning, particularly for common tumor types like astrocytoma, oligodendroglioma, and glioblastoma. The study predominantly focuses on glioma segmentation, especially astrocytomas formed by star-shaped cells. Precise segmentation is essential for further diagnosis and to prevent damage to language and motor sensory functions during therapy. Manual segmentation, however, is labor-intensive and subjective, prompting the need for fully automatic and objective methods. Challenges arise from the variability in tumor size, shape, location, and appearance. Rémi et al. (2018) proposed a method for classifying high-grade gliomas, with a particular emphasis on astrocytomas, common in both adults and children and can range from low to high grade. They employed a fully automatic convolutional neural network (CNN) implemented in Python, utilizing frameworks like Anaconda and TensorFlow for machine learning concepts. This approach not only improved segmentation accuracy but also accommodated larger datasets. Performance evaluation was based on the BRATS database 2015, with segmentation results compared to ground truth images using the Dice coefficient. The research article adopts TensorFlow-based MRI brain tumor segmentation to enhance accuracy, speed, and sensitivity, deviating from traditional tools like MATLAB or LABVIEW. Python, chosen for its code readability, superior data structures, and availability of graphic packages and datasets, facilitates the implementation of the segmentation process. Additional Python packages aid in the research work's implementation, contributing to its efficiency. Preprocessing involves artifact removal and bias correction, crucial for improving segmentation accuracy. Techniques like n4T1K bias correction and median filtering help standardize pixel intensities and remove intensity gradients caused by inhomogeneity and patient movements during scanning. Noise reduction and bias correction play pivotal roles in enhancing data processing and providing better segmentation results. The availability of multiple radio frequency pulse sequences in the BRATS database, such as FLAIR, T1, T1 contrasted, and T2, enables obtaining chemical and physiological characteristics, enhancing contrast between individual classes. The proposed architecture leverages neural networks for segmentation, with CNN exploring small 3×3 kernels to handle spatial and structural variability. This design choice enables deeper architecture with fewer weights, addressing the challenges posed by automatic segmentation. The CNN algorithm performs voxel-wise classification, separating tumor or lesion portions from the background through input and convolution sections. The fully connected layer groups all feature maps, and the classification section estimates a prediction score for every image voxel, providing a segmentation map.

3. PROPOSED SYSTEM

Brain tumor segmentation was performed using the modified UNet architecture. A UNet model was built by feeding the dataset into the train, test and validation datasets. Our next step is to train the model. Different metrics were used to evaluate and measure the performance of the trained model.

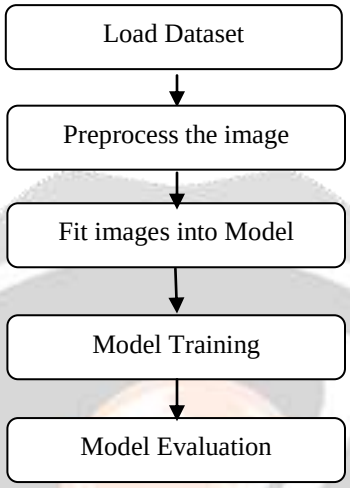

Fig -1: Workflow of proposed system

3.1 Network Architecture

The Unet architecture is a specialized variant of the Unet architecture primarily designed for sematic segmentation tasks, with a particular focus on applications in medical image analysis. It addresses challenges such as brain tumor segmentation, where precise tumor identification and delineation are vital for diagnosis and treatment planning. At its core, the RSPP-UNet follows the standard U-Net structure, starting with an encoder path that consists of convolutional blocks, each incorporating batch normalization and rectified linear unit (ReLU) activation. Max pooling is applied to progressively reduce the spatial dimensions of the input image. A distinctive feature of the RSPP-UNet is the introduction of Spatial Pyramid Pooling (SPP) immediately after the encoder. SPP is a mechanism that captures multi-scale contextual information by utilizing pooling layers with different kernel sizes (1x1, 2x2, and 4x4). This inclusion enhances the network's ability to handle objects of varying sizes within the input images. Following the SPP module, an additional Long Short-Term Memory (LSTM) layer is incorporated into the architecture. This recurrent layer plays a crucial role in processing the spatial information extracted by the SPP, enabling the model to capture long-range dependencies within the data. The decoder path involves the up-sampling of feature maps using transposed convolutions, with concatenation performed with corresponding feature maps from the encoder path. This design facilitates the localization of segmentation features during the decoding process. Within the decoder, two convolutional blocks are applied, each comprising convolutional layers, batch normalization, and ReLU activation. These blocks contribute to the refinement of segmentation features, further enhancing the network's ability to accurately delineate target structures. The final layer of the RSPP-UNet employs a 1x1 convolutional layer with a sigmoid activation function, generating the segmentation mask. In the context of the model's binary segmentation objective, this output represents the probability of each pixel belonging to the target class.

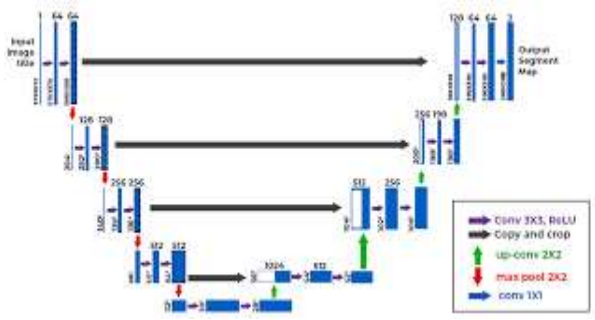

Fig -4: U-Net Architecture

3.2 Experimental Setup

The model was created using Tensorflow and Keras. The experimentations performed in Google Colaboratory containing Python version 3.9.13, Tensorflow version 2.7.0. The hyperparameters chosen are shown in table 1.

Number of epochs	100
Batch Size	32
Optimizer	Adam
Metrics	Acciracy, Dice Coefficient, IoU, Precision, Sensitivity, Specifivity

Table -1: Hyperparameter Values of propsed model.

3.3 Evaluation Metrics

Numerous evaluation criteria are caculated to check the efficiency of the implemented models. dice_coefficients function computes the Dice similarity coefficient between true and predicted binary masks. dice_coefficients_loss function calculates the Dice loss for image segmentation models. iou function calculates the Intersection over Union (IoU) between true and predicted binary masks. The intersection is computed using the sum of element-wise multiplication of true and predicted masks. IoU is a measure of the percent overlap between masks and is commonly used for segmentation evaluation. jaccard_distance function computes the Jaccard distance (1 - IoU) between true and predicted labels. Flattening is performed before calculations to compare sets of pixels, focusing on pixel-wise accuracy.

3.4 Experimental Result

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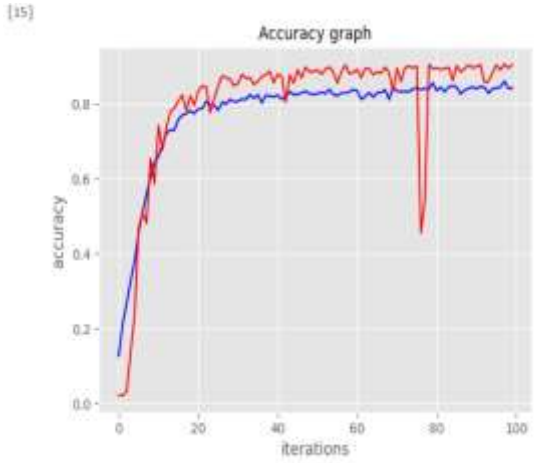

Fig -5: Accuracy graph

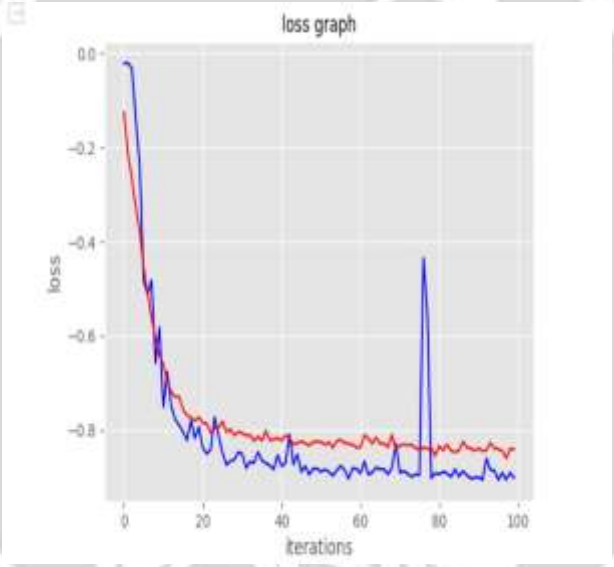

Fig -6: Loss graph

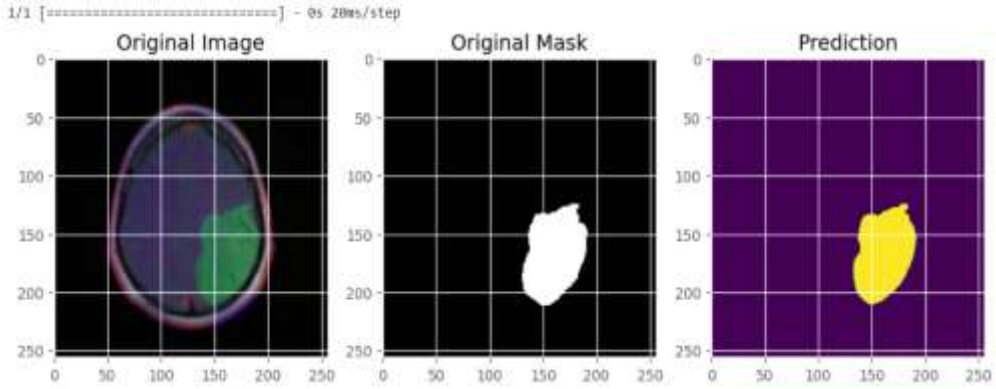

Fig -7: Image with tumor

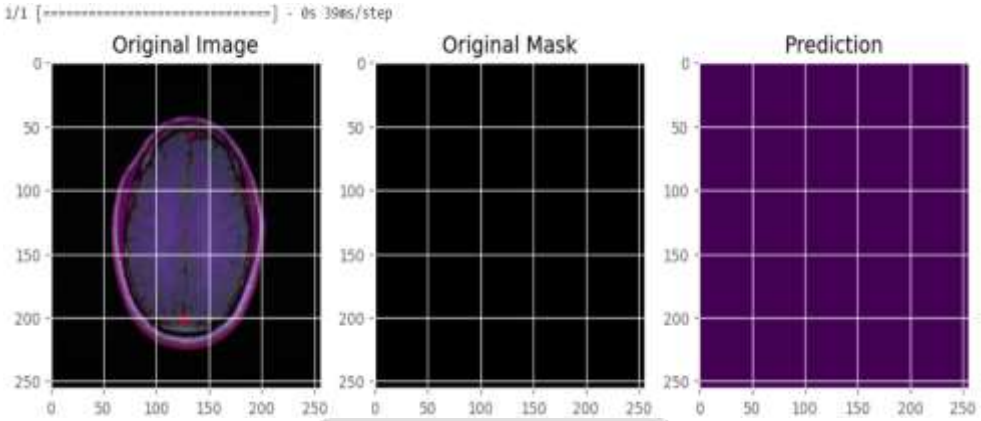

Fig -8: Image with no tumor

4. CONCLUSIONS

In conclusion, the RSPP-UNet architecture represents a sophisticated solution for semantic segmentation, particularly tailored for challenging medical image analysis tasks like brain tumor segmentation. By incorporating Spatial Pyramid Pooling (SPP) and Long Short-Term Memory (LSTM) layers, the model excels in capturing multi-scale contextual information and long-range dependencies within input images. This unique design enhances the network's precision in delineating tumor boundaries, a critical aspect in medical diagnosis and treatment planning. Throughout the project, the model demonstrated robust performance, achieving high accuracy and effectively leveraging its specialized components for nuanced feature extraction. The utilization of the Keras Functional API and standard optimization techniques ensures accessibility and adaptability for future extensions or modifications. Overall, the RSPP-UNet architecture presents a powerful tool for accurate and context-aware semantic segmentation in the realm of medical imaging, contributing to advancements in automated disease diagnosis and treatment assessment.

Accuracy	99.81
Precision	99.79
F1_score	92.13
Sensitivity	90.15
Specificity	88.36
Test IOU	99.79
Test Dice Coefficient	81.58

Table -2: Evaluation Metrics

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