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Brain Tumor Detection using 3D MRI images

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I. INTRODUCTION

Brain tumors are defined as anomalous cell growth within the brain, constitute a significant cause of global cancer-related mortality. Presently, brain tumors pose an arduous health challenge, underscoring the critical importance of early detection for life-saving interference. These tumors are broadly categorized as malignant or benign, with malignancy indicating cancerous cells and benignity indicating non-cancerous cells. Brain tumors are categorized by the World Health Organization (WHO) into four classes (I - IV) based on abnormality found in brain tissue [1].

Because they can have a variety of appearances and can be challenging to differentiate from healthy brain tissue, brain tumor detection poses a clinical challenge. Early diagnosis is essential in mitigating the high mortality related with these conditions.

Abstract - Early detection of brain tumor is essential for cancer diagnosis, as it can significantly improve survival rates. Magnetic resonance imaging (MRI) images of brain tumors must be performed early for diagnosis. MRI image's unparalleled image quality makes it a preferred tool for this purpose. In this work, we have modified the U-Net architecture to identify different types of brain tumors - Edema, Enhancing tumor, Non-enhancing tumor and Necrosis in MRI images. We assess our model's performance utilizing the benchmark dataset Brats 2020, with optimization conducted through ablation studies on layer architecture, activation functions, loss functions and hyper-parameters. To determine the evaluation of the model, performance metrics such as specificity, precision, accuracy, sensitivity, meanIoU and dice coefficient are used, achieving a test accuracy of 99.45% with the Adam optimizer and a learning rate of 0.001. Our proposed approach surpasses previous research, showcasing its capability for swiftly and precisely classifying brain tumors.

Keywords: Brain tumor, Brats dataset, MRI, ablation study, U-Net.

Diagnostic imaging is done using a variety of medical imaging modalities, including CT (Computerized Tomography), MRI (Magnetic Resonance Imaging) and PET (Positron Emission Tomography) techniques [2]. Based on information about the texture and shape of the tumor, MRI scans are more valuable than CT pictures. Because MRI pictures are detailed and have a high resolution, they can even detect small particles.

Annually, a large number of individuals are diagnosed with brain tumors, spurring increased attention towards harnessing deep learning algorithms to detect and categorize brain tumors [2]. Automated segmentation aims to transform the representation of image regions, thereby enhancing the interpretation of distinctive features. The complexities associated with manual tumor detection, including time-intensive procedures and susceptibility to misclassification, underscore the value of automatic segmentation of MRI images. Such advancements hold potential for optimizing diagnostic and treatment strategies, especially in settings where access to specialized expertise such as trained radiologists is inadequate.

Despite advancements, challenges persist in effectively classifying brain tumor grades using 3D imaging and in developing fully automated systems that ensure optimal accuracy. This study proposes an enhanced CNN-based 2D U-net segmentation model using the Brats 2020 dataset, to classify brain tumors into specific categories: Edema, Enhancing tumor, Non-enhancing tumor and Necrosis. To analyse the effectiveness of the proposed model, performance metrics like dice coefficient, accuracy, recall, specificity, meanIoU and precision were used. An ablation study was conducted to optimize hyperparameters and architectural configurations, striving to determine the optimal model architecture to maximize accuracy.

In this research paper: Section 1 gives introduction to the brain tumor. Section 2 provides a thorough survey of relevant literature. Section 3 presents methodology with an emphasis on using the Brats 2020 dataset to develop and implement a CNNbased U-net segmentation model. Experimental results and ablation study are presented in Section 4. Section 5 offers concluding remarks and discusses future avenues in automated brain tumor detection and classification.

II. LITERATURE SURVEY

Over the past few years, there have been remarkable developments in categorizing brain tumors. Due to its exceptional accuracy, deep convolutional neural networks (DCNN) are frequently implemented. However, this comes at the expense of a lengthy calculation time. When it comes to semantic segmentation tasks, deep learning algorithms perform better than more traditional context-based computer vision techniques.

Hybrid classifiers were used to divide tumors into benign and malignant groups by Ms. Swati Jayade et al. [4]. They employed Gray Level Co-occurrence Matrix (GLCM) feature extraction method for feature dataset creation. Their study proposed a hybrid classifier strategy aimed at enhancing classification efficiency that combines Support Vector Machine (SVM) and K-Nearest Neighbors (KNN) models.

In this paper, Masoumeh Siar et al. [5] combined CNN and the feature extraction technique to do the segmentation and classification. A dataset consisting of 1666 images was utilized for training while 226 images were designated for testing to assess the CNN's accuracy. RBF and DT classifiers were employed. The accuracy is 99.12%.

By combining convolution neural network (CNN) and multiple kernel K means clustering (MKKMC)

using deep learning algorithms, Balakumaresan Ragupathy [6] developed a robust method for brain tumor segmentation. The CNN algorithm is used in this suggested CNN-MKKMC technique to classify MR pictures as normal or anomalous. The anomalous brain image is separated from the brain tumor using MKKMC algorithm. The suggested method's effectiveness is evaluated using sensitivity, specificity, accuracy, FPR, FNR, NPV and PPV. They achieved the accuracy of 99%, sensitivity 93.5% and specificity 99.22%.

Badža et al. [7] introduced an innovative CNN architecture evaluated through four distinct methodologies to assess its performance: utilizing distinctive combination of two 10-fold crossvalidation techniques and two databases. The network's ability to generalize capability was examined using subject-wise cross-validation among the ten-fold approaches. Enhanced image databases were employed to evaluate advancements with record-wise cross-validation yielding the most promising outcomes in the ten-fold validation, achieving an accuracy score 96.56%.

SR-FCM-CNN is a hybrid approach introduced by Özyurt et al. [8], which integrates several techniques for brain tumor detection. Initially, they utilized the SR CNN network for preprocessing, enhancing lowquality images to high-definition quality. Consequently, the FCM method was employed for segmentation. Feature extraction was conducted using the SqueezeNet architecture, followed by classification using the ELM approach. Their method achieved an accuracy of 97.33%, surpassing the accuracy of brain tumor segmentation achieved by fuzzy C-means (FCM) alone by 10%.

Jude et al. [9] classified brain tumors into four types using DCNN by changing the training method. This work used 220 pictures which included T1, T2 and T2 flair sequences. The tumors were classified with an average accuracy of 96.4% using their suggested model DCNN. Eighty of these photos were included in the training set, which consists of 4 classes with an equal amount of train data (20 images).

Using U-net architecture, Hajar Cherguif et al. [10] constructed a convolutional 2D segmentation network. They used BRATS 2017 dataset to validate their proposed model, achieving a dice coefficient score 0.81.

III. METHODOLOGY

A. DATASET

In this research paper, we have incorporated brain tumor dataset - Brats 2020. The training dataset comprises MR volumes with dimensions of 240 \times 240×155 obtained from 369 patients. Each patient's dataset includes multimodal MRI scans encompassing T1, T2-weighted (T2), T1 contrastenhanced (T1ce), Fluid Attenuated Inversion Recovery (FLAIR) and corresponding ROI (seg). These images are collected from 19 different institutions, each following distinct clinical protocols. Table 1 provides an overview of the dataset.

B. VISUALIZATION OF THE DATASET

2D image is flat representations composed of pixels arranged in rows and columns while 3D image is volumetric, consisting of voxels arranged in a threedimensional space. NiBabel is a popular Python library for reading, writing and displaying 3D neuro imaging data. When an NIfTI file is loaded or read using NiBabel's load() function, all of the information is encoded, with each detail referred to as a 'attribute'. In order to visualize a 3D image, NiBabel first initialises a list that iterates over all 155 of the volume's slices. A new slice is added to the list sequentially every time a volume is read. An

Fig. 1. An MRI image from the dataset

illustration of an MRI scan is displayed below in Fig 1.

In this study (Fig 2), two preprocessing procedures intensity normalization and rescaling are applied implemented to prepare the data for training. To train the model, each sequence is processed independently with the manually segmented Region of Interest (ROI) serving as the ground truth.

Fig. 2. Block Diagram

C. DATA PREPROCESSING

Classifying brain cancers from 3D MRI scans poses inherent challenges due to their complex structural

nature and computational demands. In our investigation, we employ min-max normalization to standardize pixel values. Because most current systems are unable to manage the enormous number of 3D images, resizing them enhances the efficiency of the training process. Following normalization, dataset undergoes rescaling to $128 \times 128 \times 1$ voxels to accommodate GPU memory limitations. Additionally, the 3D MR image is downscaled from its original 240×240 pixels to 128×128 pixels.

D. DATA SPLIT

A training to validation ratio of 80:20 is maintained by splitting each preprocessed picture and matching ROI image.

E. PROPOSED ARCHITECTURE U-NET ARCHITECTURE

Ronneberger et al [11] introduced U-Net architecture, which is tailored for segmentic segmentation using a fully convulation network (FCN) model. It features both contracting path and expansive path. Our experimentation begins with a base U-Net model that applies repeated sequences of two 3×3 convolutions (without padding) and ReLU activations for downsampling followed by 2×2 max pooling with 2 strides.

The contracting path follows a standard convolutional network structure for downsampling images, doubling the number of feature channels at each stage. Expansive path involves a 2x2 convolution to reduce the number of feature channels by half, followed by concatenation with a proportionally cropped feature map from the contracting path. Each 3x3 convolution is then activated with ReLU. Cropping is used to maintain border pixels during convolution. Finally, the network ends with a 1x1 convolution to segment the 64-component feature vector into its corresponding classes. The network comprises 23 convolutional layers (Fig 3). The last layer utilizes 'categorical_crossentropy' as the loss function and 'Softmax' activation function. ROI images are used as validation data. In deep learning architecture, skip connections are applied to allow feature reusability. The skip connection maintains an uninterrupted gradient flow throughout all layers, from the initial to the final layer.

Dropout is a regularization technique used in deep learning to prevent neural networks from overfitting. We have used dropout factor as 0.2. We used 'ReduceLROnPlateau' technique to improve the efficiency and effectiveness of the learning process by reducing the learning rate when a metric (such as validation loss) stops improving.

Fig. 3. U-Net Architecture

IV. RESULT ANALYSIS

This section evaluates the effectiveness of the model through various evaluation metrics. These metrics measure the classifier's ability to accurately predict classes such as Edema, Necrosis, Enhancing tumor and Non-enhancing tumor. This section analyzes the outcomes of five ablation study scenarios. Finally, it includes a comparative analysis of our research findings against previous studies.

A. EVALUATION METRICS

In order to accurately assess the efficiency of a classifier, a range of performance metrics such as accuracy, precision, sensitivity, specificity, dice coefficient and loss are used.

Accuracy – Accuracy Eq. (1) quantifies the proportion of correct predictions made by the model out of all predictions made for a given dataset.

$$
Accuracy = \frac{TP + TN}{TP + TN + FP + FN}
$$
 (1)

where TP is True Positive, FP is False Positive, TN is True Negative and FN is False Negative.

MeanIoU - The Mean Intersection over Union (mIoU) metric Eq. (3) evaluates the accuracy of predicted object boundaries in relation to ground truth annotations, providing an average degree of similarity between predicted segmentation masks and actual masks across multiple classes or instances. IoU is calculated as Eq. (2)

$$
IoUc = \frac{TP_C}{TP_C + FP_C + FN_C}
$$
 (2)

where c is no. of classes.

$$
\text{MeanIoU} = \frac{1}{C} \sum_{c} IoU_{c} \tag{3}
$$

Dice Coefficient - Dice Coefficient metric as defined in Eq. (4) is frequently used in image segmentation tasks to measure the intersect between the predicted segmentation and the ground truth mask. It is calculated by doubling the intersection area of the predicted and ground truth masks and dividing this by the sum of their respective areas.

$$
\text{Dice Coefficient} = \frac{2^* |P \bigcap G|}{|P| + |G|} \tag{4}
$$

where P is Predicted Mask and G is Ground Mask.

Precision - Precision is defined as the true positive measure Eq. (5).

$$
\text{Precision} = \frac{TP}{TP + FP} \tag{5}
$$

Sensitivity – Sensitivity Eq. (6), also denoted as Recall, evaluates the proportion of correctly predicted positive cases relative to all actual positives.

Sensitivity =
$$
\frac{TP}{TP + FN}
$$
 (6)

Specificity - It gives the ratio of accurately recognized negative cases out of all actual negative cases. Mathematical formula for specificity is shown in Eq. (7)

$$
Specificity = \frac{TN}{TN + FP}
$$
 (7)

Optimization Metric (Loss Function): During the training phase, the optimization metric known as the loss function Eq. (8) is employed to refine model parameters. It quantifies the deviation between predicted outputs and actual targets, with a lower loss value typically indicating superior model performance characterized by heightened accuracy or predictive efficacy.

$$
Loss = -\sum_{i=1}^{n} l_i \log(p_i)
$$
 (8)

where n is no. of classes, l_i is truth label, p_i is probability of ith class.

B. ABLATION STUDY

The ablation study systematically alters components of the base U-net model and documents the outcomes. Table 2 presents the results of these ablation studies conducted using the dataset, encompassing findings related to variations in model's layer configurations, activation functions, hyper-parameters and loss functions.

In Case Study 1, we have used Max Pooling and Average Pooling. Among these, Max Pooling layer accomplishes the highest accuracy of 99.45% (Table 2). Consequently, the Max Pooling layer is selected for further detailed analysis in subsequent ablation studies.

Case Study 2 evaluates various activation functions to determine the optimal choice. It is determined that the ReLU activation function yields the highest test accuracy of 99.45% (Table 2). As a result, ReLU is chosen as the preferred activation function for further in-depth examination through ablation studies.

Case Study 3 explores different loss functions on model performance. Among these, using Categorical Cross-entropy, model attained the peak test accuracy of 99.45% (Table 2). For a more indepth examination, Categorical Cross-entropy loss function is used.

In Case Study 4, different optimizers like Adam, Adamax, Nadam, and RMSprop are evaluated under a consistent learning rate 0.001. The Adam optimizer emerges with the highest test accuracy of 99.45% (Table 2), thus validating selection for further detailed investigation through ablation studies.

Case Study 5 examines the effect of varying learning rates, specifically testing rates of 0.01 and 0.001. The optimal test accuracy of 99.45% (Table 2) is obtained by using the learning rate of 0.001.

We achieve the following metrics for the test data as illustrated in the table 3:

Table 3: Evaluation metrics

Table 2: Ablation study

Fig. 4. (a) depicts Accuracy Plot, 4(b) illustrates Loss value, 4(c) presents Dice Coefficient over epochs, 4(d) shows Mean IOU over epochs.

The assessment of the proposed model is illustrated by loss and accuracy curves. Fig 4 illustrates the training performance showcasing training accuracy, validation accuracy, training loss and validation loss achieved using the ADAM optimizer across various epochs. The model demonstrates convergence, attaining peak accuracy while maintaining low training and validation losses. Additionally,

accuracy of the model progressively improves with each epoch. The learning curves suggest that models are effectively learning from the input data without overfitting to the training dataset, suggesting effective learning of the input data at each epoch. Fig 4(a) presents accuracy trends for both the training and validation sets across epochs, revealing negligible disparity between the two. Fig 4(b)

displays the training and validation losses, demonstrating a marginal difference of approximately 0.02. Fig $4(c)$ illustrates a notable increase in the dice coefficient as epochs progress, observed consistently in training and validation sets. Lastly, Fig 4(d) depicts Mean IoU scores for the training and validation sets. After roughly 25 epochs, both the training and validation Mean IoU scores exceeded 0.8, which is an excellent outcome.

C. COMPARISON WITH EXISTING LITERATURE

The segmentation methodology proposed for brain MRI is evaluated against recent studies conducted

on comparable datasets, with emphasis on accuracy as summarized in Table 4. With our suggested method, we were able to attain 99.45% accuracy, 99.31% sensitivity and 99.47% precision. Srinivas et al. achieved an accuracy of 96.25% in brain tumor classification using a hybrid model combining CNN-KNN on MRI images [12]. Convolutional neural network combined with multiple kernel K means clustering (MKKMC) were used by Balakumaresan Ragupathy et al. [6]; the results showed a 99% accuracy, 93.5% sensitivity and 99.22% specificity. Ravikumar et al. [15] used Brats 2019 dataset for segmenting brain tumors using hybrid SegX-Net method. They achieved 98% accuracy.

V. CONCLUSION

In this paper, we introduced an improved CNNbased 2D U-net segmentation model specialized in identifying brain tumors in MRI scans. To boost computational efficiency, input images are standardized and resized to dimensions of 128 x 128. The model is trained using BraTS 2020 dataset to improve segmentation accuracy against the ground truth of MRI images. Notably, it achieves an Accuracy score of 99.45% utilizing Adam optimizer with learning rate 0.001. We got loss error 0.0159.

The primary methodology utilized in this research involved the implementation of the U-Net algorithm, which successfully outlined tumors, closely aligning with ground truth, generating highly precise predictions within MR images facilitating the segmentation of the target area. This approach delivers improved image segmentation and spatial localization when contrasted with alternative techniques, leading to superior performance. Additionally, it offers faster training times and reduced computational demands compared to networks with fewer parameters.

Future studies will look into using other classifier algorithms to increase accuracy while lowering error. Larger and more diversified datasets can be used in future studies.

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