Brain Tumor Segmentation Using Enhancement Convolved and Deconvolved CNN Model

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Abstract–The brain assumes the role of the primary organ in the human body, serving as the ultimate controller and regulator. Nevertheless, certain instances may give rise to the development of malignant tumors within the brain. At present, a definitive explanation of the etiology of brain cancer has yet to be established. This study develops a model that can accurately identify the presence of a tumor in a given magnetic resonance imaging (MRI) scan and subsequently determine its size within the brain. The proposed methodology comprises a two-step process, namely, tumor extraction and measurement (segmentation), followed by the application of deep learning techniques for the identification and classification of brain tumors. The detection and measurement of a brain tumor involve a series of steps, namely, preprocessing, skull stripping, and tumor segmentation. The overfitting of BTNet-convolutional neural network (CNN) models occurs after a lot of training time because training the model with a large number of images. Moreover, the tuned CNN model shows a better performance for classification step by achieving an accuracy rate of 98%. The performance metrics imply that the BTNet model can reach the optimal classification accuracy for the brain tumor (BraTS 2020) dataset identification. The model analysis segment has a WT specificity of 0.97, a TC specificity of 0.925914, an ET specificity of 0.967717, and Dice scores of 79.73% for ET, 91.64% for WT, and 87.73% for TC.

Index Terms—Brain tumor, Magnetic resonance imaging, Image enhancement, Image segmentation, Convolutional neural network.

I. Introduction

According to Gull, Akbar and Khan (2021), an estimated 29,000 individuals in the United States were diagnosed with primary brain tumors in 2015. In 2019, it was anticipated that there were 17,760 fatalities and 23,820 new cases of brain tumors in the United States. Based on the latest cancer data from 2021, there were projected to be a total of 24,530 reported instances of brain tumors in the United States. Among these cases, 13,840 were expected to be diagnosed in men, while 10,690 were anticipated in women (Siegel, et al., 2021). Magnetic resonance imaging (MRI) is a sophisticated medical imaging technique used to provide high-resolution images for the diagnosis and treatment of brain cancers. The commonly used multimodal imaging techniques for brain tumor detection in MRI include T1-weighted, T2-weighted, T1-weighted with contrast enhancement (T1CE), and fluid-attenuated inversion recovery. T1 images are capable of identifying different types of tissues, while T2 MR images provide positive signals in the image to address the presence of edema in the area. In T1CE images, the tumor edges are detected without the use of the high-intensity signal, namely, gadolinium particles, by specialists in the intricate cellular composition of tumor tissue.

Preprocessing methods and machine learning models have achieved great results in enhancing images (Taha, et al., 2021). The methodology used in this study involves using the least significant bits as a means of detecting the presence of concealed encrypted bits inside the dual-tree complex wavelet coefficient framework. Some other ML algorithms, such as the random forest (RF) algorithm, well recognized as a reliable and efficient classifier in the field of brain lesion segmentation, play a crucial role in our framework for segmenting lesions. Furthermore, our approach incorporates dense conditional random fields (CRF) as an optimizer, a commonly used technique for enhancing spatially contiguous segmentations in post-processing (Chen, et al., 2020).

The convolutional neural network (CNN)-based deep learning model demonstrates encouraging outcomes in the detection of cancers using magnetic resonance (MR) images (Ismael, et al., 2020). In the preceding automated methodologies, to optimize the performance of tumor size, position, and shape measurement

techniques, it is imperative to prioritize background subtraction, color visualization of the brain tumor region, fragmentation, size measurements, and classification. This approach will minimize complexity and enhance the segmentation process. According to the dataset that was used in the study (Bakas, S., et al. 2017), it is important to depict that the size, location and form of the tumors might vary, see Fig. 1.

It is noteworthy that tumor size, position, and shape may vary, as shown in Fig. 1. This approach is necessary to optimize segmentation and measurement efficacy. Subsequent to this stage, morphological filtering can be employed to eliminate any extraneous signals that may have arisen due to the segmentation procedure. The utilization of high-precision segmentation techniques has the potential to ascertain the benign or malignant characteristics of a tumor (Pedapati and Tannedi, 2017). The purpose of the paper is to develop a time-saving automated image processing system for appropriately segmenting and categorizing brain tumor and sub-tumor tissue from multimodal MR data. Due to its high soft-tissue contrast compared to other imaging modalities, such as computed tomography imaging (Ghadi and Salman, 2022), MRI is an effective and sensitive imaging

modality for the purpose of tumor, lesion, tissue, and disease identification/characterization. The brain tumor segmentation procedure entails distinguishing brain tumor tissues from surrounding normal tissues.

Some researchers have created unique deep learning-based systems with highly enhanced automated brain tumor recognition and delineation by concentrating on brain tumor segmentation. Havaei, et al. (2017) suggested a complicated CNN architecture for brain tumor segmentation from MR images. The goal of this project is to create a deep learning model for automatic segmentation of brain tumors from various MR sequences. Fig. 1 shows some samples of the dataset with normal cases and brain tumor cases with each class related.

II. Literature Review

The identification of brain cancer and the automated categorization of brain tissue through the utilization of MRI scans hold significant value in the realm of investigating and diagnosing human mental health. Segmentation is a critical component of medical imaging operations for MR images. It involves the separation and identification of the constituent
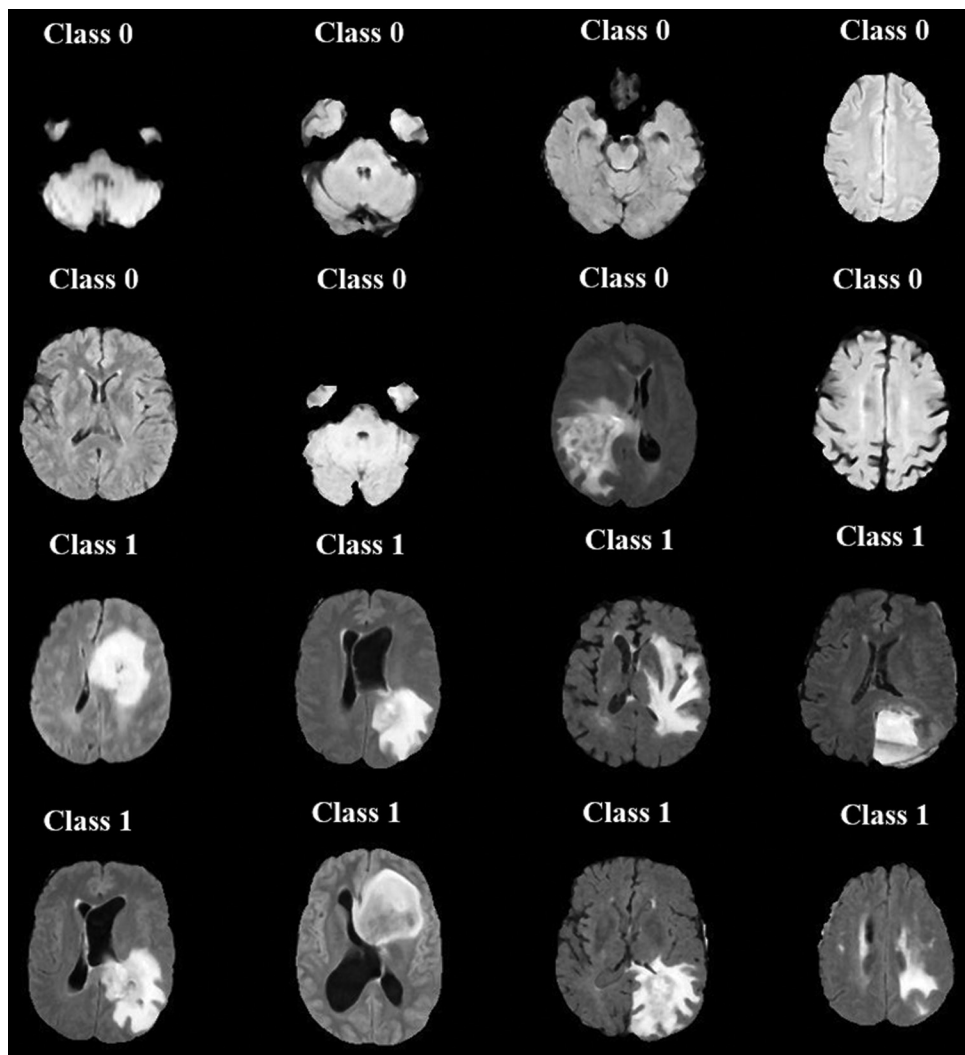

Fig. 1. Samples of brain tumor magnetic resource imaging.

parts of the image, enabling individual processing. The utilization of principal component analysis and discrete wavelet transform can facilitate the identification of the most salient characteristics of an image (El-Dahshan, Hosny and Salem, 2010). The suggested approach is useful for distinguishing between normal and abnormal human brains. MRI is considered to be the foremost diagnostic modality for the detection of brain tumors. The analysis of MR images through medical image processing has garnered significant interest in recent times (Morad and Al-Dabbas, 2020; Rao and Karunakara, 2021). Despite the diligent efforts of researchers studying brain tumors, it remains a formidable task to identify the most effective feature to target for elimination. The task of selecting suitable training and testing samples poses a significant challenge (Ortiz, et al., 2013).

The study employed a Gaussian filter to mitigate noise, followed by the acquisition of embedding, cyclic, contrast, and block appearance features for segmentation processing. The cross-validation method was utilized for classification to extract the features of the brain images. The utilization of a hybrid technique in conjunction with segmented supporting data renders this approach highly effective (Chen, et al., 2017). The utilization of particle swarm optimization and the rejection of outliers in conjunction with a level set were suggested (Huang, et al., 2020). The process of partitioning brain tumors in an MR database is frequently accomplished through the utilization of the fuzzy C-means (FCM) algorithm.

Another effective technique is to segment the lesion, and the well-known U-Net network design has met or exceeded the state-of-the-art performance standards for a variety of 2D and 3D semantic segmentation tasks as well as for a wide range of imaging modalities. When it comes to identifying patients and tracking the development of malignant entities over time, semantic segmentation of brain tumors using different MRI imaging modalities is an essential medical image processing field. The Swin UNET architecture is proposed as an innovative approach for the semantic segmentation of brain tumors, specifically using multimodal MRI data (Hatamizadeh, et al., 2021).

Wang (2021) introduced the use of the transformer model in conjunction with a 3D CNN for the purpose of MRI brain tumor segmentation. We offer a unique network architecture called TransBTS, which is built around an encoder-decoder structure. The decoder utilizes the characteristics included by the transformer model and employs a progressive upsampling technique to provide predictions for the precise segmentation map. Zhang, et al. (2017) proposed that multiple well-known fully CNNs (FCNNs) have been used for the purpose of brain tumor segmentation. These studies include conducting comparisons and modifying network designs in order to enhance performance, as assessed by metrics such as accuracy, recall, mean of intersection of union, and Dice score coefficient. The original convolutional layers of the FCNN and U-Net architectures are substituted with residual structures, along with the inclusion of batch normalization layers.

Chen (2020) proposed a two-stage automated framework for brain lesion segmentation. The system incorporates a cascaded RF algorithm and a dense CRF model, resulting in a combined approach referred to as RFDCR. The model was assessed on two segmentation tasks, namely, the segmentation of brain tumors and ischemic strokes. A two-stage supervised learning system is proposed for the purpose of automating brain lesion segmentation. In the first step, the training of the RF classifier involves the use of intensity-based statistical features, template-based asymmetric features, and GMM-based tissue probability maps (Cao, et al., 2022). This study introduces a context attention module, namely, the multiscale contextual attention, as a solution to address the issue of context information loss during feature extraction. The proposed module aims to effectively collect and filter high-level features by including spatial context information. The incorporation of the channel attention mechanism into the decoding structure facilitates the integration of high-level characteristics with low-level features.

A. Problem Statement

In Europe, approximately 60,000 individuals currently have a brain tumor, and an annual incidence of 18,000 new cases has been reported. As per the NHS (Cheng, 2017), there has been a surge in the occurrence of brain tumors in the United Kingdom, posing a significant cause for apprehension. Approximately 82% of all brain tumors, including normal brain tumors, are attributed to aggressive gliomas (Pedapati and Tannedi, 2017). The present study underscores the necessity of a meticulously planned therapeutic approach for this particular form of malignancy. Although brain tumors are prevalent globally, primary brain tumors are infrequent. The incidence of extracranial metastases originating from primary tumors in the brain and central nervous system is relatively low. Conversely, a significant proportion of brain tumors are classified as metastatic tumors, which have an extracranial origin and disseminate to the brain through the circulatory or lymphatic systems. A tumor's therapeutic response is influenced by various factors, such as its size, cellular composition, and stage. Tumor segmentation holds significant importance in the context of surgical and other therapeutic planning. Medical imaging techniques can be employed to detect and assess neoplasms. Selection of the optimal treatment modality for diverse clinical conditions aims to facilitate surgical intervention and coordinate radiation therapy (Rao and Karunakara, 2021).

B. Preprocessing Techniques

Preprocessing is a crucial step in enhancing the quality of MR images of a specific region of interest (ROI), such as brain tumors, to facilitate comprehensive analysis. In addition, Hamad, Mohammed and Simonov (2019), preprocessing produces the effect of enhancing some MRI characteristics. As demonstrated by Huang, et al. (2020), the application of preprocessing techniques has been observed to enhance certain features of MRI. In spite of the fact that, this technique makes use of a high-frequency emitter to improve the look of edges and finer details.

The grayscale image's intensity can be denoted by a set of K values ranging from 1 to K. The variable xi (i) represents the proportion of dots that exhibit a particular shade of gray, denoted by p (Shukla, 2016).

The summation of all feasible values is represented by the mathematical expression $X=x_1+x_2+....+x_L$. The frequency distribution of events is commonly used to interpret the distribution of a grayscale image. $(i)=x_i/X$, $x_i \geq 0$, $\Sigma x_i = 1$.

Every individual pixel within an image comprises two distinct components, namely, a foreground component (denoted as C_0) and a background component (denoted as C_1, which possesses a minimum value of t). The pixels that fall within the range of levels [1, 2,…,k] are denoted by the symbol C_0, while those that belong to the range of levels $[t + 1,…,k]$ are represented by the symbol C_1 (Shukla, 2016). The formulas for defining the class occurrence probability W_{c0} and the median occurrence probability are as follows in Eq. (1):

$$W_{c0} = \sum_{i=1}^{t} p(i) \tag{1}$$

$$\mu_{c0} = \sum_{i=1}^{t} \frac{i.p(i)}{w_{c0}} = \frac{1}{w_{c0}} \tag{2}$$

The formula for calculating the expected value of a random variable is expressed as in Eq. (3):

$$\mu_T = \sum_{i=1}^{L} i.p(i) \tag{3}$$

Where: $\mu_T = w_{c0}\mu_{c0} + w_{c1}\mu_{c1}$ (4)

Subsequently, by utilizing this formula in Eq. (2) (3), we can determine the value of μ_T as the weighted sum of μ_{c0} and μ_{c1}, where w_0 and w_1 represent the respective weights. The variables and in Eq. (4) represent the probabilities of the foreground and background regions, respectively. Furthermore, it should be noted that μ_{c0} and μ_{c1} correspond to the mean gray value of the image foreground and background, respectively. The image's complete gray level is denoted as μ_T (Wala'a, and Rana, 2021).

C. Classification and Segmentation of Brain Tumors

Various imaging modalities, including computed tomography, MRI, and X-ray, have been employed to examine the brain's anatomy and identify malignant tumors (Zebari, et al., 2020; Zhang, 2010). The utilization of MRI is increasingly prevalent in the identification of brain cancer, as evidenced by scholarly literature (Wang, Cheng and Basu, 2009). The technique for segmenting brain tumors in computer vision involves partitioning an image into distinct components by categorizing the image's adjacent pixels according to specific predetermined pixel characteristics or properties (Faris, et al., 2019).

Segmentation is a critical operation in the domain of image processing, particularly in the context of extracting information from intricate medical scans. These data have the potential to aid in the identification and management of medical conditions in individuals. The fundamental aim of image segmentation is to partition a digital image into discrete regions that are mutually exclusive (Joseph, Singh and Manikandan, 2014).

There exist notable dissimilarities in the attributes of tumors and malignancies. Irrespective of its composition, a tumor represents an anomalous aggregation of tissues. Tumors can be categorized as either primary or secondary based on their specific type. The nervous system is a commonly observed source of nourishment for the gradual proliferation of primary tumors. Gliomas are a type of brain tumor characterized by the presence of glass cells as their predominant structural component. These tumors are frequently observed within the central nervous system (Al-Dabbas, et al., 2019; Al Mahmud, et al., 2020; Mohammed, et al., 2021).

The advancement of a cerebral neoplasm (cancer) mandates a meticulous evaluation of the individual's clinical manifestations. MRI is the preferred modality for detecting brain tumors. The task of exposing a tumor without causing harm to surrounding healthy tissue is a highly challenging endeavor.

III. Methodology

The present investigation entails the utilization of automated techniques for brain tumor segmentation, measurements, and classification, which are known to be time-intensive. Typically, MRI scans are utilized to examine the brain's anatomy.

This study aims to investigate feature representations that can improve the precision of brain tumor segmentation and size measurements. This will be achieved by combining handmade features, which account for local dependencies, with machine-learned features that provide global information.

This study's objective is to explore the optimal combination of features extracted from multimodal MR scans, with the aim of maximizing the informative content derived from particular MR modalities.

The objective is to devise an automated methodology for producing a tumor segment that is consistent with the delineation of experts across all grades of glioma, utilizing a single, commonly employed MRI technique. The proposed methodology involves using CNN for enhancement purposes, as shown in Fig. 2, and using machine learning techniques for classification subsequent to the extraction of features from a segmented tumor and its subsequent categorization, as shown in Fig. 3. The CNN-MRI architecture was developed with consideration of the aforementioned requirements. It consists of three parallel layers, each containing 16, 64, and 64 filters, respectively. The filters in each layer are of varying sizes, specifically 3×3, 5×5, and 9×9.

Subsequently, the images that have undergone coevolution are observed. The data underwent batch normalization and rectified linear unit activations, subsequently undergoing two distinct types of pooling operations, namely, average pooling and maximum pooling. The justification for utilizing varying filter dimensions is to discern regional characteristics through the implementation of 3-by-3 filters and relatively
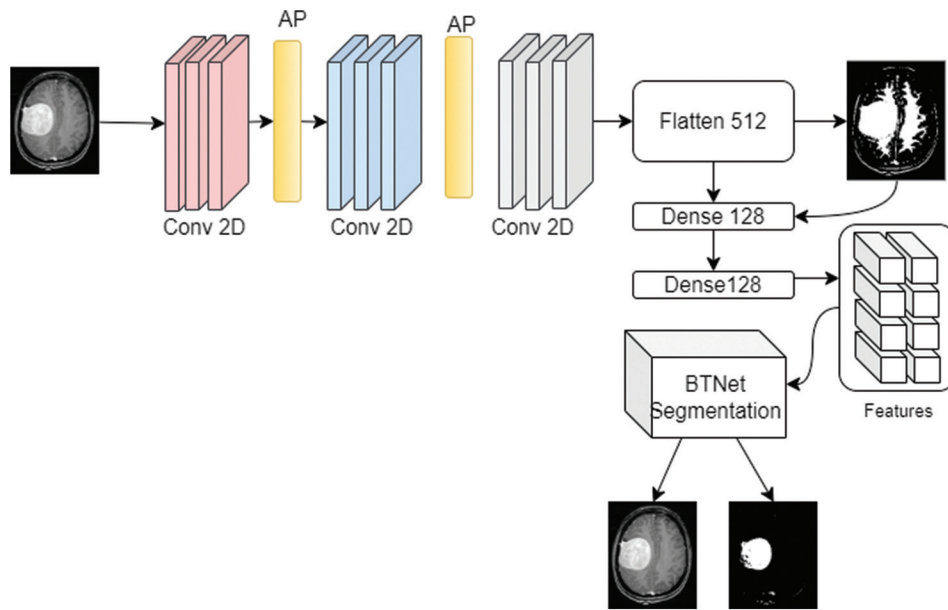
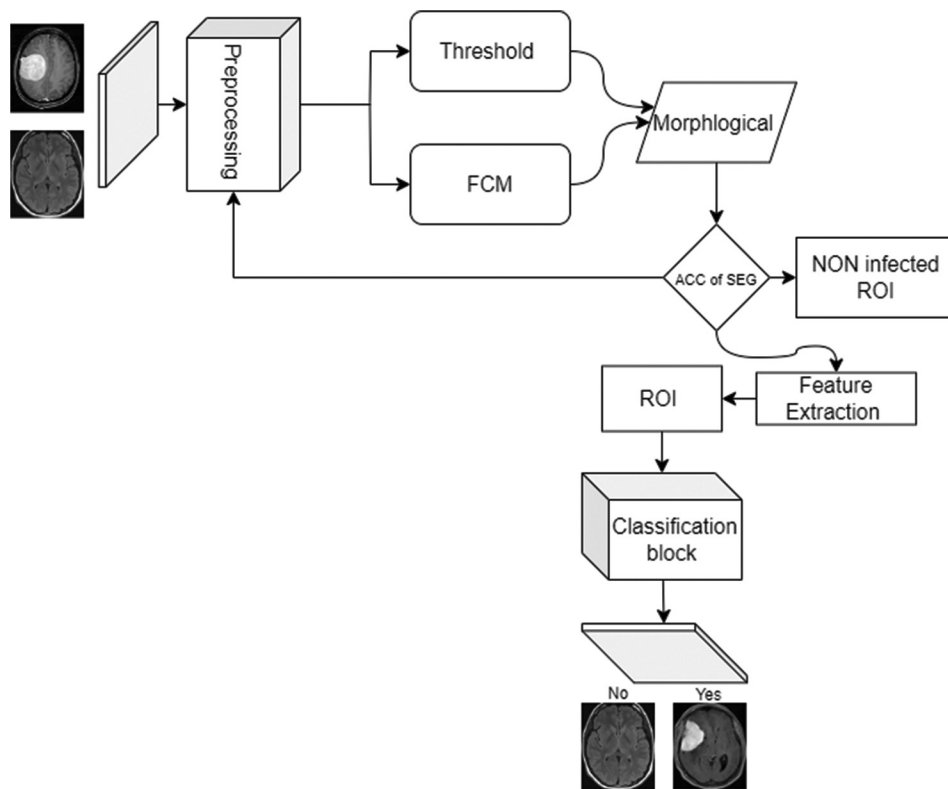Fig. 2. Enhanced brain tumor convolutional neural network model.

Fig. 3. Brain tumor classification model in magnetic resonance imaging.

broader features through 9-by-9 filters. The 5-by-5 filter size is employed to detect any features that may have been overlooked by the other two filters, as shown in Fig. 3.

Our study explores methods for classifying and segmenting MR images using an iterative approach and a methodology based on thresholds. The process of selecting an optimal starting contour for the purpose of FCM and thresholding is challenging due to the presence of gray-level variations in the pathological area of images, such as brain tumors. The process of delineating and characterizing the boundaries of regions of interest, such as the brain or pathological areas within it, as depicted in MR images, plays a crucial role in aiding medical practitioners in arriving at a diagnosis, such as the presence of gliomas or meningiomas. Segmentation enables precise delineation of the dimensions (contour) of said regions (neoplasms and healthy brain tissue).

A. Image Classification

The task of categorizing images was executed by utilizing manually designed features and advanced computational methods such as support vector machines or decision trees. CNNs have emerged as the predominant technique for image classification due to the progress made in deep learning and the accessibility of vast labeled image datasets (Abdulkareem, et al., 2019). The CNN training procedure entails inputting a vast labeled image dataset into the network, which then adapts its internal parameters (weights and biases) to minimize the disparity between its predicted class labels and the actual ground truth labels. After undergoing training, the neural network can subsequently be employed to categorize novel and unobserved images by conducting forward-propagation through the network and acquiring the probabilities or predictions for each class.

The block diagram in Fig. 3 illustrates a technique for enhancing the precision of diagnostic analysis of MR images, which has the following steps:

1. Preprocessing has been shown to enhance images' resolution.
2. Tumor segmentation is a technique utilized to quantify a tumor's size by demarcating the regions that are affected by the tumor from those that are not.
3. Morphological operations are utilized to eliminate undesirable regions from binary images and to smooth the boundaries of bulk objects.
4. The accuracy of tumor categorization can be improved by utilizing feature extraction techniques.
5. The process of classification involves categorizing segmented tumors into either malignant or non-cancerous groups.

In numerous cases, the region of the image that portrays the neoplasm exhibits greater visual prominence than the adjacent healthy tissue. The approach and code utilized in this particular scenario are based on the fundamental principles of an algorithm that has been developed to detect malignancies. At this juncture, the pertinent section of the document can be addressed as necessary during the data processing stage.

B. Threshold-based Segmentation and FCM

Pattern recognition was developed due to the importance of picture segmentation and its crucial role in object extraction within the field of image processing. The process involves partitioning the input image into multiple segments, thereby simplifying the identification and extraction of the desired region by locating the optimal matching data. A segmentation technique utilizing a localized threshold is employed to partition images containing multiple regions that correspond to distinct objects.

Pixels with a value of one denote the ROI, while pixels with a value of zero represent the background of the image. The present research utilizes a segmentation model based on thresholds, enabling the exploration of input images at different thresholds and maximum values to enhance the information obtained (Fig. 4a).

The FCM algorithm is widely acknowledged as a highly efficient technique for data clustering (Fig. 4b). The unsupervised technique known as FCM has the potential to perform various tasks, including but not limited to factor identification, grouping, and segmentation. This technology has potential applications in various fields such as horticulture construction, astronomy, biochemistry, image analysis, and medical evaluation. FCM employs multiple data regions to address the issue of partial volume impact. The method described is an iterative approach that solely analyzes the luminosity of the segmented image. The method involves
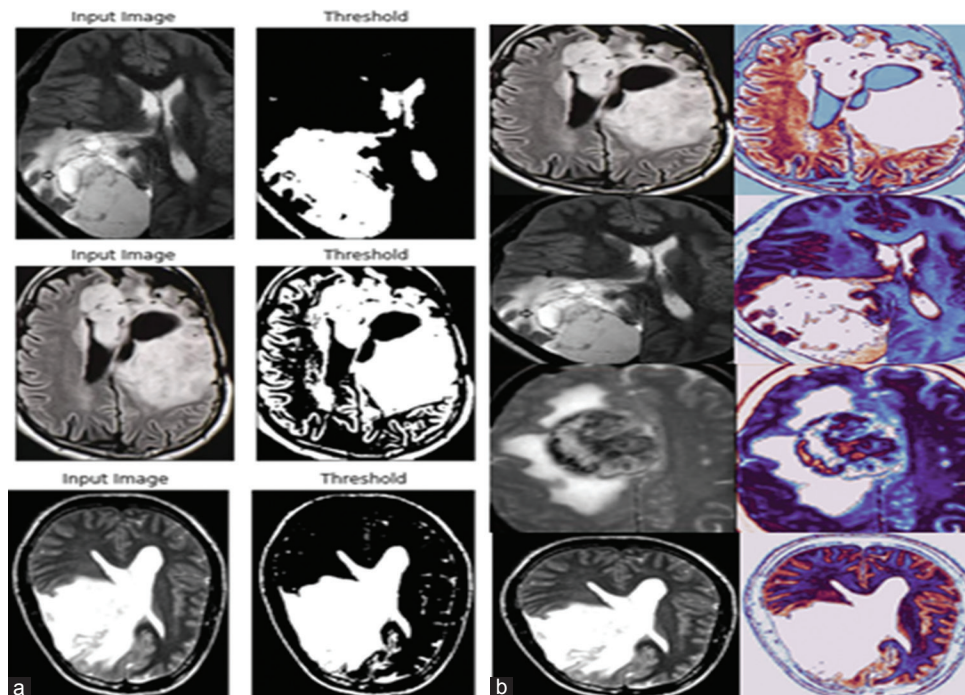

Fig. 4. Preprocessing techniques to enhance feature extraction: (a) Threshold and (b) fuzzy C-means segmentation.

conducting an incremental search to identify a sequence of imprecise clusters and their corresponding cluster centers, with the aim of achieving the most precise clustering of the given data structure.

Tumor segmentation is a technique utilized to quantify the size of a tumor. Morphological operations are utilized to eliminate undesirable regions in binary images and refine the boundaries of bulk objects. The accuracy of tumor categorization can be enhanced through the implementation of feature extraction techniques.

The process of classification involves categorizing segmented tumors into either malignant or non-cancerous groups. The developed approach is expected to facilitate the cancer diagnosis process and enable the system to be trained with a reduced quantity of data. On the conclusion of the validation process, the gathered data will be incorporated into a comprehensive report detailing the patient's health status.

C. Brain Tumor Segmentation Method

Image segmentation is frequently employed to detect boundaries and objects, such as curves and lines. The initial stage in identifying a particular attribute in medical images involves the segmentation process. For instance, brain tumors can be detected by utilizing MR images or other medical imaging techniques. This suggests that the prompt initiation of therapy is crucial in identifying the optimal treatment approach. The objective of utilizing the aforementioned illustrations is to aid radiologists in prioritizing patients with gliomas or meningiomas for diagnostic testing and therapeutic interventions, contingent on their distinct etiology. The convolution operation is a fundamental process employed in CNNs to extract local features from an input image. The process entails the utilization of a diminutive matrix, commonly referred to as a kernel or filter, which is moved across the image. During this movement, element-wise multiplications are carried out between the kernel and the corresponding pixels of the image.

The summation of the products yields a solitary numerical output that signifies a localized feature or activation. Through the implementation of various filters, a CNN can acquire distinct characteristics at diverse spatial positions within an image. Fig. 5 illustrates the process of BTNet based on a convolved algorithm. The process of upsampling or decoding the feature maps derived from the convolutional layers of a CNN is commonly referred to as "deconvolution," as per the prevailing terminology. The BTNet model is a crucial process in the realm of medical imaging. The model creates

four blocks of CONV as a convolution phase and four blocks as a deconvolution phase. Between the convolution and deconvolution phases, four FC-layers are used. Moreover, the utilization of certain architectures, such as convolutional autoencoders, variational autoencoders, and generative adversarial networks, involves the aforementioned technique. Deconvolution is a technique employed to reconstruct the initial image or produce novel images by utilizing the acquired features.

It is noteworthy that the usage of the term "deconvolution" may be somewhat deceptive. Within the realm of CNNs, it is important to note that deconvolution does not constitute a genuine mathematical inverse operation of convolution. The term in question pertains to transposed convolution or fractionally strided convolution, a technique employed to increase the resolution of feature maps by means of zero insertion or interpolation between the preexisting feature values. This enables the network to enhance the spatial resolution of the feature maps. Various techniques of image segmentation, which involves the extraction of an ROI from a larger image, have been employed to isolate specific organs and tissues for diagnostic testing. The utilization of this methodology encompasses a diverse range of fields, including but not limited to the identification of masses in mammographic images, the alignment of photographic data, the examination of cardiac imaging, and the partitioning of cardiac structures.

IV. Results

In this experiment, an MRI-scan grayscale database was employed, with each image having a size of 240*240 pixels. Preprocessing is critical in image analysis activities such as tumor identification in medical imaging. It emphasizes many major goals of image preprocessing. Fig. 6a illustrates the input image with three different preprocessing phases. We used a threshold technique after that to apply *contrast limited adaptive histogram equalization* CLAHE technology to enhance picture detail, which is important in medical imaging for improved visibility of things such as malignancies. By increasing local contrast, small details that may have been concealed by shifting lighting or noise become more visible, assisting in the accurate diagnosis of abnormalities such as tumors. However, the threshold value is determined locally for each section of the image based on the local attributes of the image. In image processing applications such as segmentation, object recognition, and feature extraction,
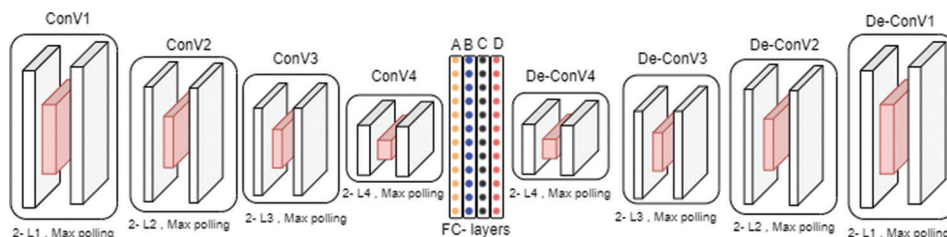

Fig. 5. BTNet convolved and deconvolved convolutional neural network model.
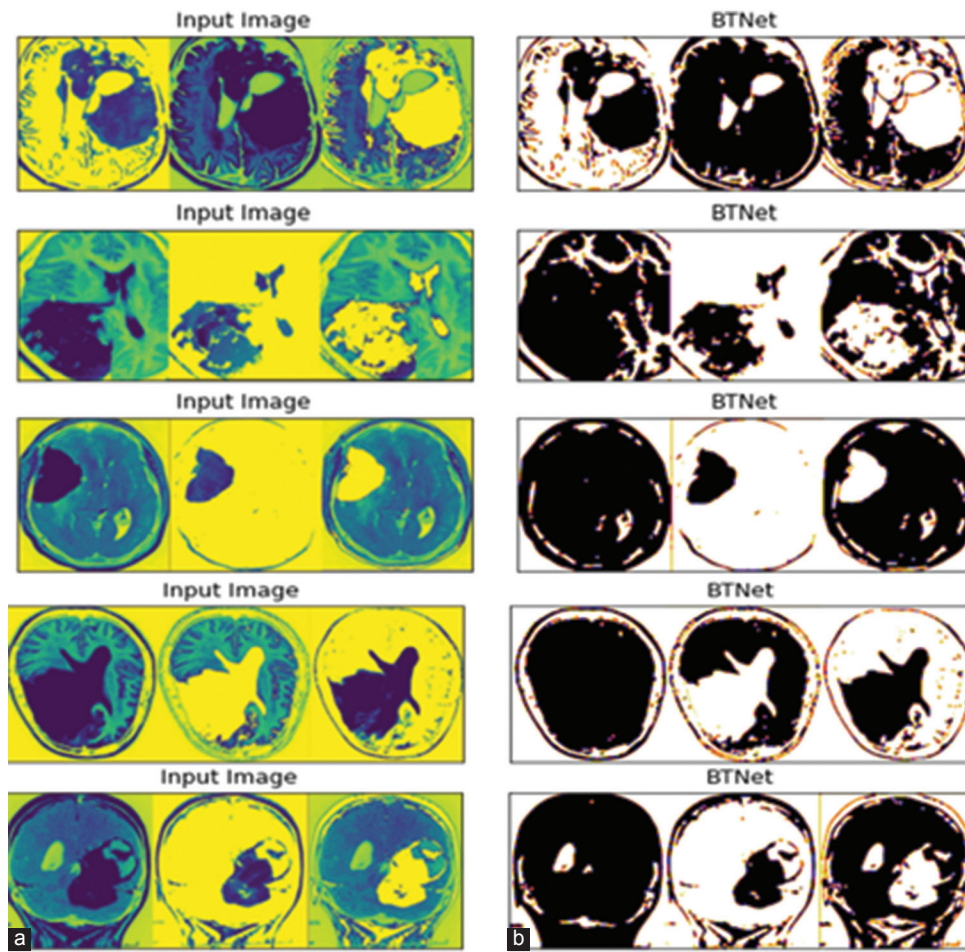
Fig. 6. (a) Input image thresholding and CLAHE and (b) brain tumor image classification phase.

thresholding is an effective strategy. It is especially useful when there is a clear divide between foreground and background intensities in the image.

Fig. 6-b shows the results of our BTNet for these three preprocessing input images in the first phase of the training model that is used to classify brain tumor lesions. The image undergoes grayscale conversion while it is being read. Next, the model retains the binary image for further training. Additionally, determine the aggregate quantity of white pixels inside the binary spectrum, and thereafter divide this figure by the overall pixel count in the image. While, CLAHE was used for the purpose of enhancing low-contrast medical photographs. Using the CLAHE approach, an input original image is segmented into non-overlapping contextual sections that are referred to as sub-images, tiles, or blocks.

The segmentation phase results are shown in Fig. 7, which depicts BTNet's segmentation of the ROI lesion. The receiver operating characteristic (ROC) curve shown in Fig. 8 is a visual depiction that illustrates the effectiveness of a binary classification model. The graph illustrates the relationship between the true positive rate and the false-positive rate across different classification thresholds. The utilization of the area under the ROC curve (AUC-ROC) is frequently employed as a metric to evaluate a model's predictive capability, where a greater AUC signifies superior

TABLE I
COMPARISON OF THE PROPOSED FRAMEWORK WITH STATE-OF-THE-ART APPROACHES FOR BRAIN TUMOR SEGMENTATION.

Author	Technique	Dataset	Metrics
Wu, et al. (2021)	V-Net dropout 0.1	NTUH dataset	Sensitivity 0.66
Hu, et al. (2019)	MCCANN1 MCCANN2	BRATS 2013	Sensitivity 0.91 Sensitivity 0.89
Tustison, et al. (2015)	supervised brain tumor segmentation	BraTS 2013	Sensitivity 0.89 Dice Score 0.87
Zhao, et al. (2018)	FCNNs and CRFs	BraTS 2013	Sensitivity 0.83 Dice Score 0.87
Siar and Teshnehlab (2019)	Deep neural networks CNN+DT	BraTS 2013	Accuracy 0.9424
Havaei, et al. (2019)	LocalCascadeCNN	BraTS 2013	Sensitivity 0.84
Kamnitsas, et al. (2017)	DeepMedic	BraTS 2015	Sensitivity 0.88
Sharif, et al. (2020)	DRLBP	BraTS 2018	Accuracy 0.92
Gull, Akbar and Khan (2021)	FCNN and CRFs	BraTS 2020	Accuracy 0.980
Proposed Method	BTNet	BraTS 2020	Accuracy 0.9823 Sensitivity WT0.987 TC 0.986, ET 0.987

performance. BTNet's ROC achieves accuracy of 0.98, as compared to the ROCs of the ResUNet model and ROC UNet++, which have both achieved accuracy of 0.97.
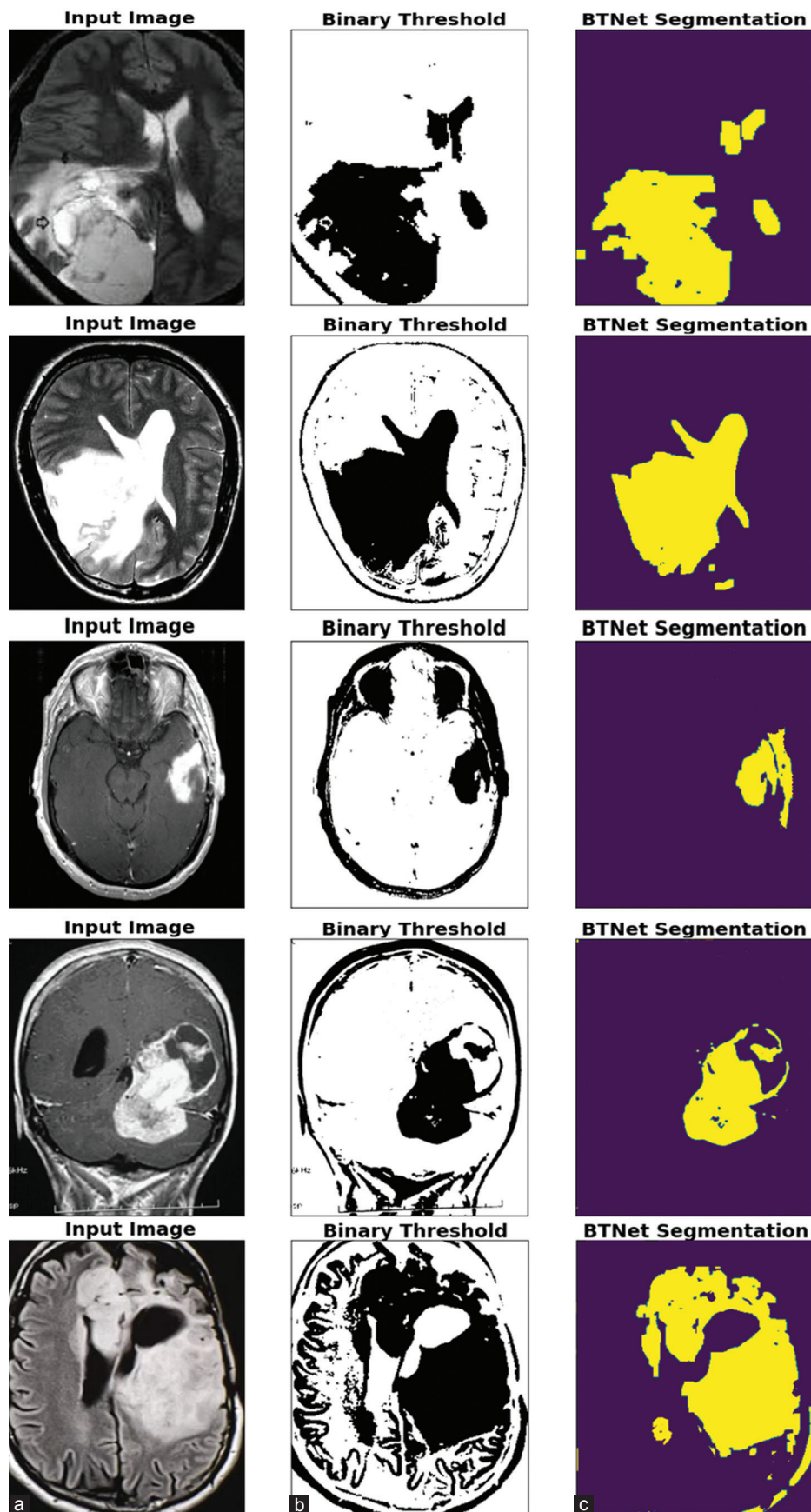
Fig. 7. (a) Input image; (b) binary threshold; and (c) ROI segmentation for brain tumor lesion.

To evaluate a model's efficacy, it is customary to calculate accuracy individually for both the training set and the test set. The training set is utilized to train the model, whereas the test set is employed to assess its performance on data that have not been previously encountered. The act of comparing the accuracy achieved on the training set and the test set offers valuable insights regarding the model's ability to effectively generalize its predictions to novel, previously unseen data. Fig. 9 illustrates the accuracy for the training and test phases of the UNet++ model, while (B) shows the training and test accuracy for the BTNet model.

Table I shows the results of other comparative methods that may discover that the axial view segmentation results are optimal in the coarse segmentation stage. Furthermore, of all the phases involved in the process of identifying malignancies, segmentation is the most important and advantageous.

Table II presents the results of an evaluation model that measures the modified CNN's efficiency in identifying tumors from the BraTS 2020 dataset. The best accurate results for 30 epochs, while the results achieved for Dice Score, Sensitivity, and Specificity. Fig. 10 depicts the assessment model employs for WT, TC, and ET to determine the efficacy of the modified CNN.

The Dice Score results for the proposed model are compared with existing techniques and shown in Table 3. which shows the ET score is 79.73, the WT score is 91.64, and the TC score is 87.73. Total number of images
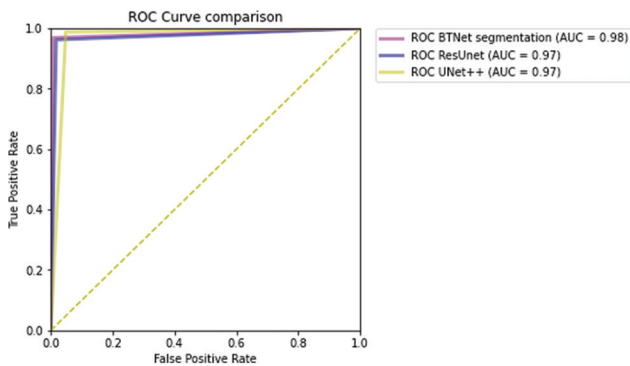
is 2470 MR images 70% for train and 30% for test as the divided datasets. For training phase, the model utilizes 1680 for training and feed 790 image for test phase. The initial learning rate is set at 0.001 at the minimum batch size of 30. The learning method used is Adam, and the optimizer used is Momentum. Accordingly, the use of a momentum optimizer leads to improved accuracy in achieving more precise results. Moreover, the value of the focal loss function is 10. However, the maximum epochs are 30 with number of

TABLE II
THE RESULTS FOR BRATS 2020 DATASET FROM ALL THREE MRI MODALITIES ARE THE BASELINE RESULTS

Epoch No.	WT dice score	WT sensitivity	WT specificity
5	0.883095	0.784932	0.78306
10	0.838448	0.83322	0.844257
15	0.935524	0.92049	0.973394
20	0.970243	0.976846	0.963729
30	0.975987	0.9879	0.945358
Epoch No.	TC dice score	TC sensitivity	TC specificity
5	0.906776	0.89741	0.679755
10	0.769711	0.84817	0.704538
15	0.850613	0.885764	0.85922
20	0.967822	0.891602	0.945632
30	0.97548	0.986997	0.925914
Epoch No.	ET dice score	ET sensitivity	ET specificity
5	0.841533	0.813294	0.871802
10	0.547767	0.754954	0.429811
15	0.803296	0.918384	0.713841
20	0.83659	0.952891	0.75439
30	0.977399	0.987276	0.967717

TABLE III
COMPARATIVE ANALYSIS OF THE AVERAGE DICE SCORES OF OUR PROPOSED FRAMEWORK ON THE BRATS 2020 TRAINING DATASETS AND ALTERNATIVE APPROACHES

| Study	Method	Dice score
Milletari, Navab and Ahmadi (2016)	Basic V-Net	ET 61.79 WT 84.63 TC 75.26
Wang, et al. (2021)	Residual 3D U-Net	ET 71.63 WT 82.46 TC 76.47
Wang, et al. (2021)	TransBTS	ET 78.73 WT 90.09 TC 81.73
Yang, et al. (2023)	ODE model	ET 0.775 TC 0.845 WT 0.773
Proposed Method	BTNet	ET 79.73 WT 91.64 TC 87.73

Fig. 8. Receiver operating characteristic curve comparative results.

Fig. 9. Training and test accuracy for (a) UNet++ and (b) BTNet segmentation model.

WT Metrics Evaluation

TC Metrics Evaluation
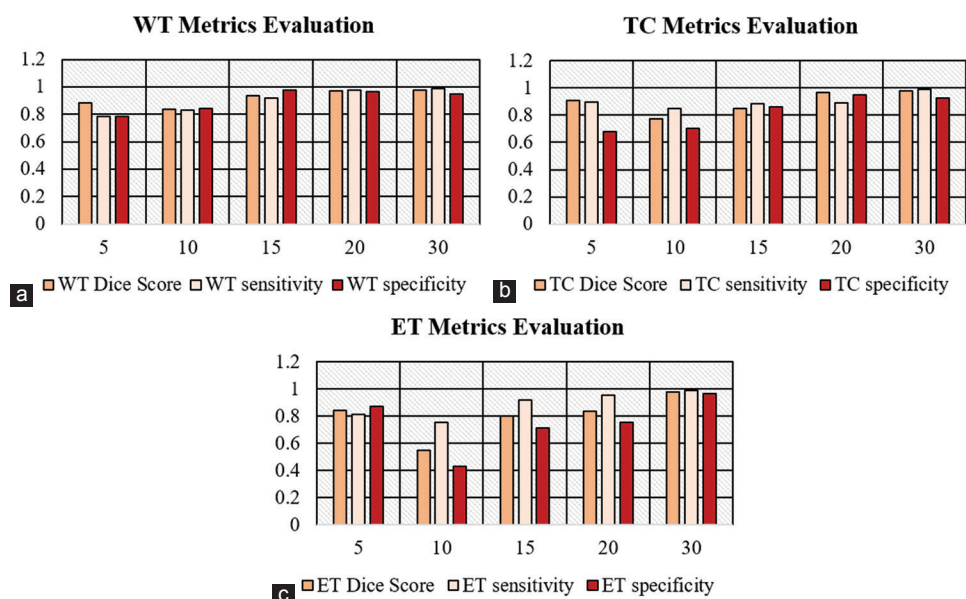
ET Metrics Evaluation

Fig. 10. (a-c) Metrics evaluation for three phases of BraTS 2020 dataset.

iterations 10,000. The presented approach obtains an overall classification accuracy of 98.23% for the BraTS 2020 dataset.

V. Conclusion

The domain of MRI-based segmentation and prediction of brain tumors has undergone significant advancements recently, primarily attributed to the utilization of machine learning algorithms. Notwithstanding this fact, MRI continues to be a complex topic that warrants further investigation. Our model combined classification and segmentation networks together for give the best accurate detection of the lesions. The central objective of this paper pertains to the utilization of deep learning techniques for the purpose of segmenting and classifying malignancies, specifically gliomas and meningiomas. The preprocessing technique used in this study shows the powerful effect to increase the accuracy of the training model. Our enhanced brain tumor CNN framework is adaptable and capable of detecting multiple types of cancer would be highly advantageous for medical professionals. BTNet used a CNN for segmentation, using both convolutional and deconvolutional layers. Improving the quality of this work may be achieved using ensemble classification methods, such as deploying a CNN with different layer configurations or a deep CNN. Future work, we want to assess the robustness of our Custom YOLO tool for use in various MRI images analysis applications. Furthermore, our goal is to enhance the model's accuracy by increasing training samples and optimizing hyper-parameters.

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