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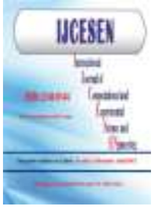

Computer Aided Based Performance Analysis of Glioblastoma Tumor Detection Methods using UNET-CNN

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Abstract:

Brain tumors are the life killing and threatening disease which affects all age groups around the world. The timely detection and followed by the perspective treatments saves the human life. The tumor regions in brain are detected and segmented using UNET-CNN architecture in this paper. During training process of the proposed work, both Glioblastoma and Healthy brain Magnetic Resonance Imaging (MRI) is preprocessed and then multi level transform is applied on the preprocessed image. The features are further computed from the transformed coefficients and these features are trained by UNET-CNN architecture to obtain trained vectors. During testing process of the proposed work, the test brain MRI image is preprocessed and then decomposed coefficients are obtained by multi level transform. Features are computed from these decomposed coefficients and they are classified using UNET-CNN architecture with the trained vectors. The simulation results of the developed methodology are compared with similar studies on both BRATS 2017 and BRATS 2018 datasets.

1. Introduction

Glioblastoma is the severe case of the brain tumor, which is very aggressive type when compared with other types of tumors in brain region. This type of tumor is mainly occurred in the conjunction region of the brain and spinal cord of the human body. Astrocytes cells are the main reason for forming this type of tumor cells. The aggressive development of these cells in the brain region forms the tumor pixels. This tumor affects the human in any age category, especially in case of older people. Severe headache with continuous vomiting and seizures are the main symptoms of this type of tumors. Timely detection of this tumor in human body increases the life span of the patient. There is lot of methods available for diagnosis this type of tumors as Neurological method, Biopsy method and imaging method [1-3]. Neurological method is based on the symptoms formation in the affected patient and the biopsy method is based on examine the affected portion or tissues for tumor detection process. The imaging method is the usage of scanning procedures for the detection of tumor.

Among these three diagnosis methods, imaging methods are mostly preferable by radiologist which detects the Glioblastoma tumors more accurately than the other procedures. In this paper, Magnetic Resonance Imaging (MRI) scanning procedure is used for the detection of tumor pixels in the image. Fig.1 shows the Glioblastoma image.

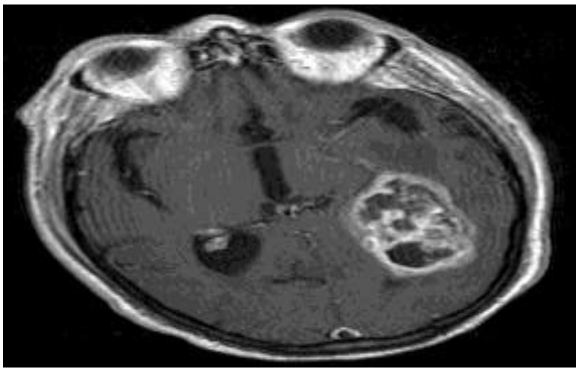


Figure 1 *Glioblastoma MRI*

The deep learning algorithms are classified into Fully Connected Convolutional Network (FCCN) and UNet architecture. Among these deep learning methods, UNet architecture has many advantages over the FCCN architecture based on the performance efficiency and reliability [4-6]. Hence, UNet architecture is used in this paper for the detection and segmentation of tumor pixels in the brain MRI image. The UNet architecture is the U-shaped architecture which is split into two distinct modules as left part and right part. The left part module of this architecture is the Encoder and the right part module of this architecture is the Decoder. Each output response from each layers of the Encoder module is integrated with each layer of the Decoder module, which is the main reason for enhancing the performance of the tumor segmentation results. The integration of feature maps from both low and high level features from both Encoder and Decoder module are used to detect the tumor pixels in the brain image [7]. The UNet structure is classified into 2D and 3D architecture. The main limitation of the 3D structure is that the requirements for memory consumption and hyper parameters are high. In order to overcome these limitations in 3D structure, this paper uses 2D-structure. Brain tumors are successfully detected in Fully connected Network (FCN) based 2D structure [8] and UNet 2D structure [9,10] in recent years. By comparing 2D model of FCN with UNet for the detection of pixels belonging to tumor category, the UNet is chosen as the most desirable solution for many biomedical applications due to its high performance efficiency while compared with other similar models [9]. Therefore, the UNet architecture is used in this work for the identification of tumor pixels in the meningioma brain images. This paper is organized into five sections. Section 1 introduces the Glioblastoma and its detection process using different methods. Section 2 discusses various frameworks for the detection of pixels belonging to tumor category. Section 3 develops the UNET architecture for segmenting tumor pixels. Section 4 details about simulation results of the developed architecture and section 5 conclude this work.

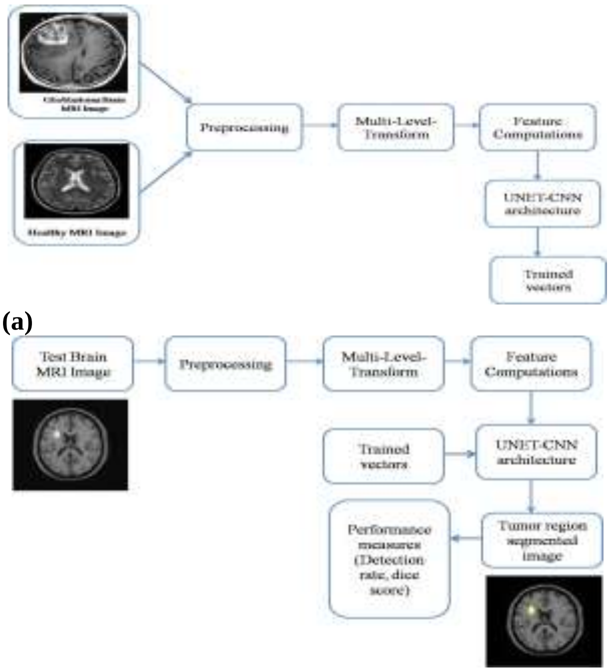
2. Literature survey

In the literature there are a number works done on this subject [10-43]. Muhammad Arif et al. [22] proposed Biologically Inspired Orthogonal Wavelet Transform (BIOWT) for decomposing the source brain images. The decomposed wavelet orthogonal coefficients were classified by the deep learning structure. Saeidifar et al. [32] integrated evolutionary approach with the active contour models to detect the tumor regions in brain images. The authors analyzed the linear kernel selection procedure of the active contour model with respect to simulation metrics. DeNoised wavelet segmented entropy classification algorithm for the classification of the brain images. The authors analyzed the performance of this method with other denoising models [29]. Irmak et al. [19] developed five different architectures for the detection of tumor pixels in the brain images. These architectures were differing with respect to the internal layers and with the different maximization structures. The output responses of each internal layer were integrated into regressive feature map and they were classified into the pixels belonging to either normal or tumor. Mobeen Rehman et al. [11] used BU-Net Convolutional neural network architecture for the identification of the tumor pixels in the brain image. Linear dropout function was implemented between each Convolutional layers with ReLu function to avoid over fitting problems in developed architecture. The obtained Loss functions or factors were low by proposing the Wide Context (WC) module. The authors obtained the simulation results of dice score as 0.9, 0.837, 0.788 DS for whole, core and enhancing set, respectively. Arif et al. [23] fused multi modal brain images using region level pixel fusion algorithm. The authors transformed the multi modal images using Fast Curvelet Transform for obtaining the transformed coefficients. Further, these coefficients were classified by the linear binary classifier to identify the tumor images. Jinisha et al. [26] used Support Vector Machine (SVM) classifier for the classification process of brain tumors. The bags of visual words were selected by the classification process to improve the classification rate. Shivhare et al. [33] combined the active contour model and the convex hull method for the classification of the brain tumor images. The authors obtained 96.1% of classification rate using their developed model. González-Villà et al. [28] detected multiple sclerosis lesions through the various abnormal tissue segmentation methods.

Hu et al. [14] used multi cascaded type CNN architecture and the Conditional Random Field (CRF) for the identification of pixels belonging to tumor category. The local dependencies of each internal module were computed and the multi core features were integrated with them to produce the cascaded feature maps. Then, the generated cascaded feature maps were fed into CRF classification architecture for the classification of pixels into either tumor or non-tumor. The authors tested their proposed CRF based brain tumor detection method on the brain images which were available in BRATS dataset and the authors obtained the simulation results for the dice scores as 0.882, 0.748, 0.718DS for whole, core and enhancing set. Khalil et al. [27] analyzed the performance of the brain tumor detection system through the feature extraction techniques. The authors also analyzed the effect of the computed features on brain tumor detection process. Glan et al. [24] used wrapper incorporated genetic algorithm for detecting and segmenting the tumor regions in brain images. This approach improved the classification accuracy through the feature selection approach. Angulakshmi et al. [25] used spectral clustering algorithm for the classification of brain tumors in source brain MRI images. The non-linear clustering kernels were used in this approach for brain tumor detection. Kermi et al. [12] detected and segmented the whole tumor and intra-tumor regions in the brain MRI images. The class imbalance issues in conventional deep learning architecture were reduced by proposing the modules Weighted Cross Entropy (WCE) and Generalized Dice Loss (GDL). The loss functions of the propose architecture were reduced using these entropy and GDL modules in the proposed CNN architecture. The authors obtained the simulation results of dice score as 0.873, 0.768, 0.716 DS for whole, core and enhancing set, respectively. Albiol et al. [13] constructed 2D CNN architecture for the problems of 3D segmentation in medical brain imaging. The non-linear feature map was constructed from the source brain image and these feature maps were fed into the classification module for the classification process. The authors verified their developed architecture using cross validation methods with neurological experts. Havaei et al. [16] used deep learning Convolutional architecture for the segmentation of tumor pixels in the brain image. The non linear negative responses were detected through the weight based modules and these negative responses were eliminated by implementing the architecture with residual blocks. The authors implemented their developed architecture on the brain MRI images of the open access datasets.

3. Proposed Methodology

The tumor regions are detected and segmented using UNET-CNN architecture in this paper. During training process of the proposed work, both Glioblastoma and Healthy brain MRI images are preprocessed and then multi level transform is applied on the preprocessed image. The features are further computed from the transformed coefficients and these features are trained by UNET-CNN architecture to obtain trained vectors. During testing process of the proposed work, the test brain MRI image is preprocessed and then decomposed coefficients are obtained by multi level transform. Features are computed from these decomposed coefficients and they are classified using UNET-CNN architecture with the trained vectors. Fig. 2 (a) shows the training methodology for Glioblastoma tumor detection and Fig.2 (b) shows the testing methodology for Glioblastoma tumor detection. It is the process of improving the dataset images for both training and testing phase of the classifier to obtain high classification rate.



(a)

(b)

Figure 2 *(a) Training methodology for Glioblastoma tumor detection (b) Testing methodology for Glioblastoma tumor detection*
Preprocessing

In this paper, data augmentation methods are used as the preprocessing technique to increase the total set of the brain images for further process. The flipping functions with respect to horizontal and vertical, translational function with respect to left and right orientations and shearing functions are used as the methods in data augmentation process. The BRATS 2018 consist of 265 Glioblastoma images and 318 Healthy brain images. Therefore, the total number of brain images which are obtained from this dataset is about 583 and these image counts are increased to 2915 (1166 flipped images, 1166 translational images and 583 shearing images) and these data augmented images are integrated with 583 original source brain images which produces 3498 images in dataset.

Multi Level Stationary Wavelet Transform (MLSWT)

Multi level transform decompose the source image into various sub bands at different stages of the transformation process. Many researchers used Discrete Wavelet Transform (DWT) for obtaining the decomposition sub bands for further feature extraction process. Implementation of DWT for the detection of tumor images has certain level of limitations which degrades the classification accuracy of the proposed system. Decomposition using wavelet transform creates translation invariance on each decomposed coefficients. These translation invariance increases the error rate on each sub band. In order to eliminate such translation invariance, MLSWT is used in this paper. This transform is otherwise called as Undecimated Wavelet Transform (UWT). The sampling modules (both up and down sampler) are removed in conventional DWT and the filter coefficients are up sampled by 2^{-1}, where j is the number of stages in MLSWT. The shift invariant property of MLSWT improves the classification rate of the proposed Glioblastoma tumor detection system.

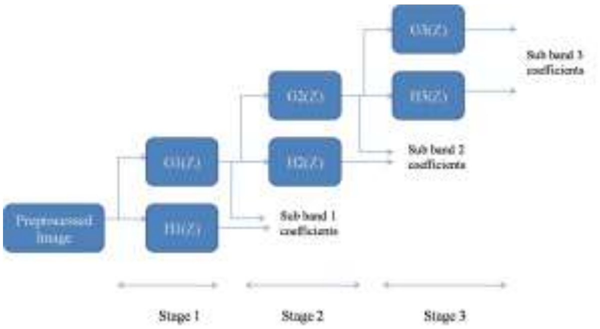


Figure 3 *Multi level SWT structure*

The MLSWT structure is depicted in Fig.3, which consists of low and high pass filters. The low pass filter has designed with its impulse function H1(Z) and high pass filter has been designed with its impulse function G1(Z) respectively. The preprocessed image is passed through the first set of low and high pass filters which produce the sub band 1 coefficient. These decomposed sub band coefficients are passed through the second stage of low and high pass filters which produce the sub band 2 coefficients. Further, the second stage sub band coefficients are passed through the third stage low and high pass filters, which produces sub band 3 coefficients.

Feature Computations

The features represent the internal pixel variation in an image. In this paper, the features are used to discriminate each pixel variation or coefficient in each decomposed sub bands which are obtained through the MLSWT structure. All the decomposed sub band coefficients from the MLSWR structure at each stage are stored in a matrix with P number of rows and Q number of columns. From this matrix, the following features are computed for differentiating the Glioblastoma image from the healthy brain image.

$$Linear\ Regression\ Metric\ Feature\ (LRMF) = \frac{1}{P*Q}\sum_{i=1}^{P}\sum_{j=1}^{Q}\frac{M(i,j)^2}{i*j}$$

Where, $M(i,j)$ is the matrix which contains the coefficients of the decomposed preprocessed image using MLSWT structure. The rows and columns of this matrix $M(i,j)$ is represented by P and Q.

LRMF feature defines the coefficient variations in the decomposed sub band with respect to its nearby coefficient values. The SOLF and TOLF features are the second and third order features which describes the correlation property of each decomposed coefficient values. The energy values of each decomposed coefficient are described by EHF features.

$$Second\ Order\ Linear\ Feature\ (SOLF) = \frac{1}{P*Q}\sum_{i=1}^{P}\sum_{j=1}^{Q}\frac{M(i,j)^2}{i^2*j^2}$$

$$Third\ Order\ Linear\ Feature\ (TOLF) = \frac{1}{P*Q}\sum_{i=1}^{P}\sum_{j=1}^{Q}\frac{M(i,j)^2}{i^3*j^3}$$

$$Schematic\ Metric\ Feature\ (SMF) = \frac{1}{(P-1)(Q-1)}\sum_{i=1}^{P}\sum_{j=1}^{Q}\frac{i^2j^2*M(i,j)}{(i-1)^2*(j-1)^2}$$

$$Energy\ Heuristic\ Feature\ (EHF) = \frac{1}{P^2*Q^2}\frac{\sum_{i=1}^{P}\sum_{j=1}^{Q}M(i,j)^2}{SMF}$$

Table 1 shows the extracted feature values of both Glioblastoma and healthy brain image which is available from the dataset.

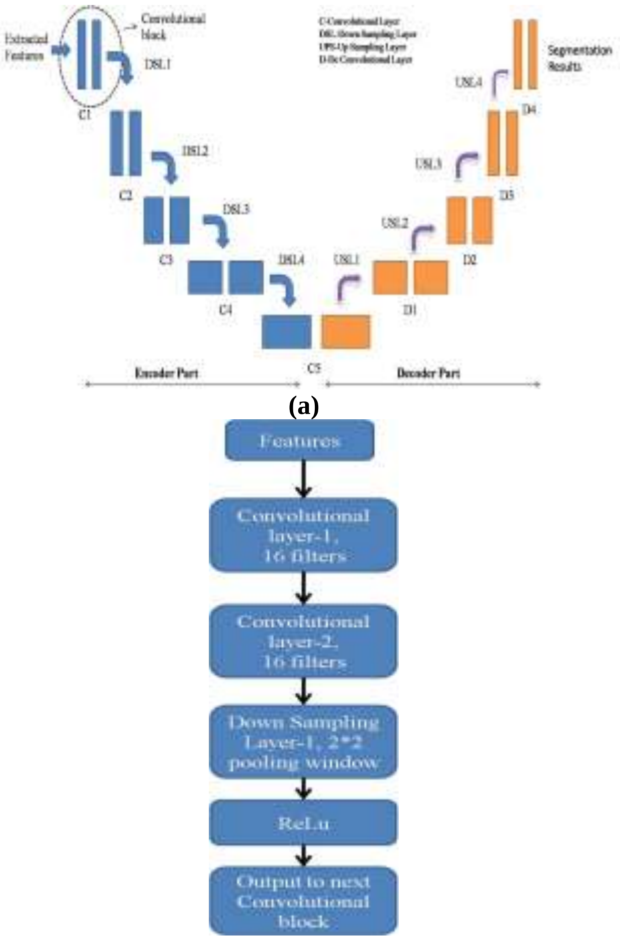
***Table 1** Extracted feature values of Glioblastoma and healthy brain images*

Feature metrics	**Glioblastoma image**	**Healthy brain image**
LRMF	$1.2*10^{-2}$	$0.879*10^{-2}$
SOLF	$3.98*10^{-4}$	$0.398*10^{-4}$
TOLF	$1.298*10^{-3}$	$0.769*10^{-2}$
SMF	$7.389*10^{-4}$	$1.83*10^{-3}$
EHF	$5.783*10^{-2}$	$0.382*10^{-2}$

Classification and Segmentation

Classification and segmentation are the two stage distinct process for the classification of Glioblastoma images and for segmenting the tumor pixels in the classified image. Past two decades, many researchers used machine and deep learning methods to perform the classification process [17,18,19]. Then, separate segmentation algorithm is applied on the classified image to identify the tumor affected pixels. This two step process increases the computation time as well as degrades the performance efficiency of the overall tumor detection and segmentation system. Therefore, there is a methodology requires for the Glioblastoma detection system with single step process. This will eliminate the problems raised in conventional two step process for tumor detection system. Hence, UNET-CNN architecture is developed in this paper to perform both classification and segmentation process for Glioblastoma detection system in this paper. The computed features from the feature computation process are classified and the tumor pixels are segmented using UNET-CNN architecture.

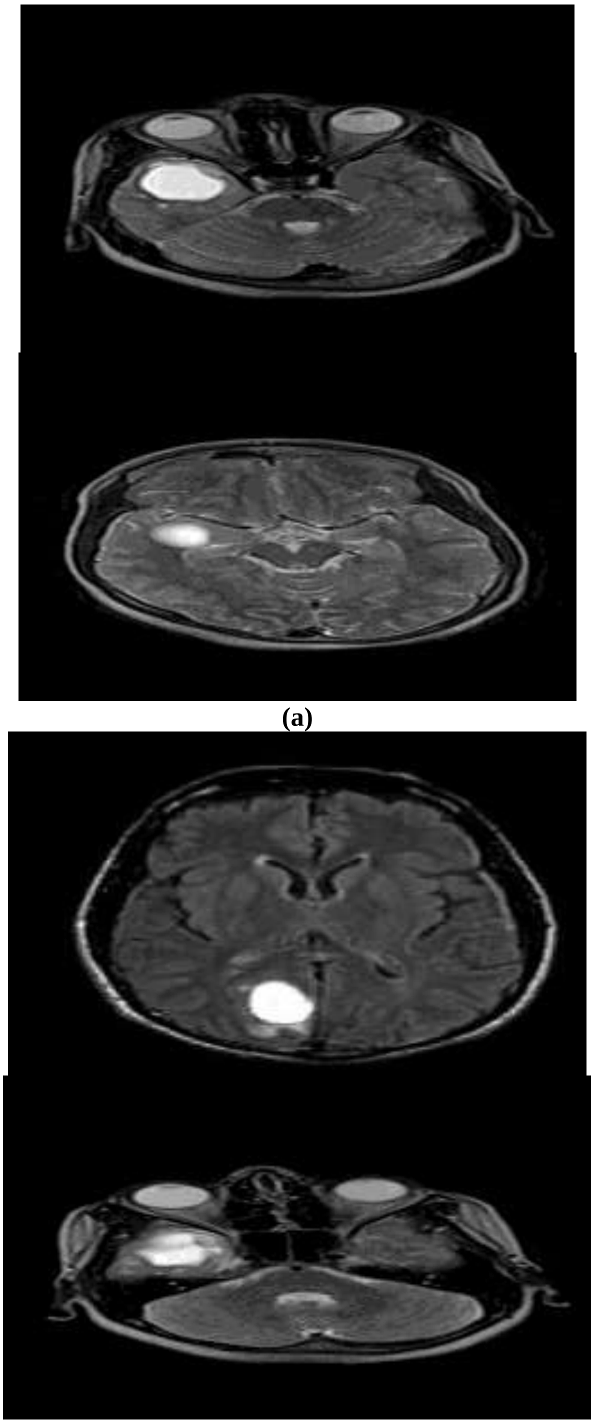
Fig.4 (a) shows the proposed UNET-CNN architecture for detecting and segmenting the tumor pixels in the Glioblastoma image and Fig. 4(b) shows the structure of each Convolutional block in the proposed architecture.This proposed structure is designed with two modules as Encoder and Decoder. The Encoder part of this structure consist of Convolutional layer (C), Down Sampling Layer (DSL). The decoder part of this structure consist of Deconvolutional layer (D) and Up Sampling Layer (USL). The first Convolutional block in Encoder part is designed with two Convolutional layers and each Convolutional layer is designed with 16 Convolutional filters with 3*3 kernel. The second Convolutional block in Encoder part is designed with two Convolutional layers and each Convolutional layer is designed with 32 Convolutional filters with 5*5 kernel. The third Convolutional block in Encoder part is designed with two Convolutional layers and each Convolutional layer is designed with 64 Convolutional filters with 7*7 kernel. The fourth Convolutional block in Encoder part is designed with two Convolutional layers and each Convolutional layer is designed with 128 Convolutional filters with 5*5 kernel. The fifth Convolutional block in Encoder part is designed with two Convolutional layers and each Convolutional layer is designed with 256 Convolutional filters with 3*3 kernel. The Decoder part of this structure is having the reverse process of the Encoder part. The responses from each Convolutional block are reduced with DSL which designed with Max Pooling function and 2*2 pool window. The negative responses in the down sampling responses are rectified using Rectified Linear Unit (ReLu). The segmentation results (tumor pixels) are obtained after fourth Deconvolutional layer of this proposed structure. Fig.5 shows the Glioblastoma images and Fig.6 shows the healthy (non-Glioblastoma) images which are classified through the proposed UNET-CNN architecture. Fig. 7 (a) shows the test brain image and Fig. 7(b) shows the tumor region segmented image by the proposed UNET-CNN architecture.



(a)

(b)

***Figure 4** (a) Proposed UNET-CNN architecture (b) Structure of Convolutional block*

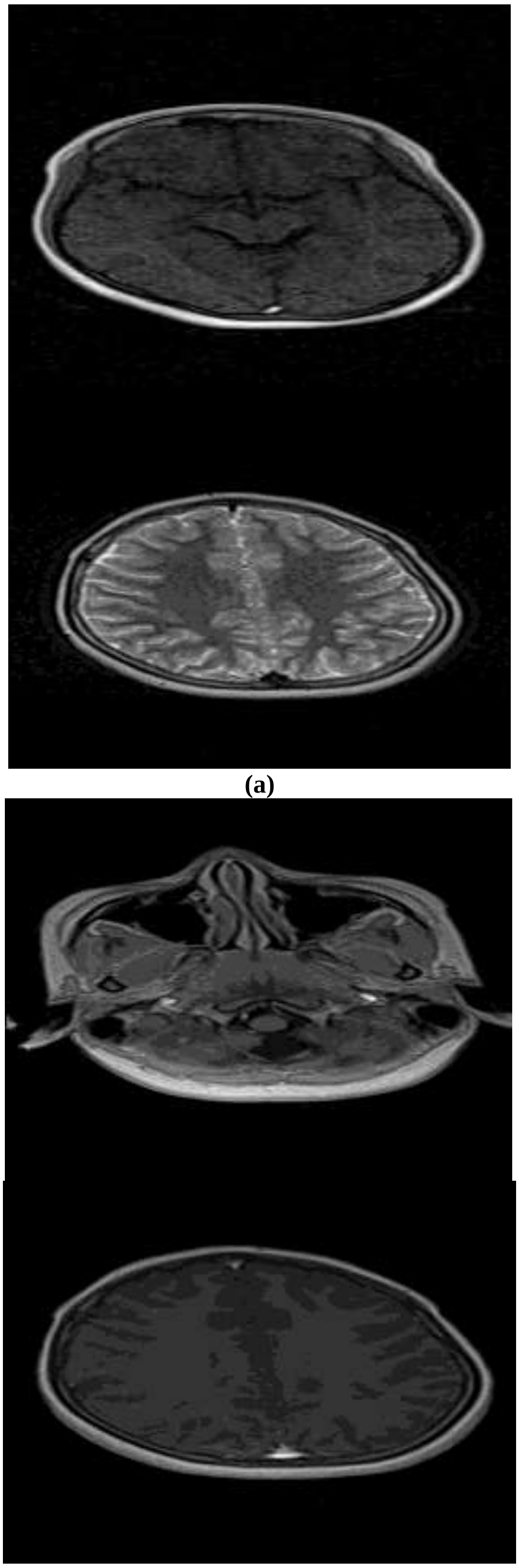

(a)

(b)

Figure 5 *Classified Glioblastoma images (a) BRATS 2018 dataset (b) BRATS 2017*

4. Results and Discussions

In this paper, the quantitative and qualitative performance measures are computed for the proposed Glioblastoma tumor segmentation methodology on BRATS 2017 [20], BRATS-2018 dataset [21] brain MRI images. The quantitative measures are computed based on the number of correctly detected brain images. The qualitative measures are computed based on the visual inspection of the tumor segmented pixels. For performing quantitative measures, Detection Rate (DR) is used in this paper which is measured


(a)

(b)

Figure 6 *Classified Healthy images(a) BRATS 2018 dataset (b) BRATS 2017*

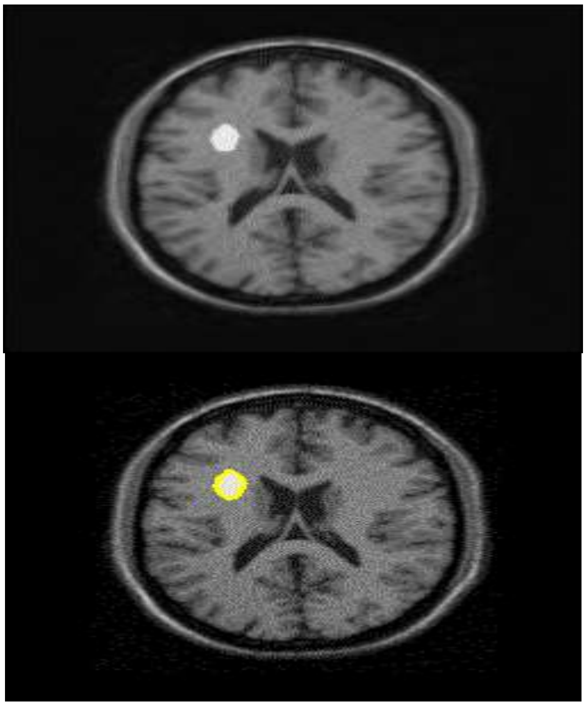

(a) (b)

Figure 7 *(a) Test brain image (b) Tumor region segmented image by the proposed UNET-CNN architecture*

between the correctly detected images counts and total number of images as described in the following equation.

$$DR = \frac{Number\ of\ correctly\ detceted\ Glioblastoma\ images}{Total\ Glioblastoma\ images} * 100\%$$

The BRATS 2018 consist of 265 Glioblastoma images and 318 Healthy brain images. The proposed UNET-CNN architecture correctly detects 263 Glioblastoma images and reaches 99.2% of DR and also correctly detects 312 healthy brain images and reaches 98.1% of DR. Therefore, the average DR for BRATS 2018 dataset is about 98.6%.

The BRATS 2017 consist of 175 Glioblastoma images and 200 Healthy brain images. The proposed UNET-CNN architecture correctly detects 173 Glioblastoma images and reaches 98.8% of DR and also correctly detects 198 healthy brain images and reaches 99% of DR. Therefore, the average DR for BRATS 2018 dataset is about 98.9%.

Table 2 shows the comparative quantitative analysis on BRATS 2017 and BRATS 2018 datasets in terms of DR. Mobeen Rehman et al. [11] obtained 96.1% and 96.4% of DR for BRATS 2017 dataset and BRATS 2018 dataset respectively.

Hu et al. [14] obtained 95.3% and 93.9% of DR for BRATS 2017 dataset and BRATS 2018 dataset respectively. Kermi et al. [12] obtained 96.2% and 92.9% of DR for BRATS 2017 dataset and BRATS 2018 dataset respectively. Albiol et al. [13] obtained 95.3% and 94.8% of DR for BRATS 2017 dataset and BRATS 2018 dataset respectively. Dong et al. [15] obtained 94.2% and 95.2% of DR for BRATS 2017 dataset and BRATS 2018 dataset respectively.

From the qualitative measures of the proposed method with other state of the art methods, the proposed Glioblastoma tumor detection method stated in this work provides better DR than other existing methods.

Table 2 *Comparative quantitative analysis on BRATS 2017 and BRATS 2018 datasets*

Authors	**Methodology**	**DR in %**	
		BRATS 2017 dataset	**BRATS 2018 dataset**
This paper	**UNET-CNN**	98.6	98.9
[11]	BU-Net	96.1	96.4
[14]	MCC	95.3	93.9
[12]	ResU-Net	96.2	92.9
[13]	Ensemble Net	95.3	94.8
[15]	U-Net	94.2	95.2

Dice Score (DS) qualitative parameter is used in this paper to measure the effective performance of the brain tumor segmentation results. The DS can be computed between the tumor segmented image by proposed work and the tumor segmented image by manual method (through radiologist). The following equation is used to compute DS and the value of the DS varies between 0 and 1. If the value of DS is greater than 0.8, then the tumor segmentation results are better for further tumor diagnosis process.

$$Dice\ Score\ (DS) = \frac{2 * (I_1 \cap I_2)}{|I_1| + |I_2|}$$

Where, I_1 is the tumor segmented image by proposed work and I_2 is the tumor segmented image by manual method.

Table 3 shows the comparative qualitative analysis on the brain images available in BRATS 2018 dataset with respect to DS.

The Glioblastoma images in dataset are split into three regions Whole Tumor (WT), Tumor Core (TC), and Enhancing tumor (ET). The regions in each brain image are categorized into these three regions and the proposed method is tested on these three regions of the same brain image to validate the effectiveness of the proposed work in this paper. The proposed methodology stated in this paper used UNET-CNN segmentation approach and obtained 0.967, 0.959, 0.943 DS for whole, core and enhancing set. Mobeen Rehman et al. [11] used BU-Net segmentation approach and obtained 0.9, 0.837, 0.788 DS for whole, core and enhancing set.

Hu et al. [14] used MCC segmentation approach and obtained 0.882, 0.748, 0.718DS for whole, core and enhancing set. Kermi et al. [12] used ResU-Net segmentation approach and obtained 0.867, 0.803, 0.768 DS for whole, core and enhancing set. Albiol et al. [13] used Ensemble Net segmentation approach and obtained 0.881, 0.777, 0.773 DS for whole, core and enhancing set. Dong et al. [15] used U-Net segmentation approach and obtained 0.86, 0.79, 0.767 DS for whole, core and enhancing set. From qualitative analysis of Table 3, the proposed UNET-CNN based Glioblastoma brain tumor detection system stated in this paper provides good tumor segmentation results when comparing other state of the art methods. Fig. 8 shows the illustration of Comparative analysis of dice score on BRATS 2018 dataset. Table 4 shows the comparative qualitative analysis on the brain images available in BRATS 2017 dataset with respect to DS. The proposed methodology stated in this paper used UNET-CNN segmentation approach and obtained 0.947, 0.939, 0.923 DS for whole, core and enhancing set. Li et al. [17] used NovelNet architecture for segmenting the tumor regions and obtained 0.809, 0.701, 0.554 DS for whole, core and enhancing set.

Table 3 *Comparative qualitative analysis on BRATS 2018 dataset*

Authors	Methodology	Dice Score		
		Whole	**Core**	**Enhancing**
This paper	**UNET-CNN**	**0.967**	**0.959**	**0.943**
[11]	BU-Net	0.90	0.837	0.788
[14]	MCC	0.882	0.748	0.718
[12]	ResU-Net	0.867	0.803	0.768
[13]	Ensemble Net	0.881	0.777	0.773
[15]	U-Net	0.86	0.79	0.767

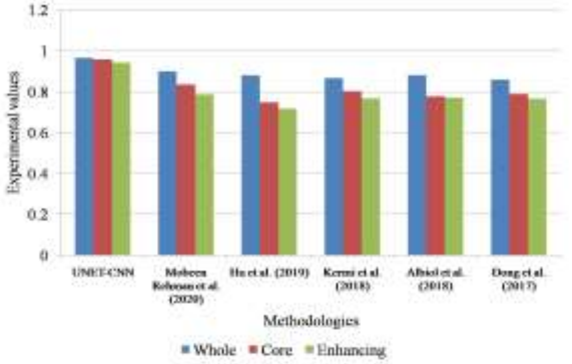


Figure 8 *Illustration of Comparative analysis of dice score on BRATS 2018 dataset*

Kermi et al. [12] used ResU-Net architecture for segmenting the tumor regions and obtained 0.873, 0.768, 0.716 DS for whole, core and enhancing set. Dong et al. [15] used U-Net architecture for segmenting the tumor regions and obtained 0.87, 0.762, 0.70 DS for whole, core and enhancing set. Badrinarayanan et al. [18] used SegNet architecture for segmenting the tumor regions and obtained 0.833, 0.703, 0.496 DS for whole, core and enhancing set. From qualitative analysis of Table 4, the proposed UNET-CNN based Glioblastoma brain tumor detection system stated in this paper provides good tumor segmentation results when comparing other state of the art methods. Fig. 9 shows the illustration of Comparative analysis of dice score on BRATS 2017 dataset.

5. Conclusions

The Glioblastoma brain tumors are detected and segmented using multi level transform based UNET-CNN architecture in this paper. The developed architecture is tested on the brain images which are available in BRATS 2017 and BRATS 2018 datasets. The proposed methodology stated in this paper used UNET-CNN segmentation approach and obtained 0.967, 0.959, 0.943 DS for whole, core and enhancing set, on BRATS 2018 dataset images. The proposed methodology stated in this paper used UNET-CNN segmentation approach and obtained 0.947, 0.939, 0.923 DS for whole, core and enhancing set, on BRATS 2017 dataset images. The simulation results of the proposed architecture are both quantitatively and qualitatively compared with other similar studies in terms of detection rate

Table 4 *Comparative qualitative analysis on BRATS 2017 dataset*

Authors	Methodology	Dice Score		
		Whole	**Core**	**Enhancing**
This paper	**UNET-CNN**	**0.947**	**0.939**	**0.923**
[11]	BU-Net	0.892	0.783	0.736
[17]	NovelNet	0.809	0.701	0.554
[12]	ResU-Net	0.873	0.768	0.716
[15]	U-Net	0.87	0.762	0.70
[18]	SegNet	0.833	0.703	0.496

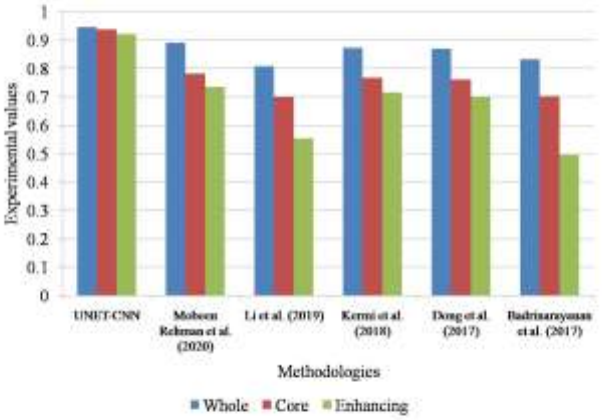


Figure 9 *Illustration of Comparative analysis of dice score on BRATS 2017 dataset*

and dice score. In future, the Glioblastoma tumors will be diagnosed into various stages for further effective treatment.

Author Statements:

- **Ethical approval:** The conducted research is not related to either human or animal use.
- **Conflict of interest:** The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper
- **Acknowledgement:** The authors declare that they have nobody or no-company to acknowledge.
- **Author contributions:** The authors declare that they have equal right on this paper.
- **Funding information:** The authors declare that there is no funding to be acknowledged.
- **Data availability statement:** The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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