Brain Tumor Detection Using Skull Stripping and U-Net Architecture

Debapriya Hazra and Yungcheol Byun

Abstract—**The formation of abnormal cells within the brain is termed as brain tumor. Brain tumors can be benign or cancerous. Brain being the major organ of the body controls every activity we perform in our daily life. Therefore, it is important to detect any kind of abnormal growth of cells in the brain at the earliest. Deep learning methods are now being hugely used in medical image analysis. Manual detection of brain tumors by radiologists are time consuming and error prone. Therefore applying Machine Learning techniques to automatically segment tumor region and to detect is very important and necessary in advancing medical image analysis. The algorithm in this paper could automatically detect brain tumor through skull stripping method and segmentation through U-Net architecture. The algorithm has been tested on 3000 Magnetic resonance imaging images (MRI) and resulted in an accuracy of 93%. Dataset of Digital Imaging and Communications in Medicine (DICOM) format brain MRI images has been used for the experimentation. The proposed method achieved mean Dice Similarity Coefficient metric of 0.82 and median Dice Similarity Coefficient metric of 0.86 for full tumor region.**

Index Terms—**Skull stripping, U-Net architecture, data augmentation.**

I. Introduction

What causes brain tumor is still unknown. Common symptoms include seizures, headache, motor weakness, vomiting and changes in vision. The most dreadful case of brain tumor is brain metastasis where the tumor keeps spreading. World Health Organization has classified over 130 types of brain tumor, among which the frequently occurred tumors are Glioblastoma, Meningioma, CNS lymphoma, unspecified glioma and many more. Brain tumors are generally diagnosed through Computed Tomography (CT) scan or Magnetic Resonance Imaging (MRI) and malignancy is checked by performing biopsy. According to the result, tumor is divided into grades of extremity.

Smart healthcare is evolving with the help of machine learning. Advanced algorithms are being implemented in critical cases like detection of breast cancer, liver cirrhosis, diabetes, cyst detection, malignancy detection and many more. In this paper, we develop an algorithm that will take MRI images as input. Implement data augmentation to enhance the existing images and increase it in amount. The images are then pre-processed, after which skull stripping method is applied. Skull stripping method is applied to remove non-brain tissues from magnetic resonance brain images. For segmentation of the brain tumor, the algorithm has used U-Net architecture. After tumor segmentation, the final output is generated which shows if the MRI images consists of brain tumor or not.

The challenging task of extracting the tumor region from the healthy tissues in the brain is achieved through segmentation. Segmentation of a brain tumor becomes difficult due to the various properties that tumor holds, such as size, shape, location, its connection to the sagittal sinus and many more. Also, the formation of a brain tumor changes the surrounding tissue structure or deforms it, due to the pressure created by the tumor. Deformable models represented by curves (2D) or surfaces (3D) are the most common method for detection of brain tumor [1]. Other segmentation techniques involve thresholding, region growing, edge based segmentation, watershed, morphological based segmentation, Kmeans, contour-based segmentation, atlas-based segmentation, deep neural network and hybrid method to name few.

Brain tumors can be divided into primary and secondary brain tumors. Primary brain tumor includes pineal gland tumors, pituitary tumor, ependymomas, craniopharyngiomas, primary central nervous system lymphomas, meningiomas, primary germ cell tumors and schwannomas. Secondary tumors are responsible for causing brain cancers. They generally start in other parts of the body, then spread and metastasize to the brain. Secondary brain tumors are always malignant.

There are many neuroimaging methods for studying brain functions such as Magnetic Resonance Imaging (MRI), Functional Magnetic Resonance Imaging (fMRI), Computed Tomography Scan (CT Scan), Positron Emission Tomography (PET) Scan, Single Photon Emission Computed Tomography (SPECT), Magnetoencephalography (MEG), Electroencephalography (EEG), Functional Near-Infrared Spectroscopy (fNIRS), X-Ray, Ultrasound.

Gliomas are the most common type of tumors in brain and are generally divided into 4 types. The Astrocytomas and Oligoastrocytomas are Grade I and Grade II tumors that are less aggressiveand are known as Low-Grade Gliomas (LGG). Anaplastic Astrocytomas and Glioblastoma Multiforme are grouped into Grade III and Grade IV which are known as High-Grade Gliomas (HGG) [2]. HGGs are very aggressive and is often life threatening. In our work we have considered both HGG and LGG tumor MR images. The modalities of

MR images that we have worked on are T1-weighted MRI (T1), T1-weighted MRI with contrast enhancement (T1c), T2-weighted MRI (T2) and T2-weighted MRI with fluid attenuated inversion recovery (T2-Flair).

Methods	References	Advantages	Disadvantages
Thresholding	Saad *et al.* [2]	Work well for homogeneous image	The selection of optimal threshold is difficult
Region growing	Viji and Jayakumari [3]	Both the spatial overlap and coefficient of similarity are increased to increase sensitivity and specificity of tumor detection	The execution time is high
Edge based segmentation	Mathur *et al.* [4]	Thresholding setting capability is increased by fuzzy logic system with kmeans clustering	Complex computation is high
Watershed	Pandav [5]	Large number of segmented region in edges is reduced by marker controlled watershed segmentation	Foreground objects and the background locations should be marked already to get better segmentation result
Morphological based segmentation	Sudharania *et al.* [6]	High accuracy of segmentation result and less processing speed is obtained. Works well with low intensity image	The method involves many repeated steps for segmentation
Kmeans	Nimeesha and Gowda [7]	K-means is able to characterize the regions effectively. FCM identifies only three tissue classes whereas; K-means identifies all the six classes	Few WM is classified as edema and vice versa in using K-means algorithm. Intensify feature alone is not viable for MR classification
Contour-based segmentation	Tanoori [2]	Simple method. Tissues are separated effectively	The result are nor satisfactory for noisy, nonuniform and high intensity images
Atlas-based segmentation	Bauer *et al.* [8]	The proposed method is meshfree and hence removes the difficulty of handling meshes. This can be used clinically without knowledge of parameterization. The computation speed is high	The method is not completely automatic as initial seed selection for tumour is done manually
Deep neural network	Havaei *et al.* [9]	The proposed method provides better accuracy for segmentation process	The GPU implementation required for more fast segmentation
Hybrid method	Sachdeva *et al.* [10]	Multiclass classification of tumour is done efficiently. High accuracy is obtained using GA-ANN and high speed is obtained using GA-SVM	Complexity increases due to hybridization

Fig. 1. Advantage and disadvantage of segmentation methods of MRI images [11].

Neuroimaging Techniques	Measures / Produces	Image Quality	Temporal Resolution	Spatial Resolution	Cost
MRI	Gray Matter Volume	Good	Low (20-50ms)	Very-High (2mm)	High
fMRI	Relative Blood Oxygenation	Good	Low (1.5s)	Very-High (2mm)	High
CT Scan	cross-sectional images of bones, blood vessels & soft tissues	Low	Medium (10s)	Very-High (1mm)	Low
PET	metabolic processes	Good	Low (1-2min)	High (4mm)	Very-High
SPECT	Blood flow to tissue and organ	Average	Very-Low (5-9min)	Medium (6mm)	High
MEG	Brain activity & small magnetic field	Average	Very-High (< 1ms)	Medium (5mm)	High
EEG	Post-synaptic electrical activity	Average	Very-High (< ms)	Medium (10mm)	Low
fNIRS	Oxyhemoglobin & deoxyhemoglobin	Good	High (0.01 s)	Low-Medium (0.5-2cm)	Very-Low
X-Ray	Changes in bone	Low	Medium (1-10s)	Very-High (1mm)	Low
Ultrasound	Direction and velocity of blood flow	Low	High (1-3ms)	Depends on probe element width	Low

Fig. 2. Comparison of brain neuroimaging techniques.

II. LITERATURE REVIEW

With the advancements in AI algorithms and applications, CNN based algorithms predominantly have become a frequently used approach in the medical imaging problems and challenges [12]. Normally, deep learning algorithms require enormous amount of labeled data for training but in medical field usually the image data is insufficient for training and it's a critical challenge. It is also a labor-intensive task to label the images by the experts in order to overcome the challenge related to training data and test data for medical diagnosis [13].

There have been many approaches proposed to solve the problem of skull stripping in brain MRIs over the last two decades. These approaches can be classified into two classes; the first class of focuses on the classical methods and others are based on deep learning methods. The classical approaches are further divided into different categories, [14] presents a comprehensive survey of all the conventional approaches. In the current the Multimodal Brain Tumor Image Segmentation Benchmarks (BraTS), CNNs have accomplished state-of-the-art performance [15]-[19].

In the paper "Automatic Brain Tumor Detection and Segmentation using U-Net based fully convolutional network" [11], author has used both up-sampling and down-sampling of U-Net architecture as in the below Fig. 3.
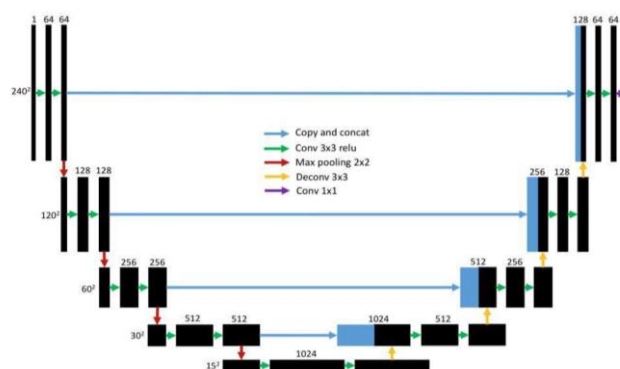

Fig. 3. Author's developed U-Net architecture.

Tatiraju and Mehta proposed a K-means clustering algorithm and introduced Expectation Maximization (EM) and Normalized Cuts (NC) for image segmentation [20]. In their work they compared two unsupervised learning methods with the graph based Normalized Cut algorithm. In K-means clustering when the value of k is small, the EM algorithm generates good results [21]. When the value of k is large, the segmentation result is not that fruitful.

Jibi Belghese and Sheeja Agustin used feedforward Pattern Neural Network (PNN) for tumor segmentation [21]. They have used Xavier initialization method for reasonable weight initialization. Author claimed that accuracy is much higher than fuzzy c-means method and using compositional pattern-producing network, the time taken for overall segmentation and post processing is much lesser than time taken by K-means clustering method or Convolutional Neural Network (CNN).

Marcel Prastawa *et al.* presented a framework for automatic brain tumor segmentation from MR images [22]. The framework is mainly composed of three stages. Firstly, abnormal regions are detected using registered brain atlas it determines the intensity property of different types of tissues. Secondly, they find whether edema appears with the tumor in the abnormal regions or not. Lastly, they have applied geometric and spatial constraints to the tumors and edema detected [22].

Stefan Bauer *et al.* in their paper used Support Vector Machine classification with hierarchical regularization based on conditional random fields to automatically segment brain tissues [23]. They have separately identified cerebrospinal fluid, white matter, gray matter, necrotic, active and edema region. Author has claimed that segmentation has greater details than previous work and the computation time is also less.

Chi-Hoon Lee *et al.* proposed a segmentation technique using Pseudo-Conditional Random Fields (PCRFs) [24]. The author argues that standard classifiers such as Logistic Regression (LR) and Support Vector Machine (SVM) treats every voxel as independent and identically distributed (iid) and therefore have limited accuracy. PCRF on the other hand is a regularized discriminative classifier that considers the labels and features of neighboring voxels and relaxes the classification decision for each voxel [24].

Abdelmajid Bousselham *et al.* proposed a segmentation technique using reinforcement learning on MRI images based on temperature changes on pathologic area [25]. To segment brain tumors in T1 contrast and Flair MRI images, author have used active contours without edges as proposed by Chan and Vese [26].

III. METHODOLOGY

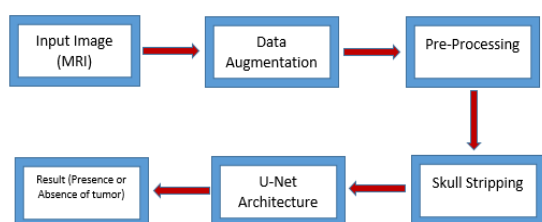Our proposed methodology consists of the steps as shown in Fig. 4:

Fig. 4. Overview of the proposed approach.

A. Algorithm of the Proposed Approach

Step 1: Start

Step 2: Read input MRI brain image (T1, T1c, T2, T2-Flair)

Step 3: Data augmentation

Step 3.1: rotations

Step 3.2: translations

Step 3.3: flips

Step 3.4: shearing

Step 3.5: scale change

Step 4: Smoothing the image using Gaussian filter of a large bandwidth

Step 5: Image enhancement

Step 6: Perform skull stripping

Step 7: Implementing 9-layer U-net segmentation process on T1, T1c, T2, T2-Flair preprocessed image

Step 8: If tumor present

Step 8:1: Trace the region boundaries and display tumor present along with tumor image superimposed with red color boundary

Else

Step 8:2: Display the original image stating tumor absent

B. Input Images

We have taken T1-weighted MRI (T1), T1-weighted MRI with contrast enhancement (T1c), T2-weighted MRI (T2) and T2-weighted MRI with fluid attenuated inversion recovery (T2-Flair) as input image. Size of the images is 512 × 512.

Tissue contrast is determined by two factors, Repetition Time (TR) and Echo Time (TE). The amount of time between successive radio frequency pulse sequences is referred to as repetition time. The time between the center of the radio frequency pulse and the receipt of the echo signal is referred to as the echo time. There are two relaxation time for tissues, T1 and T2. T1 is the longitudinal relaxation time whereas T2 is the transverse relaxation time [18]. T1-weighted images have short TE and TR times. T2-weighted images have longer TE and TR times. In Flair sequence the TE and TR times are very long. T1 contrast enhanced images includes a paramagnetic contrast agent (gadolinium) which reduces the T1 relaxation time and increases the signal intensity so that we can receive finer image of the areas affected by hemorrhage. Contrast of images in different modalities is shown in Fig. 5 [27].

Tissue	T1-Weighted	T2-Weighted	Flair	T1c
White Matter	Light	Dark Gray	Dark Gray	Light
Cerebrospinal fluid	Dark	Bright	Gray	Dark Gray
Fat with bone marrow	Bright	Light	Light	Bright
Cortex	Gray	Light Gray	Light Gray	Dark
Inflammation	Dark	Bright	Bright	Dark Gray

Fig. 5. Contrast of images in different modalities.

C. Data Augmentation

By the method of data augmentation in our algorithm, we have increased the diversity of the existing data. The algorithm has used horizontally flip, vertically flip, rotation,

translation, shearing, scale change rotation and padding. Taking two DICOM images Fig. 6 shows few examples of applying data augmentation using rotation, flipping, translation and padding.
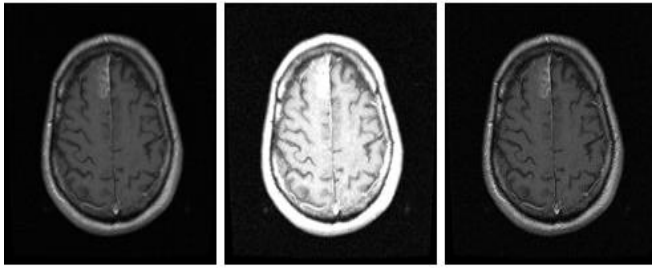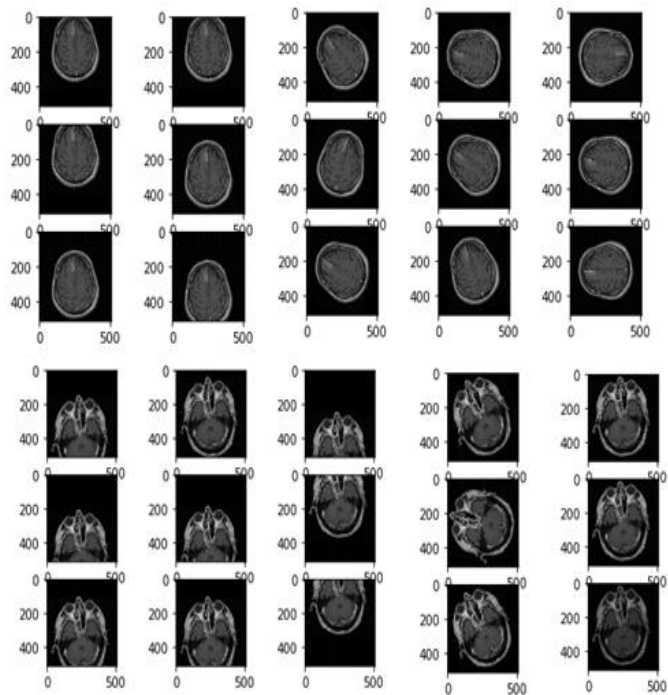

Fig. 6. T2-weighted, T1-weighted, Flair MRI images.

Fig. 7. Applying data augmentation.

D. Preprocessing

Noise created by the radio waves of the MRI is removed by using filtering techniques such as Median filtering and Gaussian filtering of a large bandwidth. We have taken specific axial slices of the brain image and then zero-mean normalized using mean and standard deviation [28]. Often there will be a dark ring in MRI images which is the brain cortex. Finer details are extracted and these dark rings are removed through image enhancement. These have been the part of the pre-processing steps.
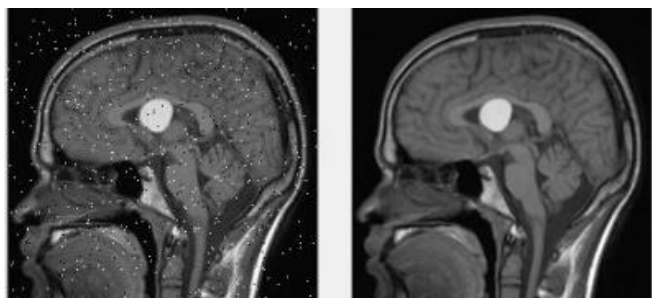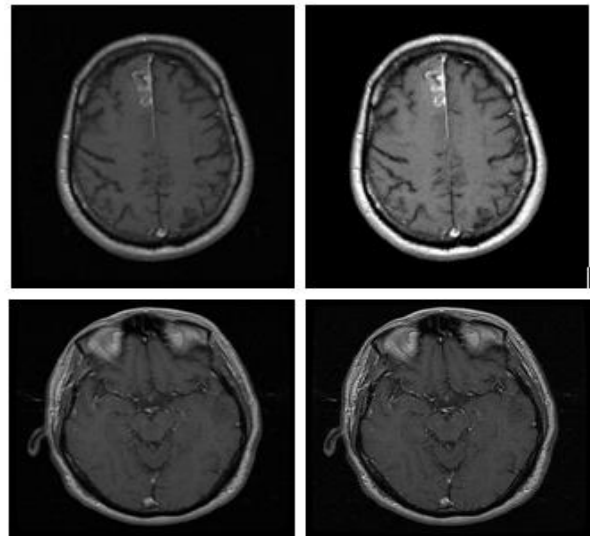

Fig. 8. Noise removal from MRI images.

Fig. 9. Original and enhanced image.

E. Skull Stripping

Skull stripping in our algorithm removes skull, dura and scalp, or we can say the non-cerebral tissues from the brain MRI image. Skull stripping has been performed by taking the threshold value of the sum of the grey and the white matter probability map [29]. Some examples of skull stripped MRI images have been shown in Fig. 10. Skull stripping in these images has been performed after removing noise and enhancing the image. Skull stripping can also be considered as a part of the preprocessing steps as before segmentation it is better to extract out the tissues that leads to incorrect detection of tumor in the brain.
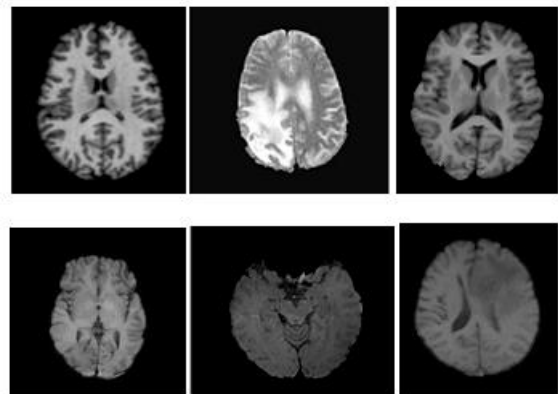

Fig. 10. Skull stripped image.

F. U-Net Architecture

U-Net architecture has been used in this algorithm to segment out the tumor from the brain MRI images. The U-Net architecture consists of a down-sampling and an up-sampling path.

The down-sampling path has 9 convolutional-blocks. For up-sampling, max pooling with stride 2×2 has been applied to the end of every block leaving the last block [30]. Every block in the up-sampling path starts with a deconvolutional layer. Zero padding has been used for all the down-sampling and up-sampling. At the end 1×1 convolutional layer has been used to reduce the feature map to two.

The convolutional layer is the main building block of the

convolutional neural network. The filter does the dot product to an input to the previous layer that result in activation. Max pooling is used to down-sample an image or input representation and helps in making assumptions about features. By using max pooling we can reduce the number of parameters and hence reduce the computation cost. A max filter is applied to non-overlapping subregions in max pooling as shown in Fig. 11.
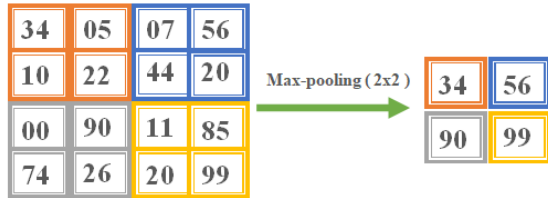

Fig. 11. Pictorial representation of max pooling.

The number of pixel shifts over the input matrix is known as strides [31]. For example if the stride is 3, filter should be moved to 3 pixels at a time. When filter does not fit the image accurately, padding is used. In our case we have used zero padding so that it fits the image. In Fig. 12, the proposed U-Net architecture has been represented. There are 4 input channels as we are using T1, T1c, T2 and Flair images for full tumor. The final output convolutional filter is one for binary segmentation. We have used nine layers U-Net structure for our segmentation algorithm.
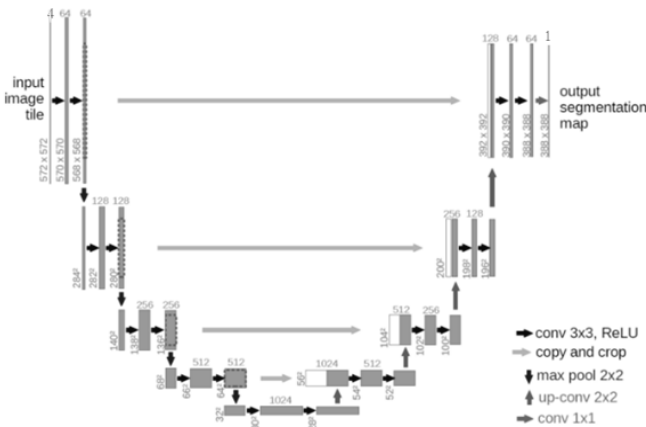

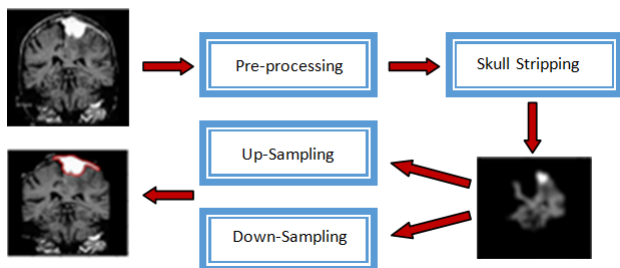Fig. 12. Proposed U-Net architecture.

Fig. 13. Detection result for T1c MRI of brain tumor.

G. Result

After going through all the processes, the algorithm produces the result of whether the MRI image of the brain consists of tumor or not. Our method is simpler and efficient in detecting brain tumor compared to other deep learning methodologies. Fig. 13 shows a result of segmentation as an example for T1c MRI image after applying U-Net architecture. Accuracy of the proposed algorithm has been calculated by equation (1):

$$\text{Accuracy} = (\text{Total no. of correctly predicted images} / \text{Total no. of tested images}) \times 100\% \tag{1}$$

H. Samples

After segmenting the tumor part using U-Net architecture, our algorithm has traced the region boundaries and superimposed the tumor part with red outline. Fig. 14 shows some of the sample result after detecting the brain tumor using our proposed methodology.
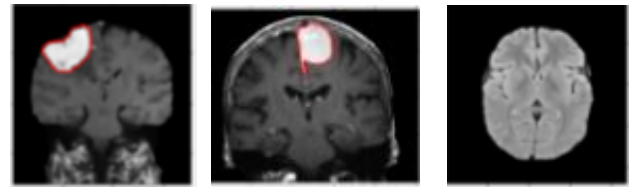

Fig. 14. Result samples.

IV. CONCLUSION

The algorithm developed in this paper has been tested on 3000 MRI images. Among those 3000 images, 2790 images were predicted correctly securing an accuracy rate of 93% by the given equation (1).

In future we would like to extend our work in detecting every kind of tumor individually according to their position and characteristics. This algorithm can also be modified and used in detecting cysts and tumors in different parts of the body.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

AUTHOR CONTRIBUTIONS

Debapriya Hazra generated the idea for this paper, designed the experiments, implemented the algorithms and wrote the paper. Yungcheol Byun conceived the overall idea of this paper, proof-read the manuscript and supervised the work.

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