International Journal of Applied Research 2017; 3(6): 1152-1159

ISSN Print: 2394-7500
ISSN Online: 2394-5869
Impact Factor: 5.2
IJAR 2017; 3(6): 1152-1159
www.allresearchjournal.com
Received: 04-04-2017
Accepted: 05-05-2017

Debjyoti Ghosh
M.Tech Student, Dept. of Computer Science and Engineering, University of Calcutta, Kolkata, West Bengal, India

Samir Kumar Bandyopadhyay
Prof. Dept. of Computer Science and Engineering, University of Calcutta, Kolkata, West Bengal, India

Correspondence
Debjyoti Ghosh
M.Tech Student, Dept. of Computer Science and Engineering, University of Calcutta, Kolkata, West Bengal, India

Brain tumor detection from MRI image: An approach

Debjyoti Ghosh and Samir Kumar Bandyopadhyay

Abstract
A brain tumor is an abnormal growth of cells within the brain, which can be cancerous or non-cancerous (benign). This paper detects different types of tumors and cancerous growth within the brain and other associated areas within the brain by using computerized methods on MRI images of a patient. It is also possible to track the growth patterns of such tumors.

Keywords: MRI, Binarization, and Segmentation

Introduction
Diagnostic imaging is a vital tool in medicine today. These imaging techniques provide an effective means for non-invasive mapping of the anatomy of an organ of a patient. These technologies have greatly increased knowledge of normal and diseased anatomy for medical research and are a critical component in diagnosis and treatment planning. With the increasing size and number of medical images, the use of computers for processing and analysis of medical images has become necessary and critical. The relative change in size, shape and the spatial relationships between anatomical structures obtained from intensity distributions provide important information in clinical diagnosis for monitoring disease progression. Therefore, radiologists are particularly interested to observe the size, shape and texture of the organs and/or parts of the organ. The recognition, labelling and the quantitative measurement of specific objects and structures are involved in the analysis of medical images. To provide the information about an object clinically in terms of its morphology and anatomy, image segmentation and classification are important tools to obtain the desired information.
Medical imaging has been undergoing a revolution in the past decade with the advent of faster, more accurate and less invasive devices. Magnetic Resonance Imaging is considered very powerful diagnostic methods to detect any abnormalities.
MRI is a medical imaging technique, and radiologists use it for visualization of the internal structure of the body. MRI can provide plentiful of information about human soft tissues anatomy as well as helps diagnosis of brain tumor. MR images are used to analyze and study behavior of the brain. A powerful, uniform, external magnetic field is employed to align the protons that are normally randomly oriented within the water nuclei of the tissue being examined. This alignment (or magnetization) is next perturbed or disrupted by introduction of an external Radio Frequency (RF) energy. The nuclei return to their resting alignment through various relaxation processes and in so doing emit RF energy. After a certain period following the initial RF, the emitted signals are measured. Fourier transformation is used to convert the frequency information contained in the signal from each location in the imaged plane to corresponding intensity levels, which are then displayed as shades of gray in a matrix arrangement of pixels. By varying the sequence of RF pulses applied & collected, different types of images are created.
Repetition Time (TR**)** is the amount of time between successive pulses sequences applied to the same slice. Time to Echo (TE) is the time between the delivery of the RF pulse and the receipt of the echo signal.
Tissue can be characterized by two different relaxation times – T1 and T2. T1 (longitudinal relaxation time) is the time constant which determines the rate at which excited protons return to equilibrium. It is a measure of the time taken for spinning protons to realign with the external magnetic field.

T2 (transverse relaxation time) is the time constant which determines the rate at which excited protons reach equilibrium or go out of phase with each other. It is a measure of the time taken for spinning protons to lose phase coherence among the nuclei spinning perpendicular to the main field.

The most common MRI sequences are T1-weighted and T2-weighted scans. T1-weighted images are produced by using short TE and TR times. The contrast and brightness of the image are predominately determined by T1 properties of tissue. Conversely, T2-weighted images are produced by using longer TE and TR times. In these images, the contrast and brightness are predominately determined by the T2 properties of tissue.

In general, T1- and T2-weighted images can be easily differentiated by looking the CSF. CSF is dark on T1-weighted imaging and bright on T2-weighted imaging.

A third commonly used sequence is the Fluid Attenuated Inversion Recovery (Flair). The Flair sequence is similar to a T2-weighted image except that the TE and TR times are very long. By doing so, abnormalities remain bright but normal CSF fluid is attenuated and made dark. This sequence is very sensitive to pathology and makes the differentiation between CSF and an abnormality much easier. The common MRI sequences and their comparisons are shown in Table 1and Table 2.

Table 1: Common MRI Sequences

	TR (m sec)	**TE (m sec)**
T1-Weighted (short TR and TE)	500	14
T2-Weighted (long TR and TE)	4000	90
Flair (very long TR and TE)	9000	114

Table 2: Comparisons of T1 vs. T2 vs. Flair

Tissue	**T1-Weighted**	**T2-Weighted**	**Flair**
CSF	Dark	Bright	Dark
White Matter	Light	Dark Gray	Dark Gray
Cortex	Gray	Light Gray	Light Gray
Fat (within bone marrow)	Bright	Light	Light Gray
Inflammation (infection, demyelination)	Dark	Bright	Bright

Human brain is the most complex organ present in the human body. The functioning of the brain is complex and various research works are being carried out to completely interpret the functioning of the brain. The brain contains complex anatomical features and different abnormalities can arise at different regions involving specific tissue structures and organs.

A brain tumor is an abnormal growth of cells within the brain, which can be cancerous or non-cancerous (benign). It is generally caused by abnormal and uncontrolled cell division, normally either in the brain itself (neurons, glial cells (astrocytes, oligodendrocytes, ependymal cells), lymphatic blood vessels), in the cranial nerves (myelin-producing Schwann cells), in the brain envelopes (meninges), skull, pituitary and pineal gland, or spread from cancers primarily located in other organs (metastatic tumors). Brain tumors are of two types: primary and secondary. Primary brain tumors include any tumor that starts in the brain. Primary brain tumors can start from brain cells, the membranes around the brain (meninges), nerves, or glands. Primary brain tumors are classified as: 1) benign; 2) malignant. Benign tumors can be removed, and they seldom grow back. Benign brain tumors usually have an obvious border or edge. They don't spread to other parts of the body. However, benign tumors can press on sensitive areas of the brain and cause serious health problems. Malignant brain tumors are generally more serious and often are a threat to life. They are likely to grow rapidly and crowd or invade the nearby healthy brain tissue. Cancer cells may break away from malignant brain tumors and spread to other parts of the brain or to the spinal cord. They rarely spread to other parts of the body. Its threat level depends on the combination of factors like the type of tumor, its location, its size and its state of development. The brain is encapsulated by the skull so tumors are not visible from outside. This paper detects different types of tumors and cancerous growth within the brain and other associated areas within the brain by using computerized methods on MRI images of a patient. It is also possible to track the growth patterns of such tumors.

Related Work

Many of the researchers proposed many methods, and algorithms for to find brain tumor, stroke and other Kinds of abnormalities in human brain using MR Images [1-4]. Some researchers focused on Meyer's flooding Watershed algorithm for segmentation and also presents the morphological operation [5-8]. Some one proposed an algorithm based on segmented morphological approach [6]. Another presented the algorithm incorporates segmentation through Nero Fuzzy Classifier. The problem of this system is to train the system by neural network and it desires many input images are used to train the network. The developed system is used only for tumor detection not for other abnormalities [7-10].

Other researchers applied preprocessing techniques like de-noising, image smoothing, image contrast enhancement and comparison of the level set methods and morphological marker controlled watershed approach and modified gradient magnitude region growing technique for MRI brain tumor segmentation [17-18].

Someone proposes automatic brain tumor detection approach using symmetry analysis. They first detect the tumor, segment it and then find out the area of tumor. One of the important aspects is that after performing the quantitative analysis, we can identify the status of an increase in the disease. They have suggested multi-step and modular approached to solve the complex MRI segmentation problem. Tumor detection is the first step of tumor segmentation. They have obtained good results in complex situations. The authors claim that MRI segmentation is one of the essential tasks in medical area but boring and time consuming if it is performed manually, so visually study of MRI is more interesting and fast [11-16].

Another compare the image enhancement techniques through histogram equalization for image enhancement using MRI brain images and presented the study of image enhancement techniques and comparison of histogram equalization basic method like Brightness preserving adaptive histogram equalization (AHE), Local histogram equalization (LHE), global histogram equalization (GHE), Dynamic histogram equalization using different quality objective measures in MRI images. They also presented the better result on contrast using BPDHE method [10].

Someone used fuzzy C means clustering for segmentation. That method given the high computational complexity. FCM shows good performance result in segmented the tumor tissue and accuracy of tumor. Segmentation was identified by applied the SVM classifier [11].

Other researchers proposed the method for brain tumor classification of MRI images. The research work applied, based on Neural Network (NN) and k- Nearest Neighbor (k-NN) algorithms on tumor classification has been achieved 100% accuracy using k-NN and 98.92% using NN [17-18].

Many researchers has proposed many algorithms and segmentation techniques to find abnormalities in the brain using MRI images. Most of them proposed various algorithms to find the abnormality in the brain like Brain tumor.

Proposed Methodology

Brain tumour detection consists of 4 stages as shown in figure 1.

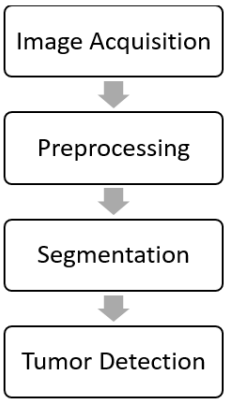

Fig 1: Proposed Method

Image Acquisition

Images are obtained by MRI scan of brain and the output of MRI provides gray level images. A gray scale image is a data matrix whose value represents shades of gray. The elements of gray scale matrix have integer values or intensity values in range [0 255]. For applying different techniques, the digital images obtained from MRI are stored in matrix form in MATLAB. Different formats of digital images like jpg, png etc. have been used in the proposed method. The MRI scan (T2-weighted & Flair) of patients suffering from tumour shows some region having high intensity. The objective of the method is to detect the exact location of this high intensity region.

Pre-processing

This phase is implemented by applying a series of initial processing procedures on the image before any special purposes processing. It improves the image quality and removes the noise. Since, the brain images are more sensitive than other medical images; they should be of minimum noise and maximum quality.

Artefacts Removal

Now a day's artefacts are principally letter or metal related artefacts or Gibbs artefact. Letter artefact is present in most of the brain MRI images due to patient's information being embedded in them. High quality of MRI machine ensures metal related and susceptibility artefact are very few.

In the first stage, threshold value is calculated over an image to binarize an image. A statistical method i.e. standard deviation is used to calculate the threshold value. In this processing statistical descriptions separate foreground images and background images. A digitized image I [m, n] and h is the intensity of each pixel of the gray image. Thus the total intensity of the image is defined by:

$$T = \sum_{I} h[I]$$

The average intensity of the image is defined as the *mean* of the pixel intensity within that image and the average intensity is defined as I_{avg} by:

$$I_{avg} = \frac{1}{T} \sum_{(m,n)\epsilon I} I[m,n]$$

The standard deviation S_d of the intensity within an image is the threshold value of the total image is defined by:

$$S_d = \sqrt{\frac{1}{T-1}\sum_{m,n\epsilon I}(I[m,n] - I_{avg})^2}$$

Or

$$S_d = \sqrt{\frac{1}{T-1}\sum_{m,n\epsilon I} I^2[m,n] - T{I_{avg}}^2}$$

Here the threshold intensity as global value i.e. the threshold intensity of the entire image is unique. The standard deviation of the image pixel of an image I[m, n] or matrix element for *I[m, n]* is given by :

I[m, n]=1 if I[m, n]≥ S_d
I[m, n]=0 if I[m, n]< S_d

In the above procedure maximum portion of MRI of brain part is extracted from the total image but due to presence of artefact, it also gets extracted from the original image and then second stage starts. In the second stage first, it is labeled the different connected components and then calculate the area of different connected components of the label image and find the components with maximum area. This is done to remove the artefact and keep the maximum component. Thus a binarized image without artefact is produced. To produce final output the convex hull of all one pixels in the binarized image is obtained. Then all pixels inside the convex hull of binarized image are set to one and the binarized image matrix is multiplied position wise to the original image to obtain MR image without artefacts. Convex hull is used for reducing metal related susceptibility and Gibbs artefact.

Noise Reduction

The noises in MRI images reduces the quality of image and also damage the segmentation task which can lead to faulty diagnosis. The most principal in image denoising is preserving the edges and fine details of an image through noise reduction.

Anisotropic Diffusion

In image processing and computer vision, anisotropic diffusion, also called Perona–Malik diffusion, is a technique

aiming at reducing image noise without removing significant parts of the image content, typically edges, lines or other details that are important for the interpretation of the image. Anisotropic diffusion resembles the process that creates a scale space, where an image generates a parameterized family of successively more and more blurred images based on a diffusion process. Each of the resulting images in this family are given as a convolution between the image and a 2D isotropic Gaussian filter, where the width of the filter increases with the parameter. This diffusion process is a linear and space-invariant transformation of the original image. Anisotropic diffusion is a generalization of this diffusion process: it produces a family of parameterized images, but each resulting image is a combination between the original image and a filter that depends on the local content of the original image. As a consequence, anisotropic diffusion is a non-linear and space-variant transformation of the original image.

Perona & Malik introduce the flux function as a means to constrain the diffusion process to contiguous homogeneous regions, but not cross region boundaries. The heat equation (after appropriate expansion of terms) is thus modified to:

$$\frac{\partial I}{\partial t} = c(x,y,t)\Delta I + \nabla c \cdot \nabla I \qquad \text{.....1}$$

Where *c* is the proposed flux function which controls the rate of diffusion at any point in the image, Δ denotes the gradient, ∇ denotes the Laplacian.

A choice of *c* such that it follows the gradient magnitude at the point to restrain the diffusion process as it approaches for region boundaries. The flux function may trigger inverse diffusion and actually enhance the edges.

Perona & Malik suggest the following two flux functions:

$$c\left(||\nabla I||\right) = e^{-(||\nabla I||/K)^2}$$

$$c\left(||\nabla I||\right) = \frac{1}{1+\left(\frac{||\nabla I||}{K}\right)^2}$$

The flux functions offer a trade-off between edge-preservation and blurring (smoothing) homogeneous regions. Both the functions are governed by the free parameter κ which determines the edge-strength to consider as a valid region boundary. Intuitively, a large value of κ will lead back into an isotropic-like solution.

Equation (1) can be discretized on a square lattice, with brightness values associated to the vertices, and conduction coefficients to the arcs. An 8-nearest neighbours discretization of the Laplacian operator can be used:

$$I_{i,j}^{t+1} = I_{i,j}^{t} + \lambda[c_N.\nabla_N I + c_S.\nabla_S I + c_E.\nabla_E I + c_W.\nabla_W I + c_{NE}.\nabla_{NE} I + c_{SE}.\nabla_{SE} I + c_{NW}.\nabla_{NW} I + c_{SW}.\nabla_{SW} I]$$

Where $0 \le \lambda \le ¼$, N, S, E, W, NE, SE, NW, SW are the mnemonic subscripts for North, South, East, West, North-East, South-East, North-West, North-West, South-West, ∇ indicates nearest-neighbor differences:

$$\nabla_N I_{i,j} \equiv I_{i-1,j} - I_{i,j}$$
$$\nabla_S I_{i,j} \equiv I_{i+1,j} - I_{i,j}$$
$$\nabla_E I_{i,j} \equiv I_{i,j+1} - I_{i,j}$$
$$\nabla_W I_{i,j} \equiv I_{i,j-1} - I_{i,j}$$
$$\nabla_{NE} I_{i,j} \equiv I_{i-1,j+1} - I_{i,j}$$
$$\nabla_{SE} I_{i,j} \equiv I_{i+1,j+1} - I_{i,j}$$
$$\nabla_{NW} I_{i,j} \equiv I_{i-1,j-1} - I_{i,j}$$
$$\nabla_{SW} I_{i,j} \equiv I_{i+1,j+1} - I_{i,j}$$

Image Enhancement

Poor contrast is one of the defects found in acquired image. The effect of that defect has great impact on the contrast of image. When contrast is poor the contrast enhancement method plays an important role.

Contrast Stretching

Contrast stretching (often called normalization) is a simple image enhancement technique that attempts to improve the contrast in an image by `stretching' the range of intensity values it contains to span a desired range of values, *e.g.* the full range of pixel values that the image type concerned allows. It differs from the more sophisticated histogram equalization in that it can only apply a *linear* scaling function to the image pixel values. As a result the `enhancement' is less harsh. (Most implementations accept a gray level image as input and produce another gray level image as output.)

Before the stretching can be performed it is necessary to specify the upper and lower pixel value limits over which the image is to be normalized. Often these limits will just be the minimum and maximum pixel values that the image type concerned allows. For example for 8-bit gray level images the lower and upper limits might be 0 and 255. Call the lower and the upper limits *a* and *b* respectively.

The simplest sort of normalization then scans the image to find the lowest and highest pixel values currently present in the image. Call these *c* and *d*. Then each pixel *P* is scaled using the following function:

$$P_{out} = (P_{in} - c)\left(\frac{b-a}{d-c}\right) + a$$

Segmentation

Segmentation is a process in which image is partitioned into its constituent salient image regions to acquire the region(s) of interest (ROI's).

Thresholding

Thresholding or image binarization is one of the important techniques in image processing and computer vision. It is used to extract the object from the background. The segmented image, which is obtained by thresholding, has the advantages of smaller storage space, fast processing speed, and ease of manipulation, compared with gray level image which usually contains a large number of gray levels (maximum 256 levels). The output of this step is the segmenting image with dark background and lighting tumor area.

Fuzzy C-Means

Fuzzy c-means (FCM) is a method of clustering which allows one piece of data to belong to two or more clusters. It is based on minimization of the following objective function:

$$J_m = \sum_{i=1}^{N}\sum_{j=1}^{C} u_{ij}^{m}\left\|x_i - c_j\right\|^2, \quad 1 \le m < \infty$$

where m is any real number greater than 1, u_{ij} is the degree of membership of x_i in the cluster j, x_i is the ith of d-dimensional measured data, c_j is the d-dimension center of the cluster, and ||*|| is any norm expressing the similarity between any measured data and the center.
Fuzzy partitioning is carried out through an iterative optimization of the objective function shown above, with the update of membership u_{ij} and the cluster centers c_j by:

$$u_{ij} = \frac{1}{\sum_{k=1}^{C}\left(\frac{\|x_i - c_j\|}{\|x_i - c_k\|}\right)^{\frac{2}{m-1}}}, \quad c_j = \frac{\sum_{i=1}^{N} u_{ij}^{m} \cdot x_i}{\sum_{i=1}^{N} u_{ij}^{m}}$$

This iteration will stop when $\max_{ij}\left\{\left|u_{ij}^{(k+1)} - u_{ij}^{(k)}\right|\right\} < \varepsilon$ and where ε is a termination criterion between 0 and 1, whereas k are the iteration steps. This procedure converges to a local minimum or a saddle point of J_m.

Threshold value has been calculated from the middle & large class labels.

$$\text{Threshold value} = \frac{\text{Maximum(Class label = Middle)} + \text{Minimum(Class Label = Large)}}{2}$$

All pixels with value ≥ Threshold are set to 1 and all pixels with value < Threshold are set to 0.

Morphological Operations
Mathematical morphology is defined as a tool for extracting image components that are useful in the representation and description of region shape, such as boundaries, skeletons, etc. I have used two morphological operations.

Fill image regions and holes
Fills holes in the input binary image. A hole is a set of background pixels that cannot be reached by filling in the background from the edge of the image.

Remove small objects from binary image
It removes all connected components (objects) that have less than a certain pixels from a binary image, producing another binary image.

Remove CSF
In T2-weighted images Cerebrospinal Fluid (CSF) appears very bright. So, after thresholding it is very important to remove those CSF area from the image, otherwise that CSF area can also be falsely identified as Tumor.
It has been observed that CSF mostly consists near center and boundary of the brain. So, I have tried to remove the CSF near the boundary of the brain. At first I have taken the gray scale image after removing artefacts and skull. Now, convex hull for this grayscale image has been computed to detect the image boundary. Now the objects from the binarized image are labelled. Convex hull for each object is also computed to calculate the object boundaries. Objects near or intersecting the image boundary are considered as CSF and hence, they are removed.

Tumor Detection
After the segmentation process, the segmented image is multiplied with original image to show tumor area in the original image. From the segmented image statistics about the connected white region. The region property internally computes bounding-box statistics. Now the bounding boxes are plotted over the input image to highlight the tumor area.

Algorithms
Algorithm to remove artefacts
Step 1: Read the grayscale MRI brain image.

Step 2: Calculate threshold i.e. standard deviation of the image intensities.

Step 3: The image is binarized using the threshold value. i.e. pixels having value greater than the threshold is set to 1 and pixels less than the threshold are set to 0.

Step 4: The binarized image is labelled and areas of connected components are calculated.

Step 5: The connected component with the maximum area is identified.

Step 6: The component with the highest area is kept and all others are removed.

Step 7: A convex hull is calculated for the one pixel in the image and all regions within the convex hull are set to one.

Step 8: Now the above obtained image matrix is multiplied to the original image matrix to obtain an image consisting of only brain and skull and without any artefact.

Algorithm for Fuzzy C-Means
Step 1: Initialize U= $[u_{ij}]$ matrix, $U^{(0)}$

Step 2: At k-step: calculate the centers vectors $C^{(k)}= [c_j]$ with $U^{(k)}$

$$c_j = \frac{\sum_{i=1}^{N} u_{ij}^{m} \cdot x_i}{\sum_{i=1}^{N} u_{ij}^{m}}$$

Step 3: Update $U^{(k)}$, $U^{(k+1)}$

$$u_{ij} = \frac{1}{\sum_{k=1}^{C}\left(\frac{\|x_i - c_j\|}{\|x_i - c_k\|}\right)^{\frac{2}{m-1}}}$$

Step 4: If $\| U^{(k+1)} - U^{(k)}\| < \varepsilon$ then STOP; otherwise return to step 2.

Algorithm to remove CSF
Step 1: Read grayscale image after removing skull and artefacts.

Step 2: Compute convex hull of the grayscale image.

Step 3: Read binarized image after thresholding.

Step 4: Objects in the binarized image after thresholding are labelled.

Step 5: Compute convex hull for each of the labelled object.

Step 6: Objects near or intersecting the boundary of the grayscale image are removed.

Let, Co-ordinates of convex hull of object O (X_o, Y_o)
Co-ordinates of convex hull of grayscale image (X_{cv}, Y_{cv})
Remove object O from the binarized image which holds any of the following conditions.

i) If ($X_o = X_{cv}$) && ($Y_o = Y_{cv}$)
ii) If ($X_o = X_{cv}$) && ($Y_{cv}-3 \leq Y_o \leq Y_{cv}+3$)
iii) If ($Y_o = Y_{cv}$) && ($X_{cv}-3 \leq X_o \leq X_{cv}+3$)
iv) If ($X_{cv}-3 \leq X_o \leq X_{cv}+3$) && ($Y_{cv}-3 \leq Y_o \leq Y_{cv}+3$)

Experimental Results and Performance Analysis

The sample image and tumour data set were collected from Institute of Neurology and Genetics, Nicosia, Cyprus [13-16] and The Cancer Imaging Archive [17-18]. After applying the proposed method on T2-weighted and Flair MRI images, results are shown in the following figures.

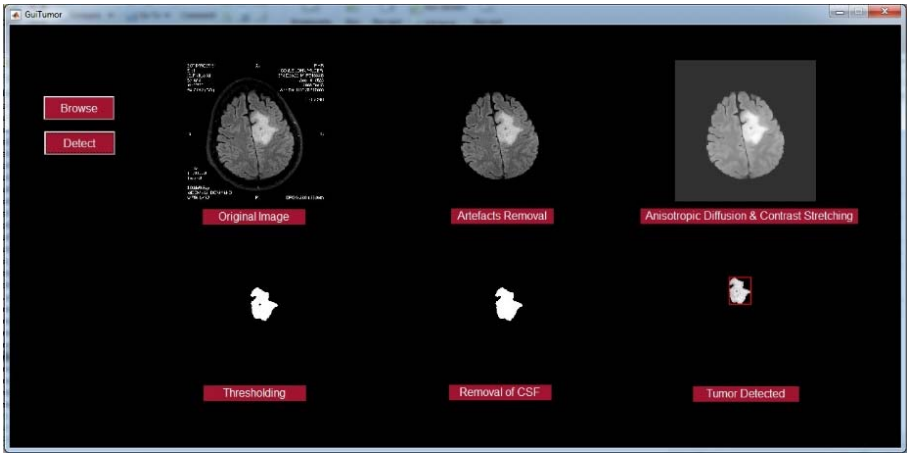

Fig 2: Screenshot of Output 1

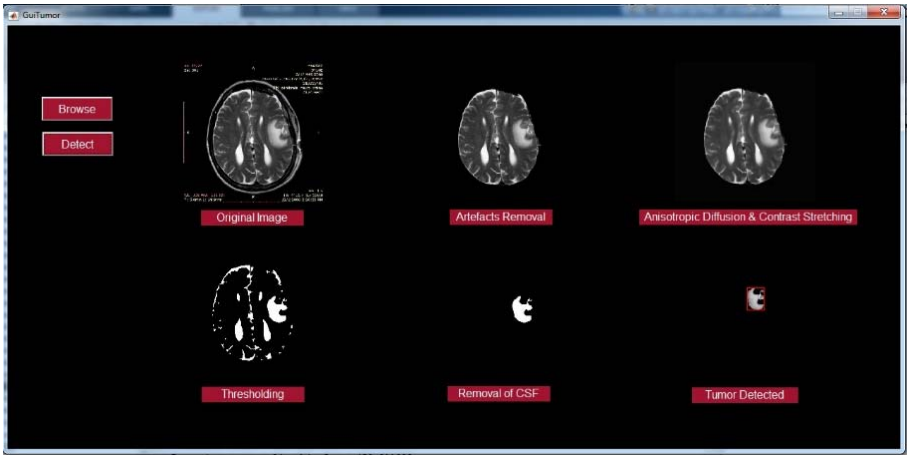

Fig 3: Screenshot of Output 2

Fig 4: Screenshot of Output 3

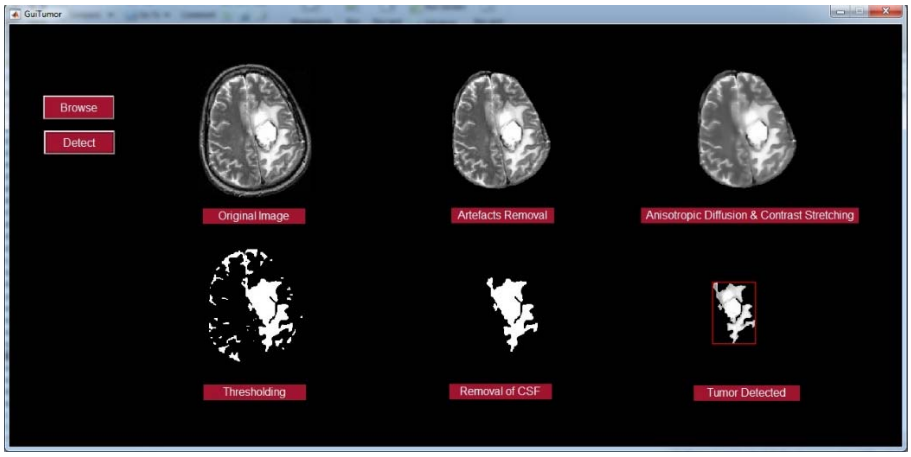

Fig 5: Screenshot of Output 4

Performance Analysis

The Proposed method has been evaluated using following evaluation parameters.

True positive (TP), Brain tumor images are correctly recognized. Which means the people who has brain tumor are correctly identified. The high is optimal.

True negative (TN), Non-Brain tumor images are correctly recognized as they do not have brain tumor. Easily Healthy people correctly identified as healthy.

False positive (FP), Non-Brain tumor images are incorrectly recognized. This indicates the people who do not have brain tumor are incorrectly identified as they have brain tumor. Simply Healthy people incorrectly identified as sick. The less is optimal.

False negative (FN), Brain tumor images are incorrectly recognized. Which represents the people who has brain tumor are incorrectly identified as they do not have brain tumor. Sick people incorrectly identified as healthy.

$$Sensitivity = \frac{TP}{TP + FN} \times 100\%$$

$$Specificity = \frac{TN}{TN + FP} \times 100\%$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100\%$$

$$Similarity\ Index = \frac{2(TP)}{2(TP) + FP + FN} \times 100\%$$

To calculate above mentioned parameters tumor images and no tumor images are needed.

Total tumor images tested = 45

TP = 40, FN = 5

Total no tumor images tested = 10

Table 3: Performance Analysis

Parameter	Value (%)
Sensitivity	88.9
Specificity	90
Accuracy	89.2
Similiarity Index	93.02

Conclusion

The proposed method was successful in extracting the tumor portion; it has provided an accurate demarcation of the boundary of the tumor, along with correct visual location of the tumor with the help of a bounding box. It has also provided a diagnosis decision whether the tumor is present or absent along with the exact size of the tumor. This decision can assist as a supportive aid which can be used at the doctor's discretion in finally declaring a decision.

References

1. Nabanita Basu, Sanjay Nag, Indra Kanta Maitra, Samir K. Bandyopadhyay, Artefact removal and edge detection from medical image. European Journal of Biomedical and Pharmaceutical Sciences. 2016.
2. Ian Young T, Jan Gerbrands J, Lucas van Vliet J, Fundamentals of Image Processing, 1995.
3. Rafel Gonzalez C, Rechard Woods E, Digital Image Processing, Prentice-Hall, 3rd Edition, 2008.
4. Manoj Kowear K, Sourabh Yadev. Brain tumor detection and segmentation using histogram thresholding. International Journal of engineering and Advanced Technology. 2012.
5. Rajesh patil C, Bhalchandra AS. Brain tumor extraction from MRI images Using MAT Lab. IJECSCSE, 2012.
6. Vinay Parmeshwarappa, Nandish S. A segmented morphological approach to detect tumor in brain images, IJARCSSE, 2014.
7. Karuna M, Ankita Joshi. Automatic detection and severity analysis of brain tumors using gui in matlab. IJRET: International Journal of Research in Engineering and Technology, 2013.
8. Dubey RB, Hanmandlu M, Shantaram Vasikarla. Evaluation of three methods for MRI brain tumor segmentation, IEEE computer society, 2011.
9. Roy S, Bandyopadhyay SK. Detection and Quantification of Brain Tumor from MRI of Brain and it's Symmetric Analysis. International Journal of Information and Communication Technology Research, 2012.
10. Senthilkumaran N, Thimmiaraja J. Histogram equalization for image enhancement using MRI brain images, IEEE CPS. 2014.
11. Preetha R, Suresh GR. Performance Analysis of Fuzzy C Means Algorithm in Automated Detection of Brain Tumor, IEEE CPS. 2014.
12. Amer Al-Badarnech, Hassan Najadat, Ali Alraziqi M. A Classifier to Detect Tumor Disease in MRI Brain Images, IEEE Computer Society, ASONAM. 2012.
13. Loizou CP, Murray V, Pattichis MS, Seimenis I, Pantziaris M, Pattichis CS. Multi-scale amplitude modulation-frequency modulation (AM-FM) texture

analysis of multiple sclerosis in brain MRI images, IEEE Trans. Inform. Tech. Biomed. 2011.
14. Loizou CP, Kyriacou EC, Seimenis I, Pantziaris M, Petroudi S, Karaolis M *et al*. Brain white matter lesion classification in multiple sclerosis subjects for the prognosis of future disability. Intelligent Decision Technologies Journal (IDT). 2013.
15. Loizou CP, Pantziaris M, Pattichis CS, Seimenis I, Brain MRI Image normalization in texture analysis of multiple sclerosis. J. Biomed. Graph. & Comput. 2013.
16. Loizou CP, Petroudi S, Seimenis I, Pantziaris M, Pattichis CS. Quantitative texture analysis of brain white matter lesions derived from T2-weighted MR images in MS patients with clinically isolated syndrome. J. Neuroradiol. 2015.
17. Scarpace Lisa, Flanders Adam E, Jain Rajan, Mikkelsen Tom, Andrews David W. 2015.
18. Clark K, Vendt B, Smith K, Freymann J, Kirby J, Koppel P *et al*. The Cancer Imaging Archive (TCIA): Maintaining and Operating a Public Information Repository. Journal of Digital Imaging. 2013.