Thresholding And Level Set Based Brain Tumor Detection Using Bounding Box As Seed

Mandeep Kaur
Research Scholar (ECE deptt.)
A.C.E.T. Amritsar, Punjab, INDIA

Dr. V. K. Banga
Professor and HOD (ECE deptt.)
A.C.E.T. Amritsar, Punjab, INDIA

Abstract

Medical image processing is the most challenging and emerging field now days. In the Brain MRI (Magnetic Resonance Imaging), the tumor part can be seen clearly but the physician needs the accurate size and the correct measurement for the treatment. This requires segmenting the tumor part from the given Brain MRI image and quantifying it. We have used axial brain MR image slices of 5 patient studies from databases maintained at Nijjar scan and diagnostic Centre for the experiment [1]. We propose an automated, fast and unsupervised technique which locates a bounding box across tumor based on search for most dissimilar region between left and right half of brain. This bounding box is used as a seed for segmentation using thresholding and level set to extract exact tumor. This technique is independent of intensity variations in MRI.

1. Introduction

A space within the skull is covered by the brain tumor which causes the disturbance of normal brain activity. Brain tumors are classified depending on the exact site of the tumor, the type of tissue involved, whether they are noncancerous (benign) or cancerous (malignant), site of origin (primary or secondary) and other factors [2]. According to World Health Organization (WHO), there are more than 120 types of brain tumors. Manual segmentation by an expert will consume more time and it is very difficult to do proper segmentation. Automatic detection and segmentation of brain tumor from brain MR images offer a mechanism for overcoming the tedium involved in the manual segmentation of large datasets. It also promises reproducibility which is affected by inter and intra observer variability. But automated systems have significant problems to achieve these objectives. The major problems are, pixel intensities violate the independent and identically distributed assumption within and between images due to the nature of brain MR images, and presence of a significant amount of artifacts and intensity inhomogeneity in MR images.
Therefore, automated method should take into account these problems to achieve reproducible segmentation results and developing clinically accepted automated methods remains an active research area [3, 4]. In this paper we proposed a hybrid approach for the detection of brain tumor which is based on fast bounding box algorithm and locating bounding box around tumor, which is used as a seed for segmentation of exact tumor.

2. Literature survey

Many techniques have been proposed to automate the brain tumor detection and segmentation in recent years. The proposed methods can be broadly classified into two, intelligent based and non-intelligent based. Most notable intelligent based systems are artificial neural network, fuzzy c-means, support vector machine and hybrid methods. On the other hand, most notable non-intelligent methods include thresholding and region growing. But there is no clear demarcation between the two, especially intelligent based systems most often use the non-intelligent based ones as a refiner of their output. Region growing based [5] tumor detection techniques suffer high time complexity. Statistical pattern recognition based methods fall short, partly because large deformations occur in the intracranial tissues due to the growth of the tumor and edema [6]. These methods detect abnormal regions using a registered brain atlas as a model for healthy brains. However, these techniques need to significantly modify the brain atlas to accommodate the tumors, which typically lead to poor results. Most of the fuzzy models work [7] well only for hyper intensity (fully enhanced) tumors and exhibit poor performance on detecting non-enhanced tumors.

3. Proposed methodology

3.1 Image acquisition

For experimental purpose database of 5 patients is collected from Nijjar scan and diagnostic Centre [1]. The medical images acquired were stored in a DICOM (Digital Imaging and Communications in Medicine) format. Each DICOM image file has both a header, contains information about the patient, type of scan and image dimensions. We removed patient data from the DICOM header due to patient confidentiality issues. In addition, we converted the image volumes from the DICOM format to Portable

Network Graphics (PNG) due to lack of portability of the DICOM format. Images are stored in MATLAB and displayed as a gray scale image of size 256*256. The entries of a gray scale image are ranging from 0 to 255, where 0 shows total black color and 255 shows pure white color. Entries between these ranges vary in intensity from black to white.

3.2. Preprocessing

The preprocessing performs intensity inhomogeneity correction, background noise removal and removes non brain tissues such as skull from head MRI scans. Image intensity inhomogeneity, also referred to as bias field. Intensity non-uniformity or shading consists of smoothly varying non-anatomical intensity variation across images. Its presence can significantly reduce the accuracy and reliability of quantitative and qualitative analysis of magnetic resonance (MR) images. Median filter is used to remove the noise like salt and pepper & the value of pixel is determined by the median of the neighboring pixels.

3.2.1. Skull stripping: Extraction of brain tissue from non-brain tissues in MR images which is referred to as skull stripping is an important step in many neuro imaging studies. In this, we used automatic threshold value selector to automatically choose threshold value. Then, mathematical morphology operations on a binarised image are applied stage by stage to achieve acceptable skull stripped brain images. The proposed skull stripping method comprises four steps [8]. Initially image binarisation is performed using threshold value and narrow connections are removed from binarised image using morphological opening. Then, largest connected component from binarised image is selected by considering the fact that brain is the largest connected structure inside the head. Thirdly, mathematical morphology operations such as: filling holes and dilation is carried out on selected largest binarised image. Finally, we obtained skull stripped brain image.

3.2.2. Create images and masks: In this, the region properties of an image are used. By using centroid property of an image, a line is drawn in the center of stripped skull. This divides the skull into two equal parts. One part is referred as a test image and other is referred as reference image.

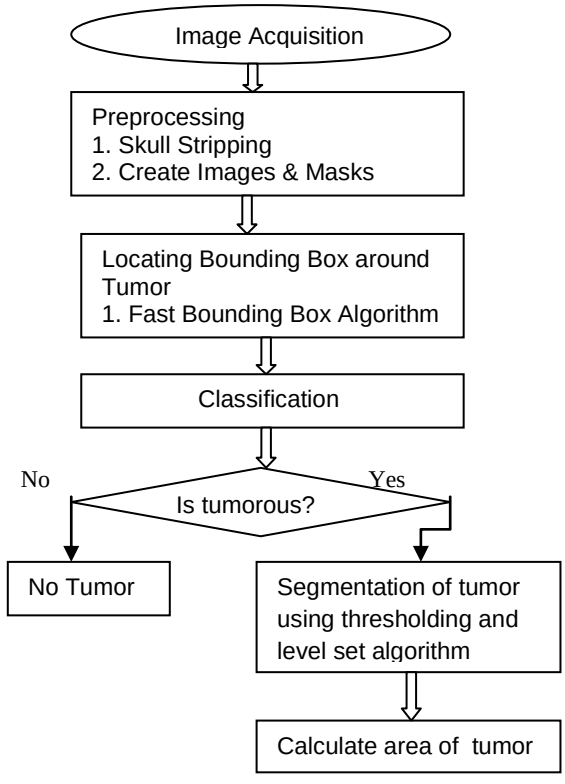


Figure1. Framework of the proposed model

3.3. Locating bounding box around tumor

In each input MR slice (axial view), there is a left–right axis of symmetry of the brain. A tumor, which is considered an abnormality in the brain, typically perturbs this symmetry. So an axis-parallel rectangle on the left side that is very dissimilar from its reflection about the axis of symmetry on the right side—i.e., the intensity histograms of two rectangles are most dissimilar, but the intensity histograms of the outside of the rectangles are relatively similar [9]. We assume that one of the two rectangles will circumscribe the tumor appearing in one hemisphere of the brain.

3.3.1 Fast bounding box algorithm (FBB): FBB is a change detection principle, where a region of change (D) is detected on a test image (I), when compared with a reference image (R). In FBB, after finding the axis of symmetry on an axial MR slice, the left (or the right) half serves as the test image I, and the right (or the left) half supplies as the reference image R. The region of change D here is restricted to be an axis-parallel rectangle, which essentially aims to circumscribe the abnormality. This method has region-based global change that differs from most techniques, which view the change as a local pixel-to-pixel changes—here tumor is considered as the ‘change’ region in the test image and all other intracranial tissues except tumor are considered as the ‘no change’ region.

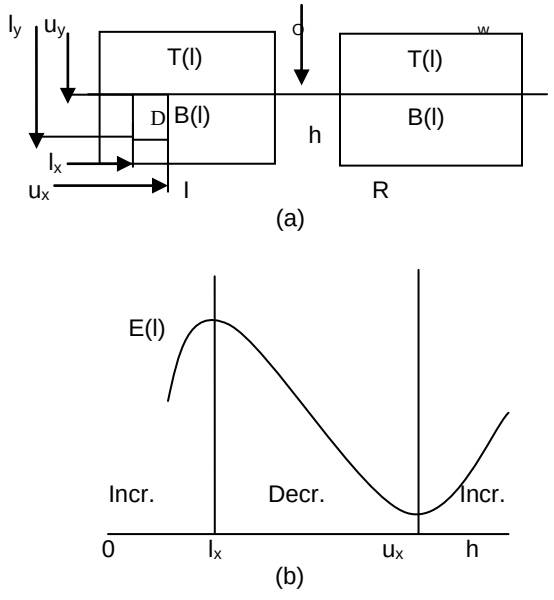


Figure 2. (a) Finding anomaly D from test image I using reference image R. (b) Energy function plot.

We utilize a novel score function that can identify the region of change D with two very quick searches– one along the vertical direction of the image and the other along the horizontal direction [9]. Fig. 2(a) represent the test and the reference images, respectively having same height h and same width w. The rectangular region D= $[l_x, u_x]$* $[l_y, u_y]$ represents the region of change between images I and R. FBB algorithm finds the rectangle D, i.e., the four unknown parameters l_x, u_x, l_y and u_y in two linear passes of the image. It first finds l_y and u_y in a vertical sweep and then finds l_x and u_x in a horizontal sweep of the pair of images. The horizontal score function corresponds to the vertical score function applied to the transpose of the images. We define our vertical score function as:

$$E(l)=BC(P_I^{T(l)},P_R^{T(l)}) - BC(P_I^{B(l)},P_R^{B(l)}) \quad (1)$$

Where $P_I^{T(l)}$ denotes the normalized intensity histogram of image I within the region T(l). $P_R^{T(l)}$,$P_I^{B(l)}$ & $P_R^{B(l)}$ are defined accordingly. BC(a ,b) = $\Sigma_i\sqrt{a(i)b(i)}$ $\varepsilon[0,1]$ denotes the Bhattacharya coefficient between two normalized histograms a(i) and b(i), with i indicating a histogram bin. Bhattacharya coefficient (BC) measures similarity between two normalized intensity histograms. When two normalized histograms are the same, the BC between them is 1 and when two normalized histograms are completely dissimilar (i.e., with disjoint supports for the histograms), the associated BC value is 0.

3.4. Classification

The region within the bounding box is extracted from the rest image. The disadvantage of FBB algorithm is that, whenever it identify any dissimilarity between test and reference image, it locate bounding box, even if there is no tumor. But the intensity level of non-tumorous area is very low and there are no variations among pixels in that area. So a particular threshold value is set and applied in that area. If the value is below the set threshold level means there is no tumor present in that area and it classify that. But if the value is above threshold, means there is tumor. So further processing is done to segment that area from rest image.

3.5. Segmentation of tumor region

Image segmentation covers objective by extracting the abnormal portion from the image which is useful for analyzing the size and shape of the abnormal region. This method is also called as "pixel based classification" since the individual pixels are clustered unlike the classification techniques which categorizes the whole image

3.5.1 Thresholding: Threshold segmentation is one of the simplest segmentation methods. The input gray scale image is converted into a binary format. The method is based on a threshold value which will convert gray scale image into a binary image format. The main logic is the selection of a threshold value. The thresholding can be done on the whole image. Each pixel is compared to the threshold: if its value is higher than the threshold, the pixel is considered to be "foreground" and is set to white, and if it is less than or equal to the threshold it is considered "background" and set to black[10]. Now the threshold result within a bounding box is checked. All the white pixels within bounding box are shown as tumor output. The tumor region is converted to color image for good visualization.

3.5.2. Level Set method: The rough boundaries of interested object are extracted by thresholding method. The extracted portion is regarded as an initialization of level set method [11]. Level-sets methods rely on partial differential equations (PDEs) to model deforming isosurfaces. Level sets methods rely on two central embedding's; first the embedding of the interface as the zero level set of a higher extension) of the interface's velocity to this higher dimensional level set function. The evolution of the contour or surface is governed by a level set equation. The solution tended to by this partial differential equation is computed iteratively by updating φ at each time interval, the general form of the level set equation is shown below.

$$\partial\varphi / \partial t = - \left| \nabla\varphi \right| .F \quad (2)$$

In the above level set equation *F* is the velocity term that describes the level set evolution. By manipulating *F*, we can guide the level set to different areas or shapes, given a particular initialization of the level set function. An initial mask for the level set function is also required, which may take the form of a square in two dimensions, or any other arbitrary closed shape. The level set iteration can be terminated once φ has converged, or after a certain number of iterations. In this paper, thresholding results act as a seed for level set method and after few iterations, the final tumor region is obtained.

4. Results and discussion

Our experiments involved axial brain MR image slices of 5 recent patient studies from databases maintained at the Nijjar scan and diagnostic Centre. After obtaining input images the first work is to remove non-brain tissues such as skull, fat and other imaging artifacts from MRI scans. The efficiency and precision of skull stripping stage is highly important since subsequent stages in the pipeline of the proposed framework use the output of this stage.

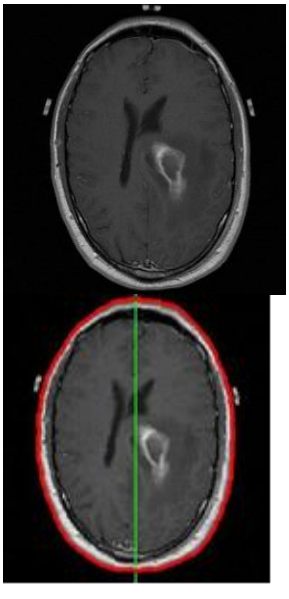
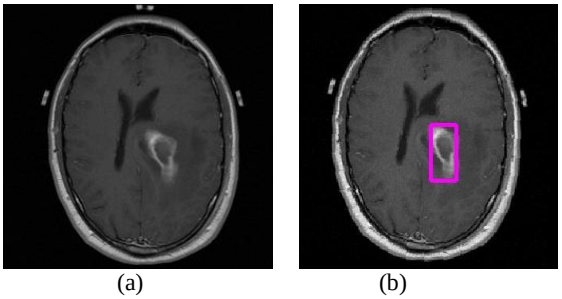


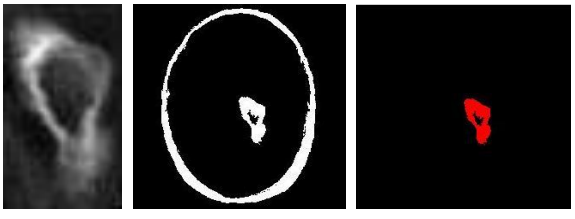
Figure 3. Skull stripped brain MR image. (a) Original brain image b) Respective skull stripped image by the proposed method.

The next module in the proposed framework is tumorous slice detection, in which bounding box is located around tumor and that act as a seed for segmentation of brain tumor. Thresholding and level set algorithm is used to extract exact tumor.



(a) (b)

Figure 4. (a) T1C axial brain MRI slice and (b) result of the FBB algorithm, which locates bounding box around tumor region.



(a) (b) (c)

Figure 5. (a) Extracted part of bounding box region from rest image. (b) Result of thresholding on the entire image. (c) Result of thresholding within the bounding box.

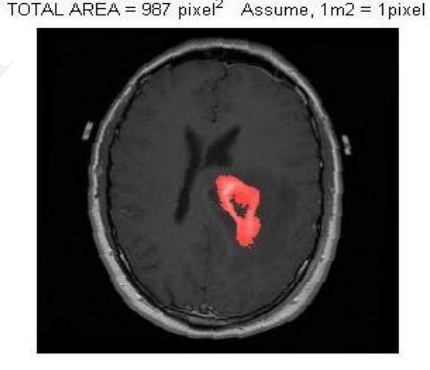


Figure 6. Final output after applying thresholding & shows the total area of segmented tumor.

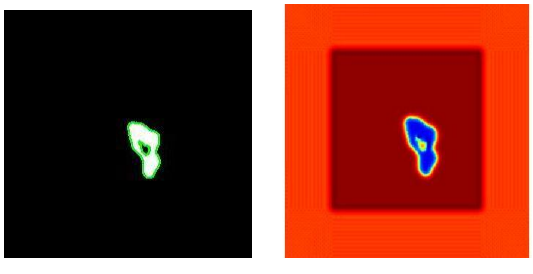


Figure 7. (a) Result of level set after 50 iterations and (b) result of final level set function.

5. Performance measure of classification

For tumorous slice detection G_T and O_M are compared based on a value manually set for a brain slice whether it is tumorous or not (1 - tumorous and

0 - non tumorous) and value set by proposed method (1- threshold > 45 and 0 - threshold < 45). Then we evaluate the performance of this tumorous slice detection phase based on the number of slices which are correctly classified as tumorous or non-tumorous [12]. Since comparison is performed based on brain slices we use metrics like, how many slices are correctly classified as tumorous slices (TP), how many slices are wrongly classified as tumorous slices (FP), how many tumorous slices are wrongly classified as non-tumorous (FN) and how many non-tumorous brain slices are classified as non-tumorous (TN).

This method is tested on 5 patient dataset and computed the performance measures as below:

Sensitivity= TP/(TP+FN)*100% = 74/(74+1)*100% = 98.66%

Specificity =TN/(TN+FP)*100% = 72/(72+2)*100% =97.29%

Accuracy= (TP+TN)/(TP+TN+FP+FN)*100%
= (74+72)/ (74+72+2+1)*100% = 98%

6. Conclusion and future work

FBB is a novel fast segmentation technique that uses symmetry to enclose an anomaly by a bounding box within an axial brain MR image. This approach avoids the challenge of dealing with the variation of intensities among different MR image slices. Moreover, FBB does not need image registration. The method is completely unsupervised. It is also very efficient—i.e., it can be implemented in real time. As this method always generates a box on a MR slice, even in the absence of the tumor, we set threshold level within bounding box to avoid this. We conclude that segmentation techniques give better result if applied within bounding box.

In the future, the work of this research can be extended to increase the detection and segmentation accuracy. By applying thresholding within bounding box for segmentation, the threshold level is needed to be set according to images. So another segmentation technique need to be applied which work on every type of axial brain images.

7. References

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