

# Detection of Tumor Cells using Symmetry Method

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## ABSTRACT

The paper focuses on identifying the tumor cells in brain of given input. This project is developed using the image processing toolkit MATLAB. The goal of our project is to detect the brain tumor cells using bounding box and symmetry method. This project can be used as an aid in many fields science, medicines. A significant medical informatics task is indexing patient databases according to size, location, and other characteristics of brain tumors and edemas, possibly based on magnetic resonance (MR) imagery. This requires segmenting tumors and edemas within images from different MR modalities. To date, automated brain tumor or edema segmentation from MR modalities remains a challenging as well as computationally intensive task. Here novel automated, fast, and approximate segmentation technique is proposed. The input is a patient study consisting of a set of MR slices. The output is a corresponding set of the slices that circumscribe the tumors with axis-parallel bounding boxes. The proposed approach is based on an unsupervised change detection method that searches for the most dissimilar region (axis-parallel bounding boxes) between the left and the right halves of a brain in an axial view MR slice.

**Keywords:** MR image, Thresholding, Bhattacharya coefficient, Fast bounding box method, Meanshift clustering

## 1. INTRODUCTION

Brain tumor is caused by an abnormal growth of cell in brain. Normally brain tumor emerges from brain cells, blood vessels or nerves that are present in the brain. Early detection of brain tumor is necessary as death rate is higher among humans having brain tumor [1]. Techniques for brain tumor detection using image processing have been present

for few decades. Researchers have proposed many semi-automatic and automatic image processing techniques to detect brain tumors but most of them fail to give effective and precise results due to the presence of noise, in homogeneity, poor images contrast that occur usually in medical images.

Brain tumor segmentation is very difficult due to complex brain structure but early and accurate detection of tumors, edema and necrotic tissues is very important for diagnostic system. Tumors can damage normal brain cells by producing inflammation, exerting pressure on parts of brain and increasing pressure within the skull[2]. Automatic brain tumor detection and segmentation face many challenges. Brain tumor segmentation requires the efficient knowledge of pathology and understanding the intensity and shape of MRI image. The main problem in tumor segmentation arises due each tumor being of different shape, size, location and intensity. Manual detection of brain tumor requires human interaction and is time consuming. Also it depends on the ability of the observer to locate the location, shape and size of the tumor. Thus, a need of completely computer aided system for brain tumor detection is inevitable.

A space within the skull is covered by the brain tumor which causes the disturbance of normal brain activity. It can increase pressure in the brain, shift the brain or push it against the skull, and/or invade and damage nerves and healthy brain tissue. The location of a brain tumor influences the type of symptoms that occur. Identifying the presence of a brain tumor is the first step in determining a course of treatment. Identification of a brain tumor generally involves a neurological examination, brain scans, and/or an analysis of the brain tissue. Doctors use the diagnostic information to classify the tumor from the least aggressive (benign) to the most aggressive (malignant). Identifying the type of

tumor helps doctors determine the most appropriate course of treatment.

Tumors can be benign or malignant, can occur in different parts of the brain, and may or may not be primary tumors. Tumors may or may not be symptomatic some tumors are discovered because the patient has symptoms, others show up incidentally on an imaging scan, or at an autopsy.

The most common primary brain tumors are,

- Gliomas
- Meningiomas
- Pituitary adenomas
- Nerve sheath tumors

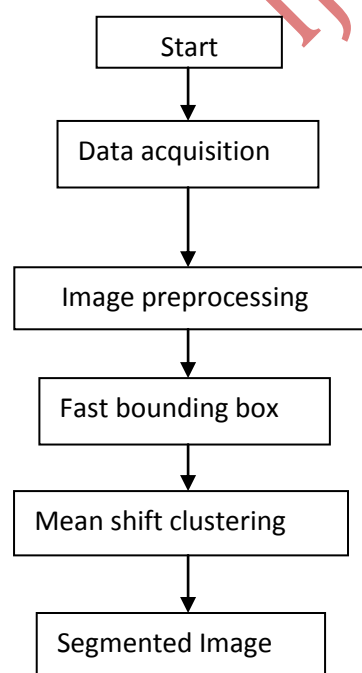
The objective of the proposed system is as follows

- Design and implement the GUI for segmentation of Tumor region.
- The input image is divided into 2 slices, one containing tumor region and other containing without tumor.
- Identify the tumor region from an MR image.
- Segmentation of tumor region using FBB method.

## 2. METHODOLOGY

The proposed system consists of four steps. They are data collection, image processing, location of bounding box and finally the clustering process. MATLAB is used in every process made throughout the project.

The block diagram of the proposed system is as follows



**Fig.1: Block diagram of Handwritten Kannada Numeral Recognition**

The steps involved are,

- Data Collection
- Image Pre-processing
- Fast bounding box
- Mean shift clustering

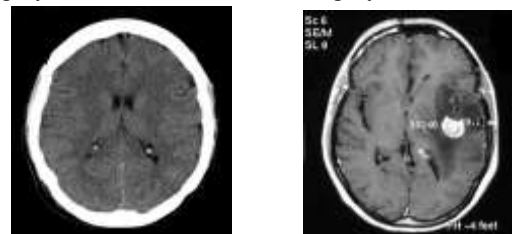
In the proposed system, the input image is pre-processed to remove the noise. Here the image is converted into binary image and it normalizes the intensity values. After preprocessing, the tumor region is identified and segmented using fast bounding box and mean clustering algorithm. The segmented region is displayed as output. The details description of the steps of the proposed system is as follows

### 2.1 Data Acquisition

The database consists of MR images which contains tumor. Each image is taken as query image.

### 2.2 Image Preprocessing

In preprocessing, the M.R. Scans images shown in the Fig 2 (a) is taken from the frontal and the centripetal side of the head of the patient. This image is of the normal person who is not having any type of tumour or any type of injury to the brain, in this image there is white boundary which resembles the bone structure of the head where as the graycolor resembles the brain (gray matter ).



**Fig. 2: Query Image**

The input image is converted in to Gray scale image because though the images are in gray matter, the Red, Green and Blue components are not visible in the image. Thus removing of this RGB component will help to perform the operations easily. This RGB images are converted to grayscale images by eliminating the hue and saturation information while retaining the luminance.

### 2.3 Fast Bounding Box

Fast Bounding Box Algorithm operates in two sequential steps. First, the input set of 2D MR slices are processed to find axis-parallel rectangles, i.e., bounding boxes on each of these slices. Next, these bounding boxes are clustered to identify the

ones that surround the tumor/edema. These two steps are described in the following subsections.

### 2.3.1 Locating Bounding Box

In this section the basic principle behind FBB is elaborated: 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.

The proposed method is different from most of the change detection methods proposed to date in that view this change as a region-based global change that differs from most techniques, which view the change as a local pixel-to-pixel changes— here tumor or edema is considered as the “change” region in the test image and all other intracranial tissues except tumor or edema are considered as the “no change” region. A novel score function is utilized 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.

## 2.4 Clustering Bounding Boxes using Mean Shift

The mean shift algorithm is a nonparametric clustering technique which does not require prior knowledge of the number of clusters, and does not constrain the shape of the clusters.

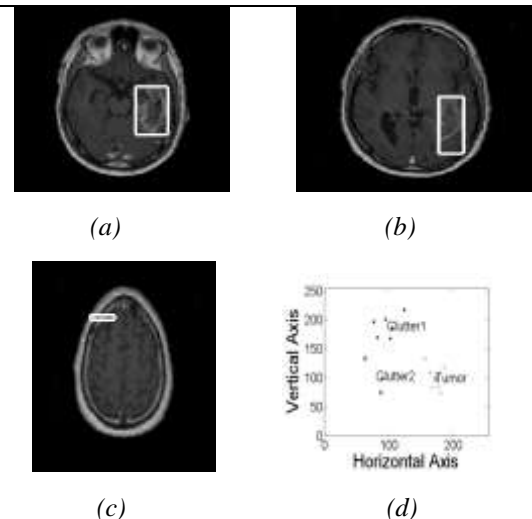
Given  $n$  data points  $x_i$ ,  $i = 1$  to  $n$  on a  $d$ -dimensional space  $R^d$ , the multivariate kernel density estimate obtained with kernel  $K(x)$  and window radius  $h$  is

$$f(x) = \frac{1}{nh^d} \sum_{i=1}^n K\left(\frac{x-x_i}{h}\right)$$

For radially symmetric kernels, it suffices to define the profile of the kernel  $k(x)$  satisfying

$$K(x) = ck, d^k (||x||^2)$$

Where  $ck$ ,  $d$  is a normalization constant which assures  $K(x)$  integrates to 1. The modes of the density function are located at the zeros of the gradient function  $rf(x) = 0$ .



**Fig.3 (a), (b), (c) Bounding boxes found on three axial brain MRI slices of a patient where only first two slices contain tumor. (d) Results of mean shift algorithm on the center position of the bounding boxes across different axial brain MR slices of a patient. FBB outputs MR slices belonging to the cluster labelled Tumor along with their bounding boxes.**

Notice that the proposed FBB algorithm always produces an axis-parallel bounding box for any MR image slice, even if that image does not contain tumor or edema. Since many MR slices do not contain tumors or edemas, simple and heuristic process is used to separate the set of input MR slices into two classes— one containing tumors and the other containing no tumors.

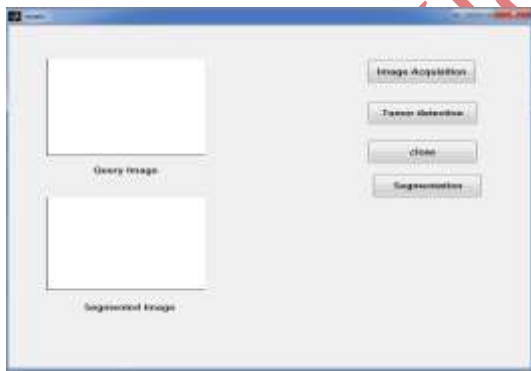
Fig. 3 (a), (b) and (c) show the results of the bounding box locating method on three MR slices of a patient, where only Fig. 3 (a) and (b) contain the tumor. The tumor positions in these two slices are close to each other (right- bottom quadrant of the slice) and consequently, the centroids of the bounding boxes found by FBB are also very close to each other. However, the centroid of the bounding box in Fig. 3 (c) is far away from the former two, providing heuristic evidence that it should be separated. Typically a patient study may consist of 20-30 MR image slices. After finding the bounding boxes on each of the MR slices, mean shift clustering (MSC) on the coordinates of the bounding boxes is applied.

The MSC algorithm climbs the probability density function or likelihood of the features (here, the centroid coordinates) to find the nearest mode (peak or bump) or local maxima. For further details regarding mean shift algorithm, the observations suggest that the centroids of the computed bounding boxes on the slices containing abnormalities are close to each other and those for

other slices are typically scattered. Thus, the largest mode found by the MSC typically corresponds to the slices containing tumors/edemas. Fig. 3 (d) shows the result of MSC on the MR slices of a patient. In Fig. 3(d) horizontal and vertical axes correspond to the  $x$  and  $y$ -position of the centroids of the bounding boxes respectively. Here MSC finds three clusters and the class corresponding to maximum mode or highest peak is labeled as „Tumor“ class and other two classes are entitled as „clutter1“ and „clutter2“. In principle other meaningful features can be utilized in the MSC for this validation purpose. However, our empirical observations suggest that the centroid feature (*i.e.*, the spatial proximity feature) is adequate for the majority of patient studies.

### 3. RESULTS

The experiments involved axial brain MR image slices of 10 recent patient studies from databases maintained at the Cross Cancer Institute. Each study contains both T1C and T2 modalities and each modality contains 20-30 axial brain MR slice which run from top of the head to the bottom of the chin. T1C modality is good at recognizing tumors and T2 modality is good at identifying edemas is observed. The database consists of tumors and edemas of different size, shape, location, orientation and types: completely enhanced, non-enhanced and border-enhancing tumors and edemas.



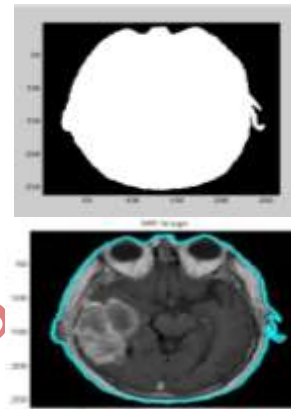
**Fig: 4 GUI of proposed System**

In Fig 4, the GUI of proposed system contains axes to display input image and segmented image. The GUI also contains push button to feed image as query image, and also to identify and to display the identified segmented tumor image from the input image. The fig 5 shows the gui which takes image as input image and displayed in an axis.



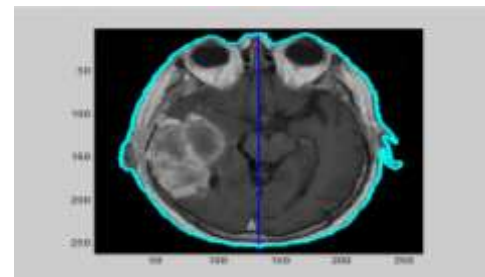
**Fig. 5 Input image in GUI**

The below fig 6 represents the edges of the image and brain part of an input image



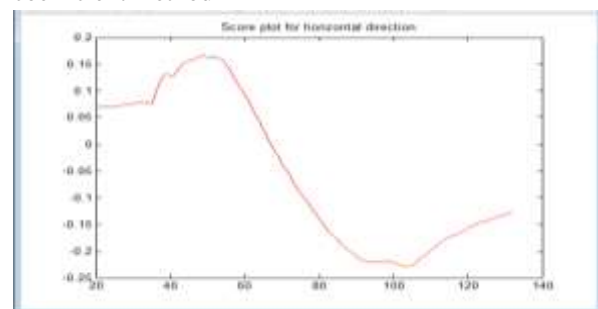
**Fig. 6 Edges of Image and brain part**

The following figure represents the 2 slices of an input image



**Fig 7: Two Slices of input image**

The following figure is used to plot the score of the vertical and horizontal direction using Bhattacharya coefficient method



**Fig 8: Score plot for Vertical direction**

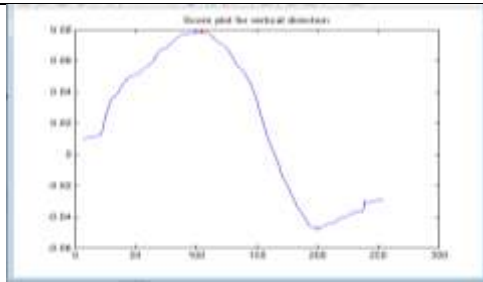


Fig 9: Score plot for horizontal direction

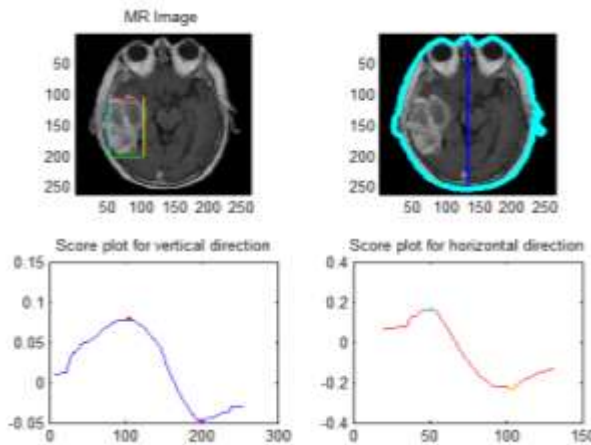


Fig 10: Output Images

#### 4. CONCLUSION

FBB is a novel fast segmentation technique that uses symmetry to enclose an anomaly (typically tumors or edema) by a bounding box within an axial brain MR image. A novel regionbased score function is utilized, which uses Bhattacharya coefficient to compute local histogram similarity between test and reference (sub) images. The analytically explained the behavior of the score function that effectively locates the brain tumors or edema quickly, showing how it exploits the symmetry of the axial brain MR image slices along the medial axis. 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 (*i.e.*, does not need any training images). It is also very efficient— *i.e.*, it can be implemented in real time.

As this method always generates a bounding box on a MR slice, even in the absence of the tumor or edema, a heuristic scheme designed to separate relevant slices (slices having tumor or edema) from normal ones of a patient— using the mean shift clustering algorithm is presented. Some standard segmentation algorithms (such

as active contour without edges or normalized graph cut) can delineate exact tumor boundary or edema if these algorithms are applied only within the bounding box is discussed. This region based approximate segmentation technique can explore new opportunities of effective MR database indexing system. The resulting method is very fast, robust and reliable for indexing tumor or edema images for both archival and retrieval purposes and it can use as a vehicle for further clinical investigations.

#### 5. REFERENCES

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