UACEE International Journal of Advances in Computer Science and its Applications – IJCSIA
Volume 3 : Issue 3 [ISSN 2250 – 3765]
Publication Date : 09 September 2013

Comparative Study of Segmentation Techniques for Extracting Brain Tumour from MRI image

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***Abstract*- Brain tumour segmentation is a crucial step in surgical planning and treatment planning. A significant medical informatics task is indexing patient databases according to size, location, and other characteristics of brain tumours and edemas, possibly based on magnetic resonance (MR) imagery. This requires segmenting tumours and edemas within images from different MR modalities. Automated brain tumour or edema segmentation from MR modalities remains a challenging, computationally intensive task.**

This paper presents a comparative study of different approaches for to segmenting brain tumour from MRI images.

Keywords: Brain tumour segmentation, MRI images, Fuzzy C-Mean, K-Mean Clustering, Bounded-box, Morphological operations.

I. Introduction

Brain tumour segmentation means segregating tumour from nontumour tissues. In medical imaging, it is one of the crucial steps in surgical and treatment planning. There are various types of malignant tumours such as astrocytoma, meningioma, glioma, medulloblastoma and metastatic, which vary greatly in appearance — shape, size and location. Magnetic resonance (MR) sequences such as T1-weighted, T2-weighted and contrast-enhanced T1-weighted scans provide different information about tumours. On these images, brain tumours appear either hypointense (darker than brain tissue), or isointense (same intensity as brain tissue), or hyperintense (brighter than brain tissue) **[5]**.

The accurate estimation of tumour size is important for clinical reasons, e.g., for treatment planning and therapy evaluation. Although maximum tumour diameter is widely used as an indication of tumour size, it may not reflect a proper assessment of this tumour attribute because of the 3D nature and irregular shape of the tumour. Tumour volume, on the other hand, may be an appropriate representation of tumour size.

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Here we present a comparative study (review) of different approaches used for medical image segmentation with their respective results in their respective papers as referenced **[3], [4]**.

One way to obtain an estimate of tumour volume is via segmentation. Such schemes implicitly acquire the tumour volume by extracting the tumour surface **[23]**. Tumour segmentation can be done using several techniques such as Region growing ([1], [9], [11], [16], [29]), Fuzzy methods ([2], [4], [15]), Kmean Clustering ([4], [7]) ects. I have studied most of the papers for

II. Methods of Segmentation

A. Fuzzy C-Mean Algorithm:

The fuzzy logic is a way to processing the data by giving the partial membership value to each pixel in the image. The membership value of the fuzzy set is ranges from 0 to 1. Fuzzy clustering is basically a multi valued logic that allows intermediate values i.e., member of one fuzzy set can also be member of other fuzzy sets in the same image. There is no abrupt transition between full membership and non-membership. The membership function defines the fuzziness of an image and also to define the information contained in the image. These are three main basic features involved in characterized by membership function. They are support, Boundary. The core is a fully member of the fuzzy set. The support is non-membership value of the set and boundary is the intermediate or partial membership with value between 0 and 1 [2] **[4] [15]**.

B. K-Mean Clustering:

K-Means is the one of the unsupervised learning algorithm for clusters. Clustering the image is grouping the pixels according to the some characteristics. In the kmeans algorithm initially we have to define the number of clusters k. Then k-cluster centre are chosen randomly. The distance between the each pixel to each cluster centres are calculated. The distance may be of simple Euclidean function. Single pixel is compared to all cluster centres using the distance formula. The pixel is moved to particular cluster which has shortest distance among all. Then the centroid is re-estimated. Again each pixel is compared to all centroids. The process continues until the centre converges **[4] [7]**.

C. A bounding box method:

The algorithm searches for 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. We assume that one of the two rectangles will circumscribe the tumour/edema appearing in one hemisphere of the brain. Once these bounding boxes are found on all input slices, an

unsupervised mean-shift clustering (MSC) uses the locations (centroids) of these bounding boxes to find the largest cluster of consecutive MR slices; FBB then outputs this volume, encoded as a set of slices with their bounding box regions **[3]**.

III. Related work

A. Fuzzy C-Mean Algorithm [4]:

The fuzzy logic is a way to processing the data by giving the partial membership value to each pixel in the image. The membership value of the fuzzy set is ranges from 0 to 1. Fuzzy clustering is basically a multi valued logic that allows intermediate values i.e., member of one fuzzy set can also be member of other fuzzy sets in the same image. There is no abrupt transition between full membership and non-membership. The membership function defines the fuzziness of an image and also to define the information contained in the image. These are three main basic features involved in characterized by membership function. They are support, Boundary. The core is a fully member of the fuzzy set. The support is non-membership value of the set and boundary is the intermediate or partial membership with value between 0 and 1.

A. The Fuzzy c-means Algorithm:

The algorithm contain following steps:

1. Initialize $M=[M_{ij}]$ matrix, $M^{(0)}$.

2. At k-step: calculate the centres vectors $R^{(k)}=[R_j]$ With $M^{(k)}$

$$R_j = \frac{\sum_{i=1}^{N} X_i . M^{m_{ij}}}{\sum_{i=1}^{N} M^{m_{ij}}}$$

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

$$M_{ij} = \frac{1}{\sum_{k=1}^{c} \left(\frac{\| X_i - C_j \|}{\| X_1 - C_j \|} \right)^{\frac{2}{m-1}}}$$

4. if $\| M^{(k+1)} - M^{k}) \| < \epsilon$ then STOP; otherwise return to step 2.

m = any real number greater than 1,
M_{ij} = degree of membership of X_i in the cluster j,
x_i = data measured in d-dimensional,
R_j = d-dimension centre of the cluster,
ϵ = termination value or constant between 0 and 1
k = no of iteration steps.

B. K-Mean Clustering [4]:

K-Means is the one of the unsupervised learning algorithm for clusters. Clustering the image is grouping the pixels according to the some characteristics. In the kmeans algorithm initially we have to define the number of clusters k. Then k-cluster centre are chosen randomly. The distance between the each pixel to each cluster centres are calculated. The distance may be of simple Euclidean function. Single pixel is compared to all cluster centres using the distance formula. The pixel is moved to particular cluster which has shortest distance among all. Then the centroid is re-estimated. Again each pixel is compared to all centroids. The process continuous until the centre converges.

Algorithm of K-Mean Clustering:

1. Give the no of cluster value as k.
2. Randomly choose the k cluster centres.
3. Calculate mean or centre of the cluster.
4. Calculate the distance b/w each pixel to each cluster centre.
5. If the distance is near to the centre then move to that Cluster.
6. Otherwise move to next cluster.
7. Re-estimate the centre.
8. Repeat the process until the centre doesn't move

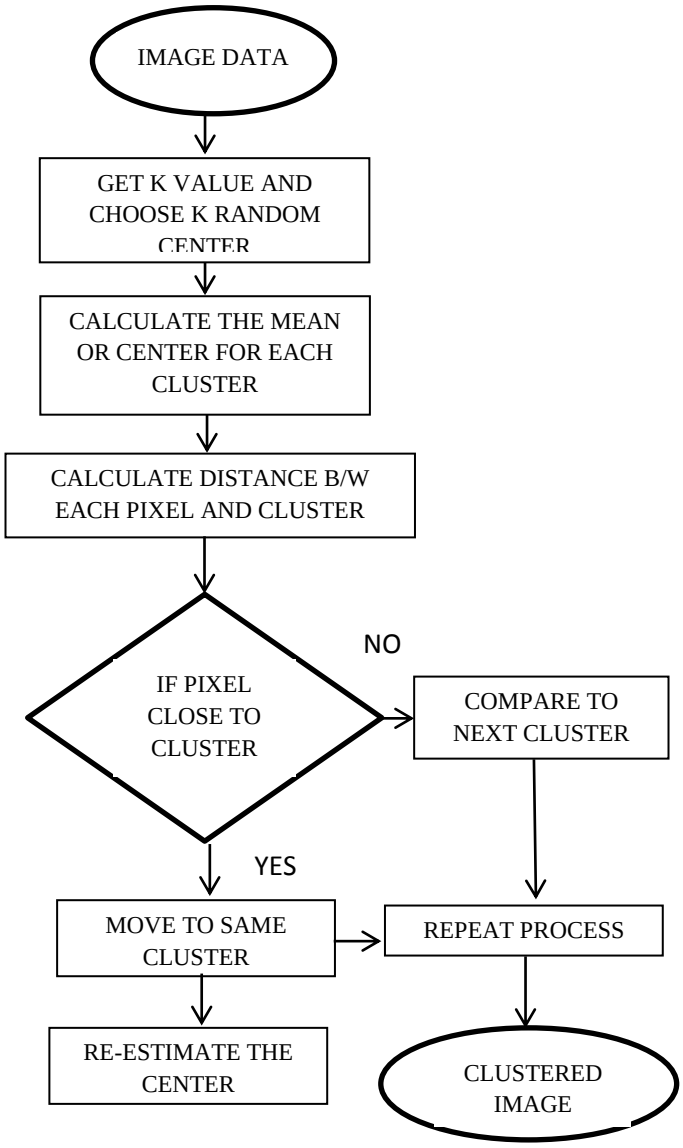

Figure 1: Flowchart of K-means Algorithm

C. Bounding-box method [3]:

Here present an automatic, fast, and approximate segmentation technique that avoids these problems by locating a "bounding box"—i.e., an axis-parallel rectangle, around the tumour or edema on an MR slices. We can then use this bounding box to answer subsequent queries that ask about tumour position and size (albeit with a response that is approximately correct).

The input to our algorithm, fast bounding box (FBB), is a set of MR slices belonging to a single patient study. The output is a subset of slices that contain tumours or edemas, which are each labelled with an axis-parallel bounding box that circumscribes the tumour and edema region. We will see that different imaging modalities are good at identifying these regions: T1C for tumour and T2 for edema.

On each input MR slice (axial view), FBB first locates the left–right axis of symmetry of the brain. A tumour or edema, which is considered an abnormality in the brain, typically perturbs this symmetry.

Fast bounding box algorithm:

FBB operates in two sequential steps. First, the input set of 2D MR slices are processed individually, to find axis-parallel rectangles (i.e., potential bounding boxes) in. Next, these bounding boxes are clustered to identify the ones that actually surround the tumour/edema.

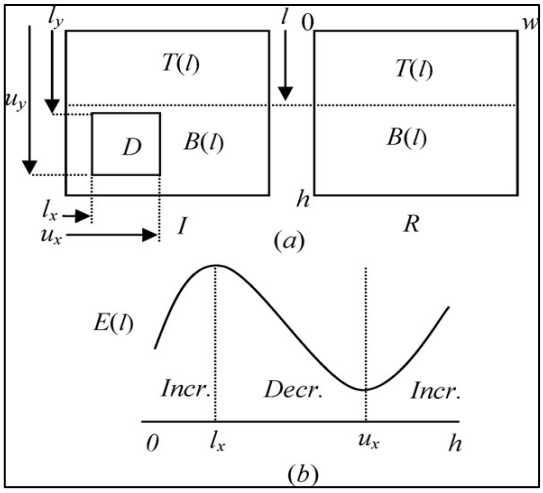

Figure 2: (a) Finding anomaly D from test image I using reference image R. (b) Energy Function plot.

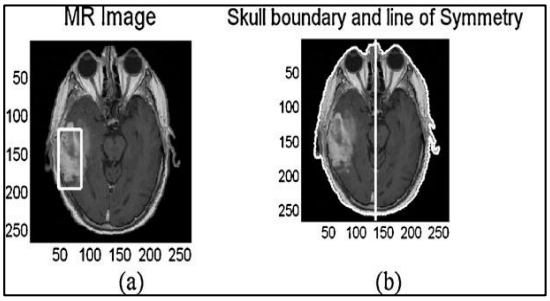

Figure 3: Locating brain tumour by the FBB method.

IV. Results and Discussion

A. Fuzzy C-Mean Algorithm [4]:

Fig. 4 is the output image for Fuzzy C-Means. It is mainly developed for the accurate prediction of tumour cells which are not predicted by K-means algorithm. It gives the accurate result for that compared to the KMeans.

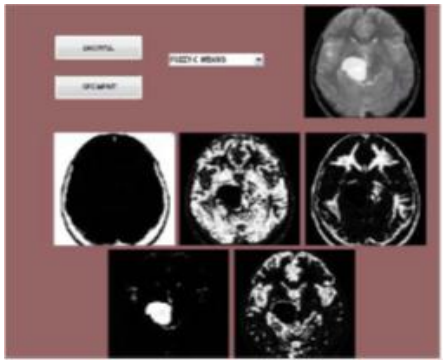

Figure 4: Output of Fuzzy C-Mean

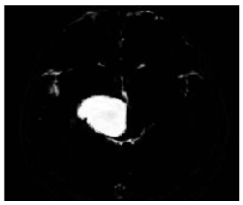

Figure 5: Output image of Thresholding

Fig.5 is the extracted tumour shape from the given image using the Fuzzy C- Means algorithm. The unpredicted tumour cells in the K-means algorithm can also be found using the Fuzzy C-Means algorithm.

B. K-Mean Clustering Algorithm [4]:

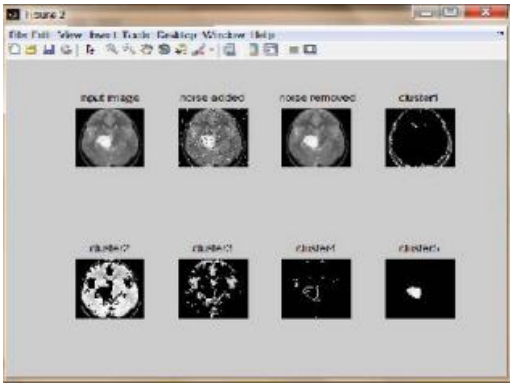

Figure 6: Output image for pre-processing and k-means for k=5

Fig.6 is the MR image given as input to the pre-processing and K-means algorithm. Here 0.02% of salt and pepper noise is added and that has been removed using the median filter. The K-mean algorithm clusters the image according to some characteristics. Figure is the Output for K-Means algorithm with five clusters. At the fifth cluster the tumour is extracted.

C. Bounding-Box Algorithm [3]:

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 that run from top of the head to the bottom of the chin.

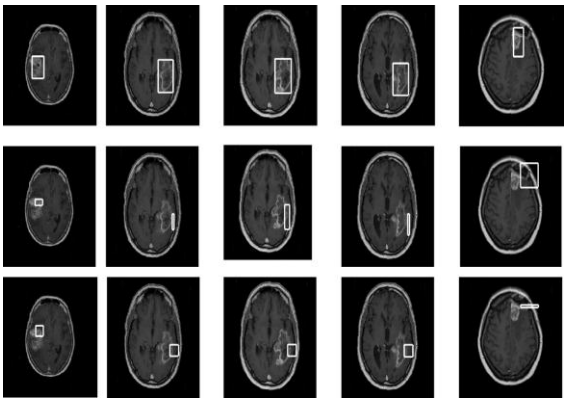

Figure 7: T1C axial brain MRI slices: top row, results of the FBB technique; middle row, results of intensity based bounding box algorithm (IBB); bottom row, results of entropy based bounding box algorithm (EBB).

We have noted that T1C modality is good at recognizing tumours and T2 modality is good at identifying edemas. Our database consists of tumours and edemas of different Size, shape, location, orientation and Types**:** completely enhanced, non-enhanced and border-enhancing tumours and edemas. The results below are results of paper [5]

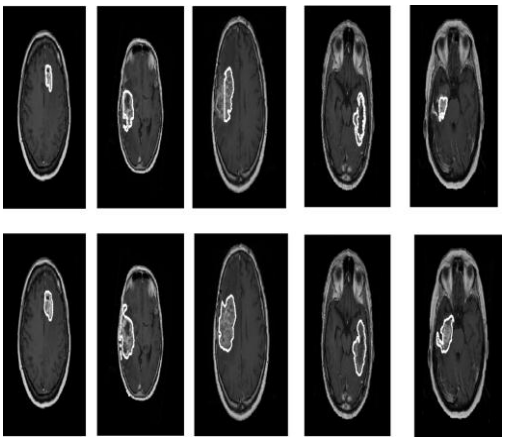

Figure 8: Tumour detection from T1C axial brain MRI slices: top row, results of knowledge based thresholding algorithm; bottom row, results of Chan–Vese algorithm within bounding box found by FBB.

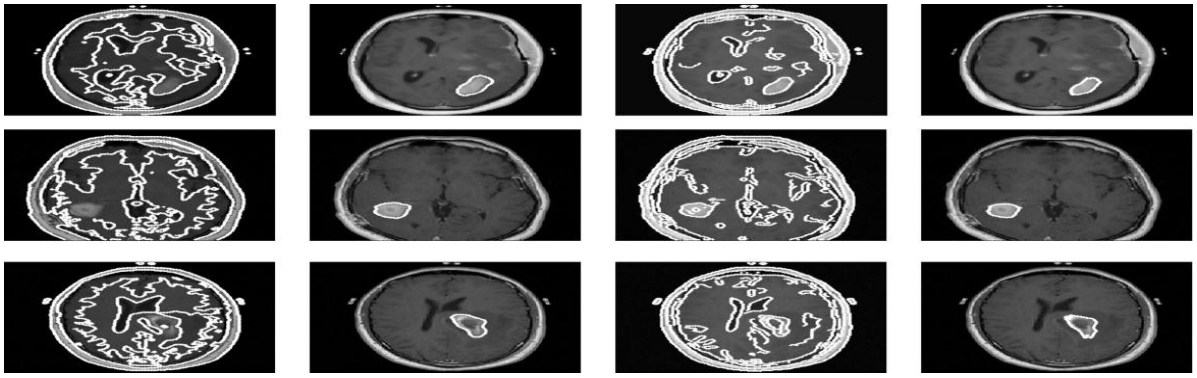

Figure 9: Tumour detection from T1C axial brain MRI slices. From left: first column, results of the Chan–Vese algorithm; second column, results of Chan–Vese algorithm within bounding box; third column, results of the normalized graph-cut algorithm; fourth column, results of the normalized graph-cut algorithm within bounding box.

V. *Conclusion*

There are different types of tumours available. They may be as mass in brain or malignant over the brain. Suppose if it is a mass then **K- means algorithm** is enough to extract it from the brain cells. If there is any noise are present in the MR image it is removed before the Kmeans process. The noise free image is given as a input to the k-means and tumour is extracted from the MRI image. And then segmentation using **Fuzzy C means** for accurate tumour shape extraction of malignant tumour and thresholding of output in feature extraction. Finally approximate reasoning for calculating tumour shape and position calculation.

FBB is a novel fast segmentation technique that uses symmetry to enclose an anomaly (typically, tumours or edema) by a bounding box within an axial brain MR image.

We utilize a novel region-based score function that uses Bhattacharya coefficient to compute local histogram similarity between test and reference (sub) images. We have analytically explained the behaviour of the score function that effectively locates the brain tumours or edema quickly, showing how it exploits the symmetry of the axial brain MR image slices along the medial axis.

As my study among these three approaches I have review the Fast Bounding Box 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. We have illustrated that some standard segmentation algorithms (such as active contour without edges [5], [14] or normalized graph cut [8]) can delineate exact tumour boundary

or edema if these algorithms are applied only within the bounding box. This region based approximate segmentation technique can enable effective MR database indexing system. The resulting method is very fast, robust and reliable for indexing tumour or edema images for both archival and retrieval purposes and it can use as a vehicle for further clinical investigations.

In this paper we present a comparative study (review) of different approaches used for medical image segmentation with their respective results in their respective papers as referenced **[3], [4]**.

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