Brain Tumor Detection and Volume Calculation Using MR (Magnetic Resonance) Images

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Objective:

Magnetic Resonance Imaging (MRI) radiologic evaluation of treatment response during clinical testing of the therapeutic drugs has become increasingly important in the brain cancer treatment process. However, exact labeling of the brain tumors is a time-consuming task, and considerable variation is observed between doctors. The current case study aims at setting up an automated system to detect and calculate the brain tumor volume. Different brain tumor detection algorithms have been developed in the past few years. Normally, the automatic and accurate segmentation is very challenging, and it is yet to be fully and satisfactorily solved. The project aims to put together a system for measuring the brain tumor volume in lesser time.

Given information in the case study:

1. Using the highest resolution scan,60 MRI scans are taken to fully image the entire brain.
2. Each scan covers 2mm thickness.
3. The texture of the tumor is heterogenous.

Methodology:

The proposed solution is divided into following stages.

1. Pre-processing.
2. Segmentation.
3. Post-processing.
4. Computing the area of the tumor in each slice.
5. Computing the volume of the tumor.

1.Pre-processing:

Pre-processing mainly involves those operations that are normally necessarily prior to the main goal analysis and extraction of the desired information and normally geometric corrections of the original actual image. These improvements include correcting the data for irregularities and unwanted noise, removal of non-brain element image and converting the data so they correctly reflected in the original image. It involves the below steps:

1. Image is converted to gray scale if it is a colored image.
2. **De-noising of the image**:
   An edge preserving smoothing filter must be applied to the image to remove the noise. This is achieved by using the Median filter as it removes the noise without disturbing the images.

Some other filters like Curvature Flow Image Filter can also be used. The idea behind the Curvature Flow Image Filter is that the regions of high curvature diffuse very quickly. This removes noise artifacts. The regions of less curvature (such as image edges) diffuse much slower, thereby preserving the features.

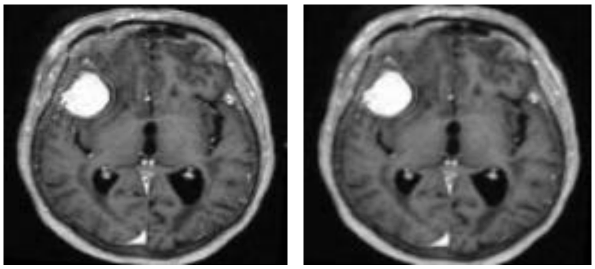

Fig 1. a) Original Image   b) Noise filtered image

3. **Skull stripping**:

This is the process of extracting brain tissues from non-brain tissues in MR images. Detection of skull defines the boundaries of the brain. The edge information helps to find out the region of interest (ROI) i.e. the portion of the image covering the tumor. Skull stripping involves the below steps.

- Double thresholding- it is a segmentation technique. This technique, converts the image into binary form, that is gray scale image to binary image. This technique generates the mask by setting each pixel in the range of 0.1*255-0.88*255 to 1 means white and remaining pixels to 0 means black. Non-brain tissues pixels were discarded in MRI image. Here two thresholds upper and lower are considered so it is known as double thresholding technique.

- Erosion- in this stage unwanted pixels are removed from MRI image after thresholding. Thus, the skull portions are removed. Here disk of radius 3 was taken as a structuring element for removing all unwanted pixels which are contributing to the brain MRI images.

- Region filling- this method is used to fill the holes in the images. After the erosion, eroded images are filled using region filling algorithm. Here the associated background pixels are converted into foreground pixels so that the holes present in the eroded regions are removed in brain MRI image.

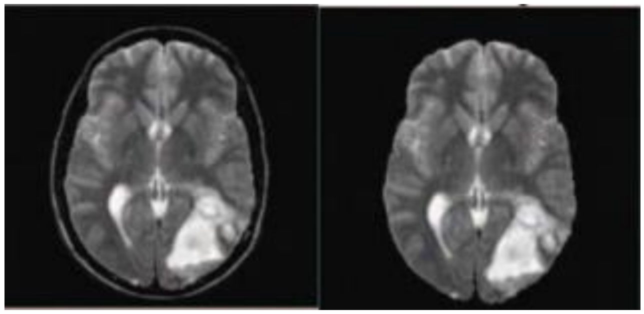

Fig 2. a) Image with skull b) Removing skull

2.Segmentation:

Segmentation is the technique of separating an image into multiple slices and object region. All the pixels in a region are similar with respect to some characteristics such as color, intensity, or texture. Each region will be considerably different with respect to its neighboring regions. There are several types of segmentation possible to segment a tumor from MRI of brain.

Thresholding based methods can be used when the contrast intensity is high. But these methods are not suitable for images with poor contrast or images with a lot of background and foreground artifacts.

Region based segmentation methods like region growing and watershed segmentation are susceptible to human error as the seed region is manually selected.

The tumor contour is fuzzy by nature because the intensity distinction between tissue classes (tumor and non-tumor) is usually blurry. The Fuzzy C-Means segmentation algorithm attempts to handle this limitation. 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 c-means(FCM) is the clustering algorithm which allows one piece of data may be member of more than one clusters.

Fuzzy C-Means Clustering method:

The aim of FCM is to find cluster centers (centroids) that minimize dissimilarity functions. To accommodate the fuzzy partitioning technique, the membership matrix (U) is randomly initialized. In the first step, the algorithm selects the initial cluster centers. Then, in later steps after several iterations of the algorithm, the result converges to actual cluster center. A good set of initial clusters is achieved, and it is very important for an FCM algorithm. If a good set of initial cluster centers is chosen, the algorithm makes less iterations to find the actual cluster centers.

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The Fuzzy C Means is an iterative algorithm that attempts to find clusters in the data by minimizing an objective function shown in the equation below:

$$J = \sum_{i=1}^{n} \sum_{j=1}^{c} u_{ij}^{m} (X_i - C_j)^2$$

J is the objective function. After one iteration of the algorithm the value of J is smaller than before. It means the algorithm is converging or getting closer to a good separation of pixels into clusters. N is the number of pixels in the image, C is the number of clusters used in the algorithm, and must be decided before execution, is the membership table – a table of NxC entries which contains the membership values of each data point and each cluster, m is a fuzziness factor (a value larger than 1), xi is the ith pixel in N, cj is jth cluster in C and difference between (xi - cj) is the Euclidean distance between xi and cj.

Algorithm:

1. Initialize with random values between zero and one; but with the sum of all fuzzy membership table elements for a pixel being equal to 1 i.e. the sum of the memberships of a pixel for all clusters must be one.

2. Calculate an initial value for J using,
$$J = \sum_{i=1}^{n} \sum_{j=1}^{c} u_{ij}^{m} (X_i - C_j)^2$$

3. Calculate the centroids of the clusters cj using
$$C_j = \frac{\sum_{i=1}^{n} u_{ij}^{m} \, |x_i|}{\sum_{i=1}^{n} u_{ij}^{m}}$$

4. Calculate the fuzzy membership table using,
$$u_{ik} = \frac{1}{\sum_{i=1}^{n} \left(\frac{|X_i - C_j|}{|X_i - C_k|} \right)^{\frac{2}{m-1}}}$$

5. Recalculate J.

6. Go to step 3 until a stopping condition is reached.

<u>Results of FCM segmentation</u>

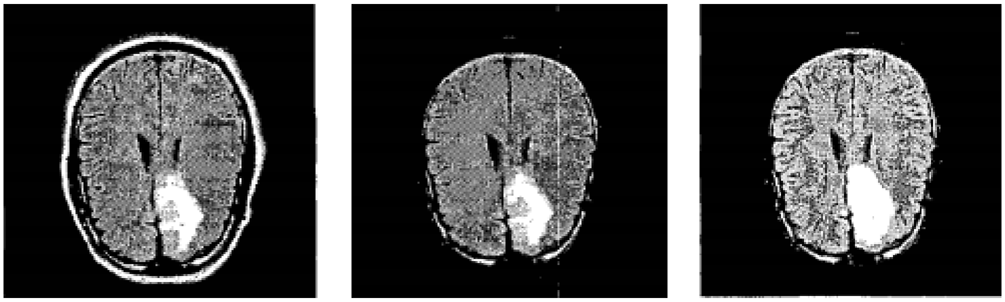

Fig. 3 a) MRI b) After skull stripping c) Segmented result after FCM clustering

3.Post-processing:

*Feature Extraction:

In this step. the cluster which shows the predicted tumor at the FCM output is extracted. A thresholding process is applied on the FCM output. A binary mask is applied over the entire image. Only those coefficients whose magnitudes are above a threshold are retained within each block. Let us consider an image block f has the k gray level, an integer value of threshold T, which lies in the grayscale range of k. The thresholding process is a comparison were each pixel in 'f ' is compared to T. Based on which, binary decision is carried out. That defines the value of the pixel in an output binary image.

$$g(n) = \begin{cases} 0 \;\; if\; f(n) \geq T \\ 1 \; if\; f(n) < T \end{cases}$$

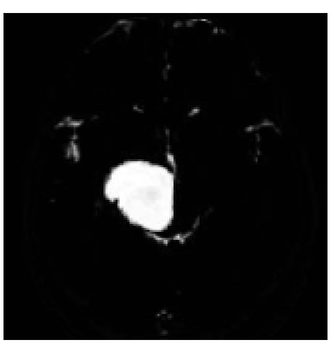

Fig 4. Output of thresholding

4.Area calculation of the tumor in each slice:

The tumor area is calculated using the binarization method.

For a 256X256 image,

Pixels = Width (W) * Height (H) = 256 X 256

f (0) = white pixel

f (1) = black pixel

Number of white pixels = $\sum_{W=0}^{255} \sum_{H=0}^{255} [f(0)]$.

If assumed that, 1 Pixel = 0.264 mm

Area 'S' is given by -> [Ref. 1]

$$S = \left[\left(\sqrt{P}\right)^{*} 0.264\right] mm^2$$

5.Computing the volume of the tumor:

Bi-dimensional measurements such as volume provide a more accurate classification of treatment response than cross-sectional area alone. Because the prior studies have shown that the tumor can grow anisotopically. And all the 60 scans must be considered.

Volume is generally computed by multiplying the area and the height together. The height in this case is represented by the MR slice thickness and the gap between any two MR slices.

Volume = $\sum_{i=1}^{N} Si$ * (Slice thickness + spacing between the slices) →[Ref. 5]

Where N = number of slice = 60

Si = Area of the slice

Slice thickness is said to be 2 mm.

Conclusion:

In this case study, an effort was made to develop a system that measures the tumor volume in substantially reduced manual time. An automation of brain tumor segmentation using combination of traditional approaches and classification like 'SVM', 'Bayesian' may overcome the problems and gives effective and accurate results for brain tumor detection.

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