



A Novel Approach for Tissue Detection in MRI Images Based on Multiple OTSU Thresholding

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Abstract—The advent of computer aided technologies image processing techniques have become increasingly important in a wide variety of medical applications. Processing of MRI images is one of the parts of this field. In this dissertation work we describes a good and efficient strategy to detect and extract the brain tissue[1][2] from patient's brain MRI images. In this method an algorithm is developed, the primary part of this algorithm is to convert given MRI image into binary image (0 and 1) using segmentation technique [3] called multiple Otsu Thresholding[4], after which morphological operations[5] [6] has been applied.

Keywords:— Graphical User Interfacing (GUI), Image processing, brain tumor, OTSU Image segmentation, Magnetic resonance imaging (MRI).

1. INTRODUCTION

The proposed work is been motivated and design because of it vital importance in current situations as for recognition of tumor in brain and still dependent on doctors observation of tumor in MRI images. Total 155 MRI images been captured by doctor form four angles top, left, right back and front, and if any patient have tumor it does not reflects in all the MRI images it basically shows in hardly one or two MRI images (normally dependent on size of tumor), and it is highly possible that it can

be ignored in some cases, hence proposed design is come up with an accurate solutions in which all the MRI images of brain been taken in a variable and first of all it get compared with MRI images of normal brain (the normal brain MRI is been taken from CC-BY-SA license and IEEE standard database SRI24) if does not matched then there is a possibility of tumor in the MRI image which further detected through proposed multi level Otsu Thresholding and detection of size after morphological filtering (erosion and dilation).

2. METHODOLOGY

Figure 1 shown below the proposed work flow diagram here the whole work is been separated in three major task

- Preprocessing
- Recognition
- Identification and calculation

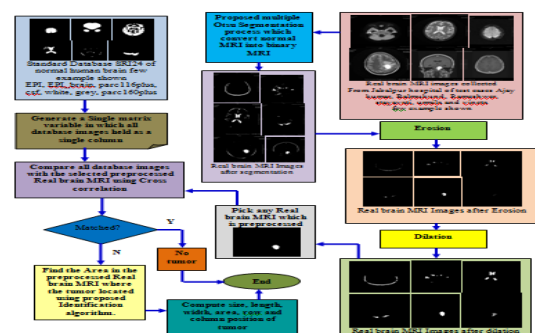


Figure 1: Proposed Work Block Diagram

Preprocessing: Pre-processing is an important required task to be done in tumor recognition system design. Pre-processing consist for two steps, Segmentation and Morphological filtering

Segmentation is done to convert gray scale image into binary image so that we can have only two object in image one is hand and other is background. Multiple Otsu algorithms [3] is used in order to segmentation purpose and real brain MRI images are converted into binary image. After converting gray scale image into binary image it must be ensure that there is no noise and undesired elements in image so use morphological filter technique. Morphological techniques consist operations: dilation, erosion.

Segmentation: A good segmentation is needed to select an adequate threshold for gray level in order to extract blood circulation (white area) .i.e. there is no part for white area should be in no blood area and no blood area also shouldn't have any part for blood area. In general, selection for an appropriate segmentation algorithm depends largely on type for images and application areas. Otsu segmentation algorithm [3] was tested and found to give good segmentation results in order to MRI images and was, therefore, selected. Otsu algorithm is nonparametric and unsupervised procedure for automatic threshold selection. Converting a greyscale image to monochrome is a common image processing task. Otsu's method, named after its inventor Nobuyuki Otsu, is one of many binarization algorithms. Otsu's Thresholding method involves iterating through all the possible threshold values and calculating a measure of spread for the pixel levels each side of the threshold, i.e. the pixels that either fall in foreground or background. The aim is to find the threshold value where the sum of foreground and background spreads is at its minimum. The algorithm will be demonstrated using the simple 6x6 image shown below. The histogram for the image is shown next to it. To simplify the explanation, only 6 greyscale levels are used.

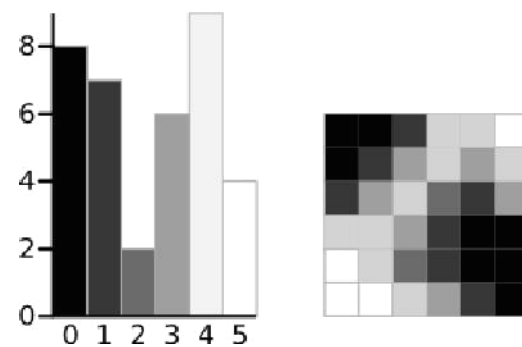


Figure 2: A 6-Level Greyscale image and its histogram

The calculations for finding the foreground and background variances (the measure of spread) for a single threshold are now shown. In this case the threshold value is 3.

$$\begin{aligned} \text{Weight } W_b &= \frac{8+7+2}{36} = 0.4722 \\ \text{Mean } \mu_b &= \frac{(0 \times 8) + (1 \times 7) + (2 \times 2)}{17} = 0.6471 \\ \text{Variance } \sigma_b^2 &= \frac{((0 - 0.6471)^2 \times 8) + ((1 - 0.6471)^2 \times 7) + ((2 - 0.6471)^2 \times 2)}{17} \\ &= \frac{(0.4187 \times 8) + (0.1246 \times 7) + (1.8304 \times 2)}{17} \\ &= 0.4637 \end{aligned}$$

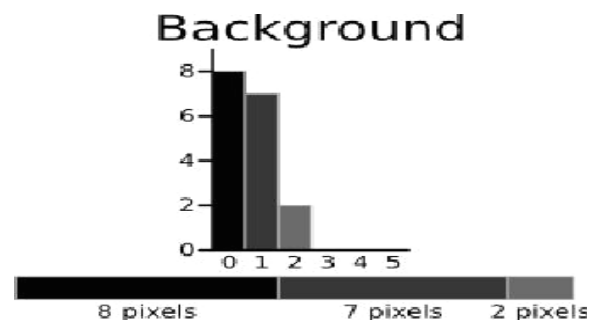


Figure 3: Background After Otsu and its Calculations

$$\begin{aligned} \text{Weight } W_f &= \frac{6+9+4}{36} = 0.5278 \\ \text{Mean } \mu_f &= \frac{(3 \times 6) + (4 \times 9) + (5 \times 4)}{19} = 3.8947 \\ \text{Variance } \sigma_f^2 &= \frac{((3 - 3.8947)^2 \times 6) + ((4 - 3.8947)^2 \times 9) + ((5 - 3.8947)^2 \times 4)}{19} \\ &= \frac{(4.8033 \times 6) + (0.0997 \times 9) + (4.8864 \times 4)}{19} \\ &= 0.5152 \end{aligned}$$

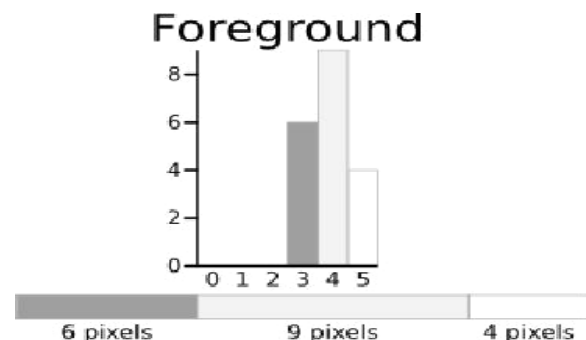


Figure 4: Foreground After Otsu and its Calculations

The next step is to calculate the 'Within-Class Variance'. This is simply the sum of the two variances multiplied by their associated weights

$$\text{Within Class Variance } \sigma_W^2 = W_b \sigma_b^2 + W_f \sigma_f^2 = 0.4722 * 0.4637 + 0.5278 * 0.5152 \\ = 0.4909$$

This final value is the 'sum of weighted variances' for the threshold value 3. This same calculation needs to be performed for all the possible threshold values 0 to 5.

Morphological Filtering: If we take close look to segmented image after applying Otsu algorithm on original gray scale image we find that segmentation is not perfectly done. Background may have some 1's which is known as background noise and MRI image may have some 0's that is known as MRI tissue noise. These errors can lead to a problem in contour detection in MRI image so we need to remove these errors. A morphological filtering [4] approach has been applied using sequence for dilation and erosion to obtain a smooth.

In morphological dilation and erosion we apply a rule on a binary image. Value for any given pixel for any given pixel in output image is obtained by applying set for rules on neighbors in input image. Dilation and erosion operation on a binary image A and with a structuring element B defined as follow:-

Dilation: If A and B are sets in 2-D integer space Z^2 , $x = (x_1, x_2)$ and \emptyset is empty set, then, dilation for A by B is

$$A \oplus B = \{x | (\hat{B})x \cap A \neq \emptyset\}$$

Where \hat{B} is reflection for B. In dilation procedure first we obtain reflection for B about its origin and then we shift reflection by x. Condition for dilation for A by B is set for all x condition is such that in order to dilation for A by B is set off all x displacement such that \hat{B} and A overlap at least one nonzero element. Set B is commonly referred to as structuring

element. Value for output pixel is maximum value for all pixels in input pixel's neighborhoods. In any for pixels is set to value 1, output pixel is set to 1.

Erosion: erosion for A by B is

$$A \otimes B = \{x | (B)x \subseteq A\}$$

Erosion for A by B is set for all point x such that B, translated by A, is contained in A. Thus value for output pixel is minimum value for all pixels in input pixel's neighborhood. In binary image, if any for pixels is set to 0, output pixel is set to 0.

Recognition: MRI matching is a one-to-many matching procedure that compares a test MRI image against all template MRI images in SRI24 database to determine identity in order to test MRI. Identification in order to test image is done by locating image in database that has highest similarity with test image. Identification procedure is a 'closed' test, which means sensor takes an observation in order to an individual that is known to be in database. Test subject's (normalized) features are compared to other features in system's database and a similarity score is found in order to each comparison. These similarity scores are then numerically ranked in a descending order. Percentage in order to times that highest similarity score is correct match in order to all individuals is referred to as 'top match score.' If any of top r similarity scores corresponds to test subject, it is considered as a correct match in terms of cumulative match. Percentage of times one of those similarity scores is correct match of all individuals is referred to as 'Cumulative Match Score', it is a curve is rank n versus percentage of correct identification, where rank n is number of top similarity scores reported.

Detection: after recognition it will be clarify that the test image is matched or not with the normal brain MRI image, if it matched any one of normal brain MRI then it will be sure that there is no tumor in the test image, but if does not matched then there is need to locate tumor

in the MRI image, this process is been done on the behalf of the histogram analysis of each rows of the MRI image.

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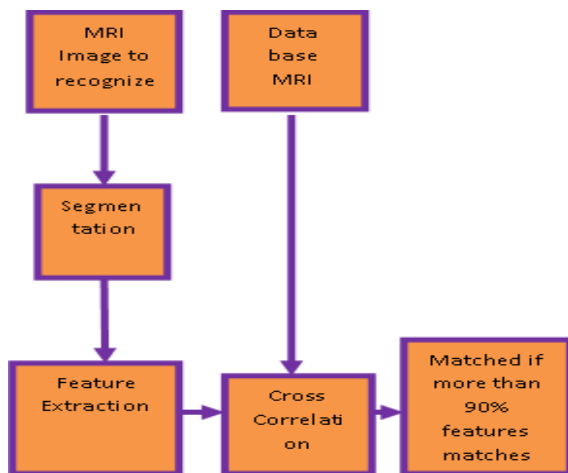


Figure 5: Proposed Recognition method

3. ALGORITHM ADOPTED

Proposed work is basically multi Otsu Thresholding for Extraction and histogram analysis to find location dimensions.

Presentably identification of ‘Contrast’ type tumors in brain MRI

Y_{ij} is MRI image of test human brain with MxN size,

$i=1, 2, 3, \dots, M$

$j=1, 2, 3, \dots, N$

‘j’ and ‘i’ are the pixel position

cnt1, cnt2, cnt3, cnt4 and cnt5 are the count values that are been assigned to get the count value so we could know the quantity of pixel values that lies in the specific range could know the quantity of pixel values that lies in the specific range

```

    if( $Y_{ij} > 0$   $Y_{ij} < 51$ )
        cnt5 = cnt5 + 1;
    elseif( $Y_{ij} > 50$   $Y_{ij} < 101$ )
        cnt4 = cnt4 + 1;
    elseif( $Y_{ij} > 100$   $Y_{ij} < 151$ )
        cnt3 = cnt3 + 1;
    elseif( $Y_{ij} > 150$   $Y_{ij} < 201$ )
        cnt2 = cnt2 + 1;
    elseif( $Y_{ij} > 200$   $Y_{ij} < 255$ )
        cnt1 = cnt1 + 1;
    
```

$$Pcnt1 = \frac{cnt1 * 100}{cnt1 + cnt2 + cnt3 + cnt4 + cnt5}$$

$$Pcnt2 = \frac{cnt2 * 100}{cnt1 + cnt2 + cnt3 + cnt4 + cnt5}$$

$$Pcnt3 = \frac{cnt3 * 100}{cnt1 + cnt2 + cnt3 + cnt4 + cnt5}$$

$$Pcnt4 = \frac{cnt4 * 100}{cnt1 + cnt2 + cnt3 + cnt4 + cnt5}$$

$$Pcnt5 = \frac{cnt5 * 100}{cnt1 + cnt2 + cnt3 + cnt4 + cnt5}$$

```

    if( $pcnt1 > 10$ )
        max = 255
    elseif(( $pcnt1 + pcnt2$ ) > 10)
        max = 200
    elseif(( $pcnt1 + pcnt2 + pcnt3$ ) > 10)
        max = 150
    elseif(( $pcnt1 + pcnt2 + pcnt3 + pcnt4$ ) > 10)
        max = 100
    else
        max = 50
    
```

Thresholding: T is the Thresholding level which decided according to Otsu Thresholding method

$$T = 50 * \sqrt{2 * \log(\text{Max})}$$

$$Z_{ij} = \begin{cases} 255 & |Y_{ij}| \geq T \\ 255 * \text{sgn}(Y_{ij}) * \frac{|Y_{ij}|^\gamma}{T^{\gamma-1}} & |Y_{ij}| < T \end{cases}$$

Where $\gamma = \sigma \sqrt{2 * \ln(N)}$

And $\sigma = \text{mean}(Y_{ij})$

Erosion: $v_t(a, b) = z(i, j) \& z_t(a, b)$

When $t=1, a=i+1, b=j,$

When $t=2, a=i-1, b=j,$

When $t=3, a=i, b=j+1,$

When $t=4, a=i, b=j-1,$

When $t=5, a=i+1, b=j+1,$

When $t=6, a=i+1, b=j-1,$

When $t=7, a=i-1, b=j+1,$

When $t=8, a=i-1, b=j-1$

Where $n=M \times N/8$ and ‘t’ repeats ‘n’ times

Dilation: $u_t(a, b) = v(i, j) \wedge v_t(a, b)$

When $t=1, a=i+1, b=j,$

When $t=2, a=i-1, b=j,$

When $t=3, a=i, b=j+1,$

When $t=4, a=i, b=j-1,$

When $t=5, a=i+1, b=j+1,$

When $t=6, a=i+1, b=j-1,$

When $t=7, a=i-1, b=j+1,$

When $t=8, a=i-1, b=j-1$

Where $n=M \times N/8$ and ‘t’ repeats ‘n’ times

Resizing: it is to be done because the MRI standard size is 240x240 in database

$$D_{i,j} = \text{imresize}(u_{i,j}, 240, 240)$$

Matching Method: The standard database is SRI24 it is an MRI-based atlas of normal adult human brain anatomy, generated by template-free nonrigid registration from images of 24 normal control subjects.

Database Preparation: Total SRI24_{240x240}(m) where m is 1,2,3....1240 MRI image of normal human brain of 240x240 pixels.

$$P_{57600 \times 1}(m) = [\text{SRI24}_{(24 \times 240.1)} \dots \dots \dots (1)$$

$$\text{SRI24}_{(240 \times 240.1)} \dots \dots \dots (2)$$

$$\text{SRI24}_{(24 \times 240.1)} \dots \dots \dots (3)$$

Where m= 1, 2, 3.....1240, m is number of MRI's in database

Cross Correlation based recognition:

$$r(n) = \sum_{k=0}^n D_{ij}(k) D_{ij}(k-n)$$

'n' is the any sample position out of total 57600 samples of D_{ij}

$$r_m(n) = \sum_{k=0}^n D(k) P(k-n, m)$$

$$S = \sum_{n=0}^{57600} r(n)$$

$$S_m = \sum_{n=0}^{57600} r_m(n)$$

$$f_m = |S_m - S1|$$

$$(Val1, K1) = \text{Min}(f_m)$$

Hard Thresholding

$$mch = \begin{cases} 1 & \text{if } val1 < 10 \\ 0 & \text{otherwise} \end{cases}$$

If mch is '1' then no need for any further calculation because the MRI is been matched with any normal brain MRI significantly

But if mch is '0' then there is tumour

Detection algorithm:

$$S_i = \sum_{j=1}^{240} u_{i,j}$$

$$rw = [rw, i] \quad \text{if } (S_i \geq 255)$$

$$Trl = \text{Min}(rw)$$

$$Tru = \text{Max}(rw)$$

$$S_j = \sum_{i=1}^{240} mu_{i,j}$$

$$cl = [cl, j] \quad \text{if } (S_j \geq 255)$$

$$Tcl = \text{Min}(cl)$$

$$Tcu = \text{Max}(cl)$$

Tcl is the column where the Tumor starts

Tcu is the column where the Tumor ends

Trl is the row where the Tumor starts

Tru is the row where the Tumor ends

4. RESULT

Simulation **results:** figures below shows the observe results after simulation of proposed work on MATLAB. This figure shows original, segmented, eroded, dilated and final detected tumor image.

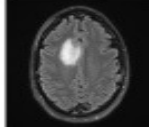

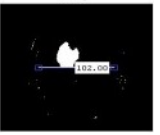
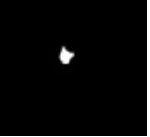


Original	Segmented	Resized
		
Erosion	Dilation	Final Tumor detection
		

Figure 6: Simulation results-

Table 1: Results Observation and Comparison

	Accuracy	Time in min
Shashwat Goel et al. [1]	92	1.24
Mariam Saii, Zaid Kraitem et al [2]	95.5	1.05
Stefan Bauer et al. [3]	87	10
Rajesh C. Patil et al. [4]	82	2.9
Proposed Work	97	12

From the results above it can be clearly observed that proposed work accuracy is found better as compare with available work and it can also be seen that proposed work time to detect tumor is less as compare with available work. Figure shown below is the GUI developed with the help of MATLAB.



Figure 9: GUI Developed for user interfacing for tumor detection in MRI image

5. CONCLUSION

Proposed procedure for detection of brain tumor from MRI images and MATLAB is been used for the design the proposed system, to make the design user friendly a GUI is been developed, the results found are very good in terms of accuracy and time delay. SRI24 (provided by International Medical Union) database is been used for matching test MRI image to ensure that it is not matched with any normal brain MRI image,. The major

application of the proposed design is to recognize the tumor out of multiple MRI images taken for any patient, for accurate detection and exact dimension of tumor is highly requires in field of medical. Hence the only application of proposed design is to identify Tumor in MRI images of brain. In near future the proposed work can be used for recognition of other body parts MRI and it and be used for detection of other disease, as the proposed work is successfully recognizing circulation of blood.

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