

Semi Automated Tumor Segmentation from MRI Images Using Local Statistics Based Adaptive Region Growing

Samiksha Chugh and S. Mahesh Anand

Abstract—Segmentation of anatomical regions of a brain is the fundamental problem in pattern recognition in medical images. It is very challenging due to ambiguity in understanding tumor boundary. Lots of work has been reported, showing various level of accuracy in segmenting the boundary of an anatomy or tumor. The motivation for our work came from the fact of accurate delineation of the contour of a tumor from Magnetic Resonance Images (MRI) with high level of precision. We have developed an algorithm by modifying the existing Region Growing (RG) algorithm, by considering the local statistics of the pixels along with Pixel Run Length (PRL) parameter. PRL based Adaptive Region Growing (ARG) algorithm gave satisfactory result with good level of accuracy. The segmented tumor is quantified by area, perimeter and form factor, which in turn helps us to classify the different shape and contour of tumor. This algorithm is a semi-automated method and it will help the radiologist and neurologist to perform the diagnosis more effectively and accurately.

Index Terms—Adaptive region growing, MRI, pixel run length, region growing, tumor

I. INTRODUCTION

A tumor is a mass of tissue that grows out of control of the normal forces that regulates growth. According to the recent report on cancer statistics [1], [2] “In terms of prognosis, cancers of the brain rate amongst the five lowest relative survival rates for males and fourth lowest for females.” Though new cases for brain tumor are comparatively low, brain tumor has a higher mortality rate when compared to more common types of cancer. This underlines the need of accurate prognosis of brain tumor in health care industry. The common diagnosis of benign brain tumor is done by Magnetic Resonance Imaging (MRI). Radiologist performs manual delineation of tumor region and imparts the details to neurologist. But this work is tedious due to the huge volume of images and it consumes more time and energy.

Accurate estimation of tumor size is important for clinical reasons, like treatment planning and various other therapies.

Although maximum tumor diameter is widely used as an indication of tumor size, it may not reflect a proper assessment of this tumor attribute because of the irregularity in shape of tumors [3], [4]. Tumor volume, on the other hand, may be an appropriate representation of tumor size. One way

to obtain an estimate of tumor volume is via segmentation. Such schemes implicitly acquire the tumor volume by extracting the tumor surface.

As mentioned above manual segmentation is time consuming and has accuracy issues. Automated segmentation will solve this problem and opened scope for medical expert system professionals. Automating this process is challenging due to the high diversity in appearance of tumor tissue, among different patients and in many cases similarity of pixel intensity exists between normal and tumor tissue.

There are numerous segmentation procedures which are currently in usage by many commercially available image processing products. Most of the algorithm doesn't give the accurate boundary and precise delineation, these are level set segmentation, watershed segmentation, fuzzy connectedness, extended graph shift algorithm etc. A main disadvantage of such algorithms is their dependency on tumor and non-tumor probability density function. Usually hand parametric estimation of probability functions may not provide sufficient accuracy as tumors generally do not have uniform intensities. Also these algorithms involve much of user interaction. The additional complexities of estimation due to such algorithms motivate us to use density independent schemes.

The algorithm proposed in this paper overcomes the above said problems by modifying existing RG technique [5]. The RG technique is encouraged as it showed excellent results in light abnormalities (Min Gray level 115-186, Max Gray Level 161-216, and Mean Gray Level 139-199). Region Growing Technique requires minimum user interaction and less computation time. The user has to select a random seed point within the tumor suspect region and the algorithm takes care of rest of all computation and finally it gives a precise delineation of contour of tumor. Pixel Run Length (PRL) based ARG is implemented in two stages. First stage gives the rough estimation of tumor region using which some calculations are been made. These calculations are used in stage 2 which finally gives the precise boundary of tumor region as its output as explained in later sections.

II. METHODOLOGY

The input image used for the algorithm is shown in Fig.1. The qualitative assessment of the image shows that there is a difference of gray level intensities, inside and outside the tumor region.

This intensity difference is used in developing algorithm for RG technique. RG technique is the one in which one pixel is chosen randomly inside tumor region. This pixel is called as seed point [6]. Then the region start growing from seed point in all directions till the intensity of the pixels is approximately same as average intensity of tumor region.

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Usually boundary pixels are of high intensity so the region stops growing at the boundary pixels. There may be few pixels inside tumor region where intensity is same as intensity outside tumor region. PRL-ARG algorithm should be robust to all such unfavorable conditions.

Few pixels inside tumor region as explained above may have intensity same as boundary pixel. In spite of the fact that such pixels are part of tumor region, those pixels are not connected in the extracted region, as after encountering high intensity pixel, the simple RG technique stops growing in that direction. To overcome this, ARG technique is used to extract the tumor region accurately. The algorithm developed here, is independent of selection of seed point. Seed point can be selected anywhere in tumor region. ARG algorithm works in two stages.

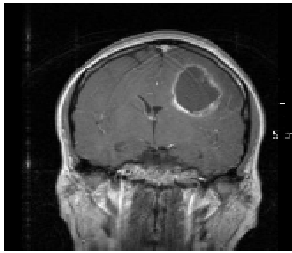


Fig. 1. Input MRI coronal slice 1

A. Stage 1

Unlike simple RG technique, ARG algorithm start growing the seed point in all directions until following conditions are not satisfied. In spite of considering intensity of individual pixels for calculation, all 8 neighbors of individual pixels are considered and average intensity is calculated. Region grows by moving pixel by pixel by comparing the average intensity of all 9 pixels, that is 8 neighbor pixels and the pixel which is in focus, is calculated and this average intensity is considered as intensity of the pixel which is in focus throughout the algorithm. The combination of 9 pixels explained above is called as mask. It is observed that mean value difference of the mask of two adjacent pixels is not more than 5 units. The condition in which the mean value difference of mask of two adjacent pixels, when exceeded the value 5 then, that is the indication that boundary pixel is reached and algorithm automatically stops growing further. Also it is estimated that Standard Deviation (SD) difference of the mask of two adjacent pixels is not more than 3.8. Hence, if this difference is more than 3.8, that indicates the boundary pixel has reached. These two preliminary conditions form basis for the stage 1 level of tumor extraction with rough estimation. Minimum and maximum intensity of the rough estimated tumor region are calculated and passed to the second stage of the algorithm.

B. Stage 2

The second stage of the algorithm starts working with the same seed point selected by the user. The region starts growing in all directions with new constraints. That is, first, algorithm calculates mean and standard deviation in same way as it calculated in stage 1.

If difference between mean and standard deviation of two adjacent pixels (mask of adjacent pixels) is less than the values specified in stage 1 then that pixel is included in tumor region. Otherwise maximum and minimum intensity

calculated in stage 1 is used to identify that the abnormality in mean and standard deviation is due to noise or it is basically the fact that boundary of tumor region is reached [7], [8]. A counter is set for next 8 pixels in same direction (This 8 is called pixel run length.). If any pixel having intensity less than minimum intensity obtained in stage 1 or intensity more than maximum intensity obtained in stage 1 is encountered, then counter is incremented by 1. If count value is more then it means that majority of pixels belong to non tumor region so further growth in that direction is stopped. If count value is low then it means that, that particular pixel belong to tumor region and had high intensity due to noise. That pixel is included in tumor region and algorithm keeps growing in that direction. The inclusion of additional constraint pixel run length statistics in stage 2 increases the efficiency of algorithm and gives precise boundary as its output.

III. IMPLEMENTATION

The algorithm is implemented in Matlab in two stage execution. The user has to randomly select any seed point in the tumor suspect region. This seed point is passed to first level approximate estimation of tumor region. The first level stage one implementation is summarized as follows,

Phase1 ()

Input: MRI Image

begin

seedX and seedY are assigned.

Its 8 neighbors,

(seedX-1,seedY), (seedX+1,seedY),

(seedX,seedY-1), (seedX,seedY+1),

(seedX-1,seedY-1), (seedX+1,seedY-1),

(seedX-1,seedY+1), (seedX+1,seedY+1)

are initialized.

Mean intensity mean0 and standard deviation std0 are calculated for 9 pixels.

mean2= mean0;

std2 = std0;

for i=1 to 60, **for** j=1 to 60

A1=seedX + i; B1=seedY + j;

Mean1 and std1 for 8 neighbors of

(A1, B1) were calculated

If (mean1-mean2) < |5| and (std1-std2) < |3.8|

then the region is grown.

Else same operation is performed for next 8

pixels

End

End

Repeat for all directions in similar way.

Maximum and minimum intensity from tumor region obtained in stage 1 are assigned to variables max, min.

End

Later it is passed to stage 2 calculations.

The second level estimation performs the accurate boundary by eliminating the noisy pixel and non tumor tissue regions. The second level estimation is summarized as follows,

Phase2()

Input: Output of phase1()

Output: Segmented tumor region

Begin

The same seed point seedX, and seedY is continued in stage 2.

Its 8 neighbors
(seedX-1,seedY),(seedX+1,seedY),
(seedX,seedY-1),(seedX,seedY+1),
(seedX-1,seedY-1),(seedX+1,seedY-1),
(seedX-1,seedY+1),(seedX+1,seedY+1)
are initialized.

Mean intensity mean0 and standard deviation std0 are calculated for 9 pixels.

mean2= mean0;
std2 = std0;
for i=1 to 60, **for** j=1 to 60
A1=seedX + i; B1=seedY +j;
Mean1 and std1 for 8 neighbors of (A1, B1) were calculated

If (mean1-mean2) < |5| and (std1-std2) < |3.8|
then the region is grown.

Else

count=0,

for runs=1 to 8, b1=seedY ;

if (seedX, b1+runs)> max

Then count=count +1

End

End

if count>=5

thenAlgorithm stops growing further in the same direction i and j loops are stopped.

End

End

End

Repeat for all directions in similar way.

Tumor region with precise boundary is obtained.

The advantage of this two stage computation is that even if any pixel has high intensity it is balanced by other pixels of comparatively lower intensities hence region growing doesn't stop at abnormal pixels inside tumor region. Also there is a possibility that we may get a group of around 15 pixels (in continuous) inside tumor region which have intensity higher than tumor intensity. So in that case, mean value and variance difference for the pixels will also be higher. Hence both conditions will fail. In certain situation, there are group of pixels after non tumor pixels, we may have tumor region which is eliminated in simple region growing algorithm. To avoid that we include one more condition regarding pixel run length , that is if both mean and variance condition fails then we keep a counter value and increment it. If counter value is high we stop growing in that direction else we do not stop and continue calculation in that direction.

IV. EXPERIMENTAL RESULTS

The results are shown in two stages, according to the algorithm implementation. Fig. 2 shows the coronal MRI

slice 1, with seed point coordinates selected at (115, 225). Fig.3 shows the segmented tumor with RG technique. We can observe lots of missing pixels inside the region and also the contour is not accurate. Whereas Fig.5 depict the accurate delineation of tumor by PRL-ARG algorithm. The intermediate stage of the algorithm is shown in Fig.4, which is the approximate estimate of tumor region.

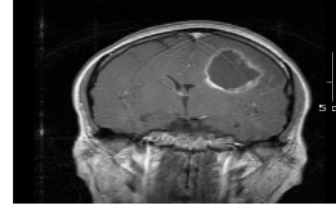


Fig. 2. MRI Coronal Slice

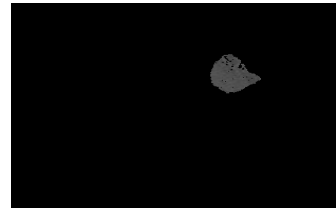


Fig. 3. Segmented Tumor by RG Algorithm

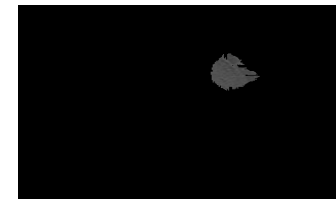


Fig. 4. Stage 1 output of PRL-ARG algorithm

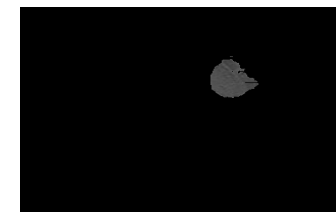


Fig. 5. Stage 2 output of PRL-ARG algorithm

The algorithm is tested with another coronal MRI slice. The seed point coordinates for the slice 2 is selected at (108, 214). Fig. 7 shows the segmented tumor with by simple RG technique, which has missing pixels inside the tumor region and also the boundary is not precise. The final snap shot of the PRL-ARG algorithm is shown in Fig.9 which indicates the accurate boundary and better estimate of tumor region.

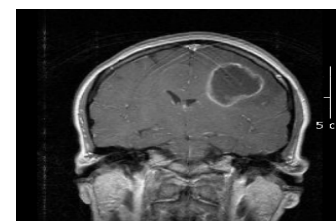


Fig. 6. Coronal MRI Slice 2



Fig. 7. Segmented Tumor by RG algorithm



Fig. 8. Stage 1 output of PRL-ARG algorithm

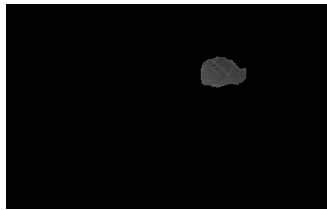


Fig. 9. Stage 2 output of PRL-ARG algorithm

Qualitative analysis of segmented tumor was cross validated with manual procedure done by a radiologist. In addition to qualitative analysis, a quantitative description of tumor is done with area, perimeter and form factor calculation. Form factor is a feature used for determining circularity of the extracted tumor. These features can be used for the classification of different shapes of tumor. Equation 1 shows the formula for measurement of form factor from area and perimeter:

$$Formfactor = \frac{4 * \Pi * Area}{Perimeter^2} \quad (1)$$

where, Area represents the number of pixels occupying the segmented tumor region and perimeter is a measurement of number of pixels along the boundary of the segmented tumor region.

A. 3-Dimensional View of the Results

The four Coronal MRI Slices tested are:

Fig.10. shown above is the 3D view of the brain image slices. Every image is segmented using the algorithm explained in this paper. Approximately 27 copies of segmented tumor are generated by duplicating these four brain images. The resultant tumor image can be viewed in 3-dimensional as shown in fig. 11. This 3D view will give a more visual insight into the shape and structure of tumor for the neurologist, before they plan for surgical procedures

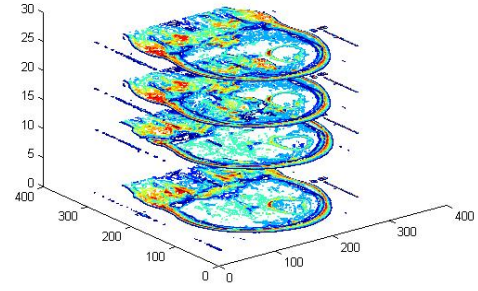


Fig. 10. 3-Dimensional view of segmented brain tumor

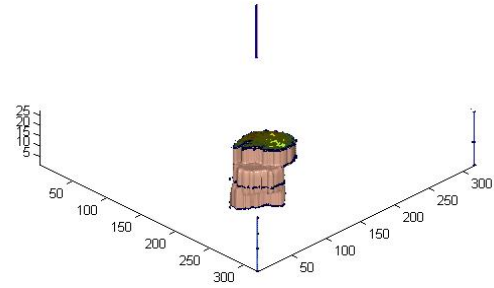


Fig. 11 3-Dimensional view of the tumor region found in MRI coronal slices

B. Quantitative Analysis

Table I shows the statistical parameters calculated from the segmented tumor region and it can be used as classification parameter to classify different size and types of tumor.

TABLE I. QUANTITATIVE ANALYSIS OF SEGMENTED TUMOR

Input Image	Statistics	RG Technique	PRG-ARL Technique
MRI Coronal Slice 1	Area (pixels)	1764	1754
	Perimeter (pixels)	171	197
	Formfactor	0.7577	0.5677
MRI Coronal Slice 2	Area (pixels)	1602	1486
	Perimeter (pixels)	167	190
	Formfactor	0.7215	0.52

V. CONCLUSION

In this paper we presented semi-automated tumor segmentation from MRI images using the modified RG technique with PRL local statistics approach. The results obtained from PRL-ARG technique shows that it outperforms simple RG technique. Moreover the qualitative and quantitative studies confirm the accuracy of boundary delineation of tumor and homogeneity of the extracted tumor is appreciable. This work can be further extended to train a neural network algorithm for complete automation of medical expert system. This expert system will improve the quality of healthcare by improving the existing diagnosis procedure in radiology.

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