

3D Morphological Tumor Analysis Based on Magnetic Resonance Images

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Abstract

In this paper, the Glow Cut Algorithm will be applied on MRI data retrieved in order to learn more about tumors morphologically analyze them. In the proposed Glow Cut Algorithm, the tumor area will be analyzed by applying the color threshold criteria. Next, the needed tumor area will be selected, beginning from the outer layer to the inner. The tumor area is analyzed from the area that has the largest amount of pixel size. After dissecting the tumor area, the tumor areas will be calculated based on the four types of morphological coordinates: AT, ATT, ADT, and TN. Using and applying the method described on the brain tumor of a thirty year old human male, the following comparative experiments have been conducted. In order to demonstrate the effectiveness of the proposed scheme, a 3D printer is used to extract the morphology of the tumor. Results have shown that using the four morphological methods and automatic methods have made little difference, showing only an average of a 3% error rate, which enables this paper to suggest a more efficient method than the current manual method.

Keywords: MRI Slice Image, Morphologically Analysis, Tumor, Glow Cut Algorithm, 3D printer

INTRODUCTION

Magnetic Resonance Imaging, or better known as MRI, provides with detailed information about tumors, such as its structure, size, and influence during medical treatment. As there have been many advances in MRI technology and its uses in structurally analyzing tumors, there have also been many tools to aid its efficiency in analysis.[1]

The first step in analyzing tumors was efficiently separating healthy cells from those that were cancerous. Examples of such a step currently would be where a medical expert would separate tumors by marking each territory manually, one by one. However, even for one tumor, there are usually hundreds of MRI photos that medical experts have to analyze, which is not only time consuming but also largely inefficient. To solve this problem, there have been various kinds of solutions proposed, to differentiate healthy and cancerous cells automatically. Such examples of automatic differentiation are the double threshold criteria, the morphological operator, the median filter, and the Gaussian filter. These ideas are easy to establish, and they have performed well in gathering data. However, there is a problem: because of the morphological calculations involved, there is a possibility that separation between the tumors might not be accurate. This will be best fixed if the filter parameter was chosen with trial and error [2].

Furthermore, the filter's parameter should be selected again for a new data set. Other ways to fix this problem would be to use the analysis of the intensity histograms, incorporated with the use of our calculated threshold and morphological values [3,4].

In this paper, morphological calculations will be used to simply differentiate tumors and healthy body cells, using the Glow Cut method. First part of the procedure will begin with differentiating between healthy and diseased cells and then calculating the morphological coordinates involved, which will then allow a detailed analysis of the proliferation and structure of the tumor. We have done this by using the four indices, AT, ATT, ADT, and TN. These indices are fundamentally retrieved by using the 3 dimensional space involved. To calculate the AT, the whole area and actual space of the tumor have been depicted on the 3 dimensional mesh, to calculate the space took in the mesh itself. To calculate the volume in the mesh, the VTK's (Visualization Toolkit) [5,6] library functions have been used, and of those numerous functions, the function designed specifically to calculate the volume in mesh have been exercised. The index AT have been used to calculate the 3 dimensional mesh's average thickness, and the index ATT have been used to estimate the average thickness in 3 dimension by [7] manipulating the thickness of the sphere of tumor area. Joining the point of the sphere means that the particular point has been defined as the center of the sphere that will encompass the tumor to the largest extent, without overstepping the boundaries previously selected. The thickness of each point may be set by another sphere junction so that it will only be updated when the newly selected points are thicker than before. ADT and ATT will also use the sphere junction as well. For ATT, the sphere junction has been selected, based on the inner points within the tumor. As for ADT, the sphere junction will be applied in all of the areas, while basing only on the points within the empty areas. These so called 'empty areas' can be found by contrasting the tumor areas.

The TN can be found by using ATT and ADT incorporated with equations. The proposed method will be based on how well the tumor and healthy cells are separated, compared to the conventional manual use of separation. Furthermore, the proposed method will be further validated by printing out the extracted region of the tumor with the 3D printer.

Of the proposed dividing methods, as well as the manual dividing methods, the four representable coordinates, AT, ATT, ADT, and TN have been compared. Results have shown that the four coordinates have shown an average of 3% or less of error, and of those, AT has shown the biggest percentage of

error. With this amount of error difference, it has been concluded through our analyses that using this method instead of the cumbersome manual method would be efficient, as well as effortless.

2. Using Glow Cut Method to Divide Between Healthy Cells and Tumor Cells

The proposed algorithm will be using images of the tumor that is shown in Figure 1, as can be seen below. Figure 1 (a) shows arecreated model of the tumor image. Figure 1 (b) depicts a vertical slice image.

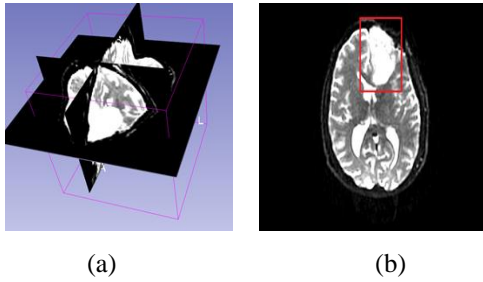


Figure 1. An example of an MRI scan

(a)Recreated 3 dimensional model (b)Vertical slice

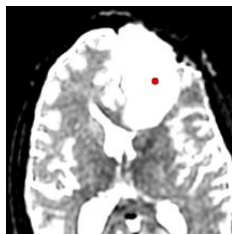
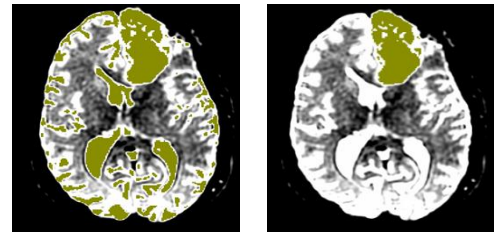


Figure 2. Selecting the area for analysis

When analyzing the tumor’s indices, it is normally done by dividing the length evenly, which is 2 dimensionally based. In Figure 2(a), we can see the divided areas that will be further discussed throughout this paper. In this paper, the areas that will be further studied will be divided in the z axis direction, by 2mm, centering the starting point at the point of origin in the 3 dimensional axes. Slices have been set to automatically designate the slices that are 2mm and below.

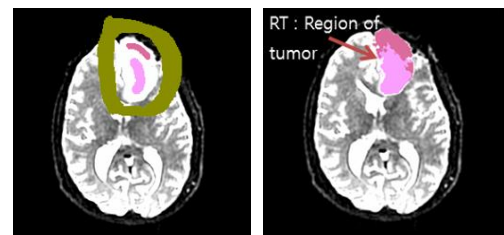
In the proposed algorithm, the particular tumor area will be selected by using the given threshold incorporated with binarization. In this paper’s images, the threshold has been selected as 330. In Figure 3, the original tumor area, before extraction, can be seen. We can see the result of binarization applied to Figure 2(a) in Figure 3(a). If the proposed threshold is applied without the extraction of the tumor area, noise can occur in the image. Noisy images have been excluded by saving the larger areas and deleting the rest. In Figure 3(b), the noise excluded image can be seen. Figure 2 shows the 2 dimensional MRI slice image, morphologically analyzing the tumor according to the Glow Cut Algorithm.



(a) (b)

Figure 3. Extraction of noise and binarization on sliced image

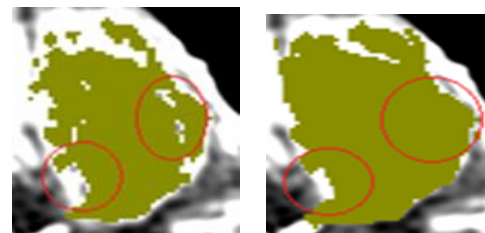
(a)Result of binarization (b)Result of noise extraction



(a) (b)

Figure 4. Tumor and the periphery of the tumor

(a)Area of Tumor (b)Region of tumor



(a) (b)

Figure 5. Example of a normally applied filling

(a)Sliced image before applied filing

(b)Sliced image after applied filing

Separating the healthy cells from the tumors cells after determining the tumor area is critical. In this paper, as can be seen in Figure 4, the range will be selected from the direction of the outer periphery of the tumor to the inner part of the tumor. The healthy and unhealthy cells, based on the coordinates of the K Pixel will be differentiated. Based on this separation, the average pixel value of the RT area (area of tumor) can be found. The largest host can be set as the value for center of the separation between tumors. Comparatively, healthy body cells are much bigger in pixels and high in density compared to tumors. This is the reason why selecting the RT area’s average pixel value as the separating standard for healthy and tumor infected cells can be justified.

The RT area can be found by filling the insides of the RT tumor, and then by applying the dilation. The RT area is the area extracted when K^{th} dilation is applied. The calculations

needed to fill the inner area can be found by the 3 dimensional hole-filling algorithm. In Figure 5 (a), the state before the 3 dimensionally mended hole can be seen, whereas in Figure 5 (b), the sliced image of the hole after the filling can be seen.

However, in cases where tumors have crevices, as can be seen in example Figure 6(a), the 3 dimensionally hole-filling methods will not be properly applied. Such instances can be seen in Figure 6(b). This paper will thus focus on repairing methods that fraudulently attempted to fill tumors with crevice. As can be seen, in Figure 7 (a), tumors with separated crevices can be repaired as in Figure 7(b). If the erosion is applied afterwards, the size comes back to normal, but with the separated cracks mended.

The standard thickness has been determined to be 1/8 of the tumor. The lower value has been chosen according to the vertical and horizontal thickness of the tumor. By setting the dilation thickness as N, crevices that are less than 2N can be filled. It is possible to mend the gap if the dilation thicknesses are set as 1/8 of the tumor. However, in special cases, it is also possible that the crevices are much bigger than formerly predicted, so the user must incorporate both the erosion and the dilation thicknesses in such cases.

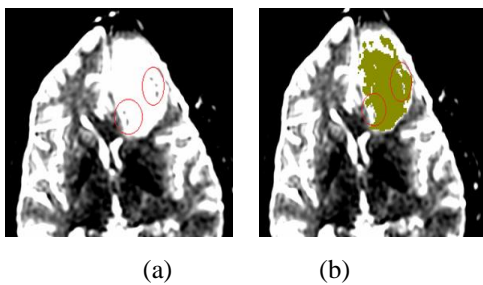


Figure 6. An example of filling the inside of tumors with crevices

(a)Image of tumors with crevices (b)Result of applying 3 Dimensional hole-filling method

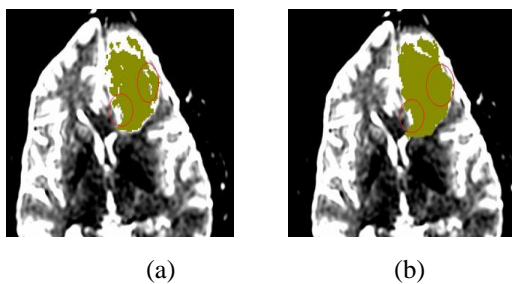


Figure 7. Applying filling method after dilation

(a)Original image of filling (b)Image of filling after dilation

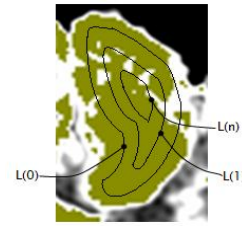


Figure 8. Lines with the same difference from the periphery

After filling the tumor area, the next step is to search the differentiating line between tumors. To find the possible tumor area RT, the value of K will be steadily increased from 1 to find the average of the pixel value of the input image. To increase the task speed and efficiency, the tasks will be separated. In the first step, lines that are the same distance from the periphery will be found, much like a contour line. Second, using the values of the pixels and the summation of the pixels that were found formerly, RT area found was increased from a K value from 1. Thus the average pixel value of the input image could be estimated.

A contour line was selected on the premises that it is the same distance from the periphery. As can be seen in Figure 8, the outermost separation line was set as L(0), and the line just inside of it as L(1). Based on this pattern, the line that is just inside of L(n) was then set as L(n-1) continuously. The tumor's thickness is limited to the ratio of the overall tumor's thickness; finding the innermost lines of the tumor is not particularly emphasized. In this paper, set values will be found until 1/6 of the horizontal direction's size or vertical direction's size, is reached. Directionality will be selected depending on the smaller value. In Figure 8, where the image's inner side is filled, the vertical direction is smaller than the horizontal direction, so it was determined that lines spanning 1/6 of the vertical direction were selected, ranging from L(0) to L(54) – a total of 55 lines. In this paper, the lines L(i) (0 = 1,2, ..., n) have been found by morphologically analyzing dilation MRI tumors through the Glow Cut Method.

L(0) was first found, which can be found by applying erosion in tumors. Tumors such as those depicted in Figure 8's 1 pixel are filled inside. Here, erosion method will be applied to examine the different kinds of pixels to be extracted. By applying 1 pixel erosion on the already erosion applied image, the periphery 1 pixel can be easily extracted. Applying this same method by examining which pixels have been extracted, the L(1) can be found. By applying this on the recently found line L(i), the appropriate image's pixel numbers and the summation of pixel values can be calculated.

In the second step, the K value will be increased from 1 to find the possible tumor area, the RT Area and the region's average pixel value. This can be found by incorporating the usage of the line's input image pixel numbers and the summation of the pixel values. Let the result of the first step be as so the input image pixel number will be set as N(i), and the summation of the pixel values will be set as S(i). The average summation of pixel values when K is m in the RT Area can be found when S in S(i) and N in N(i) is found separately within the range of L(0) to L(n-1).

3. Extracting the coordinates of the morphologically analyzed tumor

The tumor's four morphological coordinates AT, ATT, ADT, TN are extracted. These coordinates are extracted in a 3 dimensional space, with the standard set for 3 dimensional tumor data. Figure 9 shows the 3D shape of tumor extracted on the Figure 2's whole area analysis.

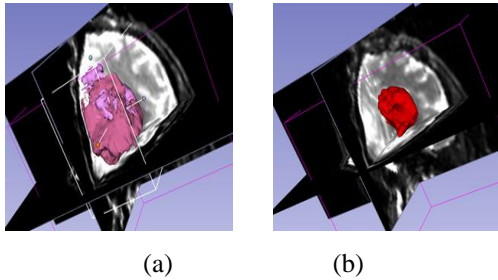


Figure 9. The result of tumor extraction on Figure 2's whole area analysis

(a)Tumor and health cell area from Figure 2's whole area analysis (b)Tumor extraction

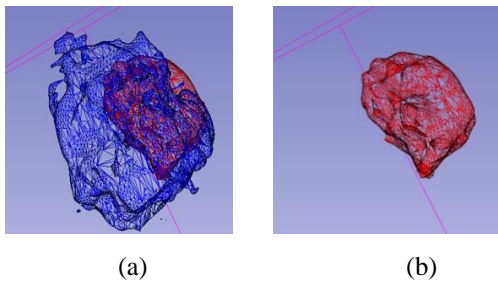


Figure 10. Expression of VTK Mesh

(a)The total area of the divide tumor(mesh data)
 (b)Tumor area extracted from Figure 10.(a)

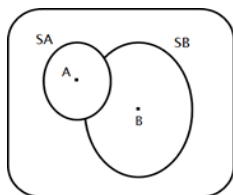


Figure 11. Spherical junction of the rectangular shape tumor

To calculate AT, the total space that the actual and virtual tumor possesses in the recreated 3 dimensional mesh plane must be estimated. In short, the volume taken up by the mesh must be calculated. Figure 10 represents the rendered result of the total area and the actual area converted into mesh form by using VTK. The total area that the tumor possesses can be found by filling the inside of the tumor area that is shown in Figure 8, as well as by applying the dilation in tumor's thickness slices. The mesh's volume can be calculated by

using the 3 dimensional mesh volume calculating function of VTK (Visualization Toolkit)'s library of functions.

The index ATT is the average thickness of the tumor as the value increases, the stronger the tumor is. The tumor's thickness is not even and varies depending on the location of the tumor, so finding the average thickness of the tumor is essential. In this paper, the tumor will be found by basing the tumor's area in 3 dimensional space, and using the thickness by the adjoining sphere [7] can be found. Figure 11 shows the cross section of the junctional sphere. When the rectangular shape of the tumor area is set as the cross section, of the tumor, the largest sphere that does not go over the peripheral lines can be set as the SA (Sphere A). This method can be applied to point B as well, rendering the result of SB (Sphere B). In reference [7], it can be seen that the thickness of the point is defined by the largest sphere's diameter. Thus, as can be seen in Figure 11, Point A not only applies to SA, but also to SB as well. As SB's diameter is larger, in Point A's case, the thickness is set as SB. This paper performed the sphere junction by collecting each tumor area's points, and updated the thickness by analyzing each of the points found inside of the sphere. The point's thickness can be set by the other joints of spheres, so presently when the new sphere junction is thicker than the set thickness, the Glow Cut Algorithm will instead be carried out to morphologically analyze the tumor.

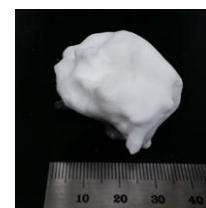
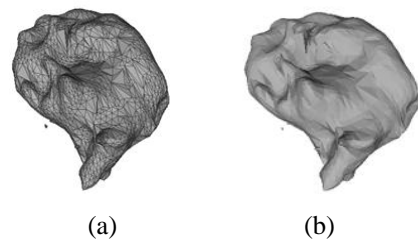


Figure 12. New values are updated for gaps of tumors.

(a)Mesh data of tumor (b)Surface data of tumor
 (c) Printing out of tumor region with 3D printer

The index ADT represents the average distance between tumors. Thus, the index foretells whether the tumors are set in a tight, compact formation or not. A smaller value correlates with a stronger tumor. ADT, as well as ATT, applies the sphere joint. To find ATT, the sphere junction was applied to the inner points of the tumor, but as for ADT, the sphere junction will only be applied to the empty areas out of the total area of the tumor. This can be found by inverting the empty area with the total area that the tumor possesses. The

meshed result of the tumor's empty area of Figure 10 can be seen in Figure 12. Index TN shows how much tumor is needed to pass TN's unit length in this paper. The proposed scheme is further validated by printing out the tumor region with 3D printer. Figure 12(c) shows the photograph of 3D printing out of the tumor region.

EXPERIMENT RESULTS

This paper has proposed methods to automatically discover ways to separate healthy and tumorous cells with MRI Imaging and to find the four indices based on the separated tumors. The paper has also compared the proposed automatic separation method with the manual method of separating. This comparison was done on a human male in his thirties afflicted with cancer. The 3 dimensional tumor data have been extracted through the MRI DICOM, and through the dividing processes of the Glow Cut Method and the manual method to extract and compare the four representative indices of a tumor's morphological analysis, AT, ATT, ADT., and TN. All of these tumors have been scanned with 1024 slices, and 291 slices have been selected to be analyzed in a 3 dimensional space with the z axis as the standard. The manual method has been carried out single handedly, and the separation has been done by drawing the inner surface of the tumor. The binarization threshold has been used for the same values for the total tumor, and the values can be changed based on the MRI equipment and the filmed conditions, so special care was taken to examine and determined the scanned images.

Table 1 portrays the manual and automatic method, and the four indices values based on the divided tumor. Basing on the manual diving method, the difference in the two values can be seen, as well as the error percentage. All indices have been, on average, to show less than 3% of error rates, and the AT have been the largest in error percentage. With this amount of error, it is perfectly plausible to use the automatic, rather than the manual method of division. Figure 14 shows the contour shapes for tumor region. The contour shapes show that the indices calculation of Table 1 and the tumor's state match each other.

Table 1. Calculation results of the tumor

No.	AT			
	Manual (%)	Glow Cut Method (%)	Deviation (%)	Error rate (%)
1	39.1	38.9	0.2	0.51
2	55.8	55.4	0.4	0.71
Average Error rate				0.61

(a) AT

No.	ATT			
	Manual (um)	Glow Cut Method (um)	Deviation (um)	Error rate (%)
1	93.7	93	0.7	0.74
2	120.3	118	2.3	1.91
Average Error rate				1.33

(b)ATT

No.	ADT			
	Manual (um)	Glow Cut Method (um)	Deviation (um)	Error rate (%)
1	185.6	185.7	-0.1	0.05
2	147	147.2	-0.1	0.13
Average Error rate				0.09

(c)ADT

No.	TN			
	Manual (um ⁻¹)	Glow Cut Method (um ⁻¹)	Deviation (um ⁻¹)	Error rate (%)
1	2.97	2.87	0.1	3.36
2	3.13	3.06	0.07	2.23
Average Error rate				2.79

(d)TN

CONCLUSION

This paper has proposed a new way of analyzing MRI data by implementing the Glow Cut Algorithm on tumors detected. This algorithm, which combines the Glow Cutted tumor and the manually divided tumor with the four morphological indices, AT, ATT, ADT, and TN, along with the jointed sphere from VTK algorithm, calculates the data in a 3 dimensional space. In this paper, the threshold of the tumor has been selected by the user, and as the values can differ based on the crevices within the tumors, a parameter variable must be selected. To decrease the parametric variable, ways to calculate the threshold value or automatic methods to find the distance between the crevices in tumors must be further investigated in the future. The proposed method and the manual methods have shown minimal difference; the research conducted in the paper suggests that the paper's proposed method decreases the manual burden of calculations while also increasing efficiency.

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