

Tumor Volume Determination Technique Using Pixel Filling and Discrete Integral Function

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Abstract—The subject of tumor has generated lots of interest from the medical point of view and recently from engineering/research perspective owing to advancement in medical equipment and increased computerization in many areas including medical field. This paper discusses a post-segmentation tumor volume determination technique that employs mainly pixel filling, and the application of discrete integral function to determine tumor volume. The prior steps taken involve finding pixel area resolution, image field of view (FOV), then FFT-Based interpolation to achieve smaller decimation of tumor area, and finally the use of discrete integral function (DIF) to accurately determine tumor volume. The result of the work will enhance the field of oncology in general, and image guided surgery (IGS) in particular.

Index Terms—pixel filling, tumor quantification, FFT-based interpolation, discrete integral function

I. INTRODUCTION

Image guided surgery (IGS) is the use of radiological images for medical diagnosis, surgical planning and intervention, and post-operation monitoring of patients. The above shows wide application of IGS in medical field largely because of its advantages [1]-[3]. Meanwhile, IGS is by far more applicable in areas requiring minimal invasiveness [4], [5] like neurosurgery because of the difficulty in getting into target site without disturbing adjacent structures, and it offers the ability to plan and practice surgical intervention before actual surgical operation and then tailor the surgical intervention in-line with the earlier plan and practice which could be shown in the operation theatre (OT) during operation [6].

Tumor or neoplasm is technically defined as abnormal tissue growth that is different from surrounding tissues in its structure [7], and which if unchecked may spread within the body anatomy, and are responsible for a range of diseases. The central nervous system tumor represents only two percent (2%) of all new cases in the United State [8], but they are the third leading cause of cancer related death in the people of less than 60 years of age and that over 95% of tumor recurrence is close to the primary site of initial resection [9]. The researchers in [9] stated further that in year 2002 alone, over seven thousand five hundred (7,500) deaths were caused by neurological diseases (in which brain tumor and metastasis are in the top) in Malaysia. Furthermore, the appalling ratio of one (1) neurosurgeon to twenty million (20,000,000) individuals in less developed countries (LDCs) imply that the proficiency of the surgeon(s) and the team alone cannot guarantee success in surgical intervention, therefore, the need to provide a non-human aid in computation form is crucial. According to world health organization (WHO), any form of surgical intervention involves lots of decisive steps with likelihood of failure and possible harm to patients. Furthermore, the world health organization (WHO) admitted the fact that in surgical intervention, “even the most straight forward procedures involve dozens of critical steps, each with an opportunity for failure and the potential for injury to patients”, and “Assuming a 3% perioperative adverse event rate and a 0.5% mortality rate globally, almost seven million (7,000,000) surgical patients would suffer significant complications each year, one million (1,000,000) of whom would die during or immediately after surgery” [10].

This paper approached these problems from the point of view that, should there be adequate knowledge of tumor

volume by the surgical team, it would be helpful in deciding incision size, and equally guide tumor resection during surgical intervention. Therefore, following careful segmentation of region of interest (ROI) from each of the affected slices as reported in Ref. [11], a tumor quantification technique that is very accurate on implementation on patients' images slice is applied and presented in this paper. Fig. 1(a) and Fig. 1(b) pictorially show previous steps taken at isolating (segmenting) tumor from adjacent non-tumorous tissues, and then the steps leading to tumor volume determination technique begin.

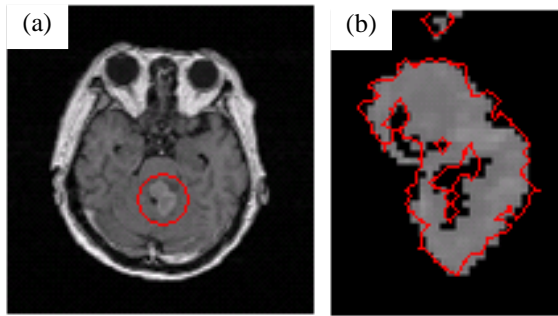


Figure 1. (a) MR axial slice with ROI encircled, and (b) Complete isolation of Tumor from MRI slice.

II. METHODOLOGY

Apart from the steps taken to arrive at accurate tumor volume determination as designated in the subheadings A to D in this section, a prior approach of single tumor at a time was adopted at the segmentation stage whenever multiple tumor are encountered on an image slice.

A. Determining Tumor Area (TA)

Owing to the usual irregular shape of tumor, researchers in computational biomedical are constrained to apply only methods capable of actualizing the fit such as traditional Graphical method, the classic-based Iterative Spatial Sectoring (ISS) [12], and the computer-based Fractal Analysis method, the Monte Carlo method, Pixel Filling, et cetera. The Pixel Filling method is applied in this paper. The pixel filling method of determining area of irregular close 2D space is based on populating the close 2D space with pixels of known size(s), and then sum up the total size of the pixel that fully occupy the 2D close space. Hence, the way to determine tumor area (TA) is specified as in equation (1).

Given that tumor pixel is designated as tup , then the total number of tumor pixel called ttp will be the summation of all tup . The area resolution of the slice is called Ar , then the tumor area (TA) per slice is calculated from equation (1) thus:

$$TA = Ar \left(\sum_{i=1}^{ttp} tup_i \right) \quad (1)$$

More so, Ar depends on two parameters namely; slice field of view (FOV) and the matrix size, hence Ar is given in equation (2) as:

$$Ar = \frac{FOV \text{ Square}}{Matrix \text{ size}} = \frac{FOV^2}{R_T \cdot C_T} \quad (2)$$

in which R_T and C_T represent tumor matrix row and tumor matrix column respectively. Hence, equation (2) is substituted into equation (1) to determine tumor area (TA).

B. Tabulation of Tumor Area (TA) Versus Slice Thickness (ST)

Having determined TA for all patient tumor affected slices, these are then tabulated as shown in Table I. That is, tumor area (TA) per slice, and slice thickness (ST) which depends on the radiological equipment used in obtaining the image. Tumor area (TA) and slice thickness (ST) are plotted against each other in Fig. 2.

TABLE I. SLICE THICKNESS (ST) AND TUMOR AREA (TA) PER SLICE

SN	ST $\times 10^{-2}$	TA $\times 10^{-3}$
1	0	0.086
2	0.02	0.116
3	0.04	0.144
4	0.06	0.164
5	0.08	0.144
6	0.10	0.108
7	0.12	0.052

In Fig. 2, slice thickness is on the horizontal axis, while tumor area is on the vertical axis. Assuming the curve to be a plot of points, and because the plot is undefined, the area under the curve can only be estimated using any of the approximate integral methods. However, noting that approximate methods are inaccurate due to gaps between data points, steps are taken to reduce the gaps, and in this paper the use of FFT-Based Interpolation is found appropriate for that purpose.

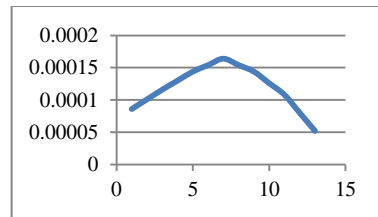


Figure 2. Plot of tumor area versus slice thickness.

C. FFT-Based Interpolation

Interpolation is desired to minimize error in finding the numerical quantity of tumor (volume) when using approximate integral function on curves such as the one represented in Fig. 2. And the choice of FFT-Based Interpolation in the paper is because it is a straight forward technique which implements interpolation by performing N-dimensional interpolation using frequency-domain-zero-stuffing.

Given that $f(X_i)$ is a series of numbers representing TAs and conceived as a time domain vector. Its frequency domain equivalent $f(X_i)$ after Fourier transform is as in equation (3).

$$f(X_i) = \sum_{x_i=0}^{N_d-1} f(x_i) e^{-j \frac{2\pi}{N_d} x_i x_i} \quad (3)$$

Furthermore, every pair of the frequency domain vector $f(X_i)$ is then zero-stuffed to produce Dx_i -point vector noted as $f(X_{zi})$, and transformed back to time

domain vector; equation (4). It should be noted that the number of zero stuffed inbetween a pair of number must be uniform throughout the vector, and it determines the number of decimated points needed inbetween the numbers. In the research work reported in this paper, single zero is stuffed inbetween a pair of number of the frequency domain vector.

$$p(x_i) = \frac{1}{N_d} \sum_{x_i=0}^{N_d-1} f(X_{zi}) e^{(-j\frac{2\pi}{N_d})x_i x_i} \quad (4)$$

Table II represents post-interpolation slice thickness and tumor area indicating that only one point (zero) is stuffed between data points (tumor area) bringing the slice thick to 1mm from 2mm. And Fig. 3 is the plot of Table II.

TABLE II. POST-INTERPOLATION SLICE THICKNESS (ST) AND TUMOR AREA (TA) PER SLICE

SN	ST $\times 10^{-2}$	TA $\times 10^{-3}$
1	0	0.086
2	0.01	0.101
3	0.02	0.116
4	0.03	0.130
5	0.04	0.144
6	0.05	0.154
7	0.06	0.164
8	0.07	0.154
9	0.08	0.144
10	0.09	0.126
11	0.10	0.108
12	0.11	0.080
13	0.12	0.052

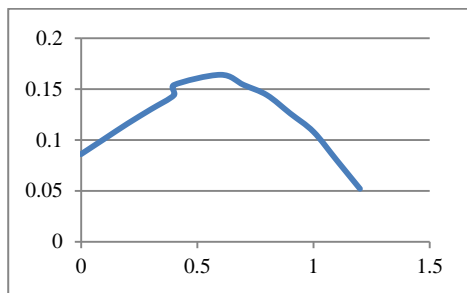


Figure 3. Post interpolation plot of tumor area versus slice thickness.

Furthermore, since the curve is made up of discrete points (discrete area in actual sense), the use of discrete integral function (DIF) which is a form of approximate integral is adopted instead of classical approximate integral subsequent to the application of FFT-Based Interpolation to refine data points.

D Determining Volume via Discrete Integral Function

The Simpson's rule of approximate integral is redeveloped into discrete integral function (DIF) of equation (5) for discrete integration. In equation (5), st , Fta , Lta , and Xa stand for ST , first TA , last TA , and the rest of TAs respectively. While n is the number of data point or TA , and the range of i from 2 to $n - 1$ is to exclude the first and last tumor areas which have been taken care of by Fta and Lta in the equation. Since Fig. 2 is not just points but areas, its integration results in tumor volume. Thence, equation (5) is

$$Volume \approx st \left(\frac{Fta + Lta}{2} + \sum_{i=2}^{n-1} X_{ai} \right) \quad (5)$$

III. DISCUSSION OF RESULT

The volume determination technique used in this paper is pivoted on the tumor area (TA) versus slice thickness plots of Fig. 2 and Fig. 3. The final Fig. used is Fig. 3 based on further refining that has been brought upon it due to the application of the FFT-Based interpolation.

Comparing Fig. 2 and Fig. 3, a slight difference is noticed around the peak (on the rising side of the curve in Fig. 3). This happened at around 5mm thickness into the tumor volume which was not observable in Fig. 2 due to the gap in slice thickness, that is, 2mm as against 1mm in Fig. 2.

Another feature of Fig. 2 and Fig. 3 is that both curve got to the peak at around the centre indicating mid-point in the tumor volume. This shows that for the particular patient, and based on the imaging elevation (axial in this case), the tumor progressed gradually suggesting the likelihood of the tumor to have started around 7mm into the tumor volume, or alternative the tumor became malignant (spreading faster) around that point.

IV. SUMMARY

Novel tumor quantification scheme that determines tumor volume using sound methodological approach is here presented. It is a post-segmentation approach that relies on careful calculation of tumor area per slice, and the use of FFT-Based interpolation to reduce gaps/errors and finally the application of DIF to determine tumor volume. This approach to tumor volume determination could also give a hint on tumor origin or point of accelerated growth.

V. CONCLUSION

The quest to find novel way of quantifying tumor is borne out of the usefulness of accurate and fast method of tumor quantification. Tumor quantification could serve two purposes of assisting surgeons to plan surgical intervention, as well as, as a secondary guidance (by knowing the quantity of tumor intended for resection) during surgical intervention. These apart, the method also increase the frontiers of the field of oncology in that tumor point of origin or tumor malignant point could be known using this approach. Finally, in spite of its accuracy and fastness, the method and its approach are altogether simple.

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