An Accurate Segmentation Method for Volumetry of Brain Tumor in 3D MRI

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ABSTRACT

Accurate volumetry of brain tumors in magnetic resonance imaging (MRI) is important for evaluating the interval changes in tumor volumes during and after treatment, and also for planning of radiation therapy. In this study, an automated volumetry method for brain tumors in MRI was developed by use of a new three-dimensional (3D) image segmentation technique. First, an expert radiologist identified the central location of a tumor. Then a volume of interest (VOI) was determined automatically. To substantially simplify tumor segmentation, we transformed the 3D image of the tumor into a two-dimensional (2D) image by use of a "spiral-scanning" technique, in which a group of radial lines originating from the center of the tumor scanned the 3D image spirally from the "north pole" to the "south pole". The voxels scanned by the radial lines provided a transformed 2D image. We employed dynamic programming to delineate an "optimal" outline of the tumor in the transformed 2D image. We then transformed the optimal outline back into 3D image space to determine the volume of the tumor. The volumetry method was trained and evaluated by use of 16 cases with 35 brain tumors. The agreement between tumor volumes provided by computer and an expert radiologist was employed as a performance metric. Our method provided relatively accurate results with a mean agreement value of 88%. Our proposed method is reliable and would be useful for the management of various brain tumors.

Keywords: brain tumor, volumetry, segmentation, MRI, dynamic programming

1. INTRODUCTION

The incidence of primary benign and malignant brain tumors is approximately 14 patients per 100,000 individuals per year in the United States[1]. The treatments such as surgical resection and radiation therapy play important roles in the management of brain tumors[2]. An accurate volumetry of brain tumors in magnetic resonance imaging (MRI) is important for evaluating the interval changes of tumor volume in post-treatment, and also for planning of radiation therapy. However, manual volumetry of brain tumors in MRI is a tedious and time-consuming task for radiologists[3]. During the past few years, several approaches investigating brain tumor volumetry based on two-dimensional (2D) in MRI have been published. Clarke et al.[4] developed a semi-automated method based on k-nearest neighbor. A medical physicist selected training data from each MRI slice. Clark et al.[5] developed an automated volumetry method by use of knowledge-based information as a guide. This method extracted intracranial region and remove normal intracranial tissue of brain by use of intensity features and anatomical shape features of brain tumors. Other approaches using level set[6], neural network[7], and fuzzy theory[8] can also be found in recent publications.

On the other hand, three-dimensional (3D) analysis method substantially improves spatial information concerning the relationships of anatomical structures and disease. Kaus et al.[9] developed a 3D segmentation method for brain tumor in MRI. This method used the iteration of statistical classification to assign labels to tissue types and also employed

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nonlinear registration to align a digital anatomic atlas to the patient data. Liu et al.[10] developed a 3D brain tumor segmentation scheme using multiple MRI protocols to gather information about different aspects of the tumor and applied fuzzy connectedness framework for the tumor segmentation. However, the main limitation of 3D brain tumor volumetry method is the long processing time and the complex computerized algorithm.

In our previous studies[11, 12]and Timp et al.'s work[13], the CT images or mammography images were converted to polar coordinate space, and dynamic programming was used for obtaining the optimal outline of lung nodules and mammographic masses. Because such segmentation methods achieved a good performance, we extended this concept to brain tumor segmentation in 3D images. First, a spherical volume of interest (VOI) was generated at the central location of a tumor and was converted to a polar coordinate system by use of a spiral-scanning technique, in which a number of radial lines originated from the center of the VOI formed a spiral scanning line that covered the VOI. The voxels scanned by the radial lines were arranged sequentially to create a transformed 2D image. The surface of a brain tumor in 3D image thus became a curve in the transformed 2D image. We employed a dynamic programming technique to find the "optimal" outline of the tumor in the transformed 2D image. To determine the volume of a tumor in 3D MRI, each edge candidate on the 2D outline of a tumor was transformed back to 3D image space. After the 2D to 3D transformation, we obtained a sparse point cloud, from which the volume of a tumor was determined by use of a new interpolation technique. Because this segmentation was performed in 2D image space, the segmentation scheme was simplified significantly.

2. MATERIALS

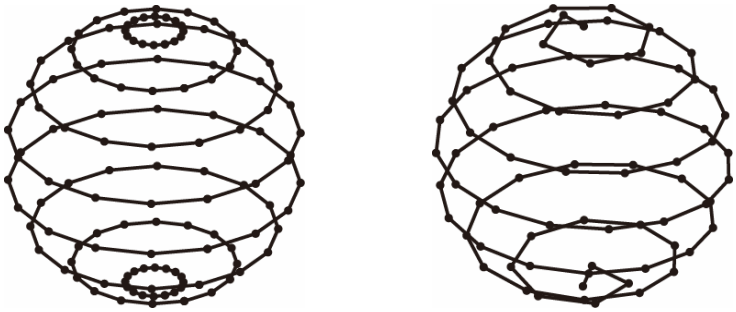
Our database includes 16 MRI scans, each of which may contain one or multiple brain tumors. The data used in this study were acquired by use of T1 weighted images with contrast-enhancement scanned with Magnetom Vision (Siemens, Germany) at the Kumamoto University Hospital, Japan during June 2005 and March 2007. The slice thickness ranged from 0.9 to 1.6 mm. Each slice had a matrix size of 256×256 pixels. The pixel size ranged from 0.8 to 0.9 mm with a 12-bit gray scale. In order to establish reference standards for evaluating the performance of the new volumetry for brain tumors, an expert radiologist delineated the outlines of tumors in MRI slices on an LCD monitor. The radiologist drawn outlines for 91 tumors in the 16 MRI scan. Because the volumetry for tiny tumors is meaningless in clinical practice, we selected 35 tumors that were 6 mm and larger to train and test our brain tumor volumetry system. The selected tumors had a mean diameter of 14 mm (range: 6 mm - 33 mm).

3. METHODS

3.1 Transformation of 3D image to 2D by use of spiral-scanning

For tumor segmentation, we first selected a spherical VOI for each tumor at the central location of a tumor identified by a radiologist. Tumor segmentation was then performed to separate the tumors from background. To simplify the segmentation significantly and to improve the segmentation accuracy, we transformed the 3D VOI to a 2D image by use of a spiral-scanning technique, so that we could segment the tumor in 2D, while still retaining the 3D information of the tumor.

We first created a number of radial lines originating from the center of the VOI. A radial line was determined by an azimuth (longitude) angle and an elevation (latitude) angle in 3D space. The range of the azimuth angle was between 0 and 2π, and that of the elevation angle was between 0 and π, where 0 and π correspond to the "north pole" and the "south pole", respectively. As shown in Fig. 1 (a), initially the azimuth and elevation angles were evenly partitioned into 2N and N sectors, respectively. With this method, the VOI was represented by the voxels on $2N^2$ radial lines. However, there are two disadvantages if we evenly partition the azimuth angles and the elevation angles. The first is the difficulty of specifying a sequential order for these radial lines. Because we planned to use dynamic programming to find an "optimal" boundary voxel on each of the radial lines, we had to overcome this disadvantage. The second disadvantage is the uneven distribution of the radial lines.



(a) (b)

Fig. 1. (a) The sample points created by evenly partitioning azimuth and elevation angles, and (b) the sample points on a spiral curve with even spatial distribution by use of spiral-scanning technique.

The key to overcome the first disadvantage was to let the elevation angle change evenly for all $2N^2$ points rather than for N circles. To further make the points evenly distributed on the sphere, we needed to determine the appropriate number of radial lines.

In this study, the curvilinear distance between two consecutive points on the equator, π / N, was used as the "standard" distance for any two adjacent points. For simplicity, we assumed that the radius of the sphere was equal to 1. When the azimuth and elevation angles were evenly partitioned into 2N and N sectors ($\alpha_k = k\pi / N$, $\beta_k = k\pi / N$), the circumference of a circle at an elevation angle β was $2\pi|\sin(\beta)|$. Thus, the number of points on the circle should be $2\pi|\sin(\beta)| / (\pi/N)$, i.e., $2N\sin(\beta)$. The total number of the points on the surface of a sphere was thus determined to be $2N\sum_{k=0}^{N}|\sin(k\pi / N)|$, which is approximately $4N^2/\pi$, when N is large enough.

Thus, we can re-sample the spiral-scanning line with $4N^2 / \pi$ "sample points" to cover a sphere evenly. Figure 1(b) shows the sample points produced by use of the above technique. A straight line between the center of the VOI and each of the sample points forms a radial line. We arranged all the voxels on the radial lines to form a transformed 2D image. Figures 2(a) and 2(b) show the VOI of a brain tumor and its transformed 2D image, respectively.

3.2 Determination of optimal outline by use of dynamic programming

After the spiral-scanning-based transformation, the surface of a tumor in the 3D image becomes a curve in the transformed 2D image, as shown in Fig. 2(b). Therefore, this transformation considerably simplifies the task of tumor segmentation. In this study, we applied dynamic programming to the transformed 2D image to find the optimal outline of a tumor[12]. Dynamic programming is an algorithm for solving optimization problems by use of a multiple-stage decision process. For our purpose, the problem of determining an optimal curve with $4N^2 / \pi$ sample points was divided into a problem of $4N^2 / \pi$ successive and sequential stages. Each stage would select an optimal "edge candidate" on a radial line based on a total cost function determined from the first stage to the current stage. The set of optimal edge candidates constitutes an optimal curve representing the outline of a tumor. Therefore, the optimal curve was defined as a series of sequential pixels from the leftmost to the rightmost column with a minimum cumulative cost, which is the sum of the local costs of all of the edge candidates on the path.

3.2.1 Definition of local cost

The local cost of an edge candidate is defined as a weighted sum of an internal cost and an external cost. The internal cost measures the smoothness between edge candidates on adjacent radial lines. A curve with a relatively smooth shape was assigned a low internal cost. Because, in 3D space, we have to consider the smoothness in both the longitude direction and the latitude direction, the internal cost was defined in two ways: a longitude internal cost along the spiral-scanning line and a latitude internal cost perpendicular to the spiral-scanning line. The longitude internal cost is given by the difference in *y* coordinates between an edge candidate and its adjacent edge candidate in the transformed 2D image.

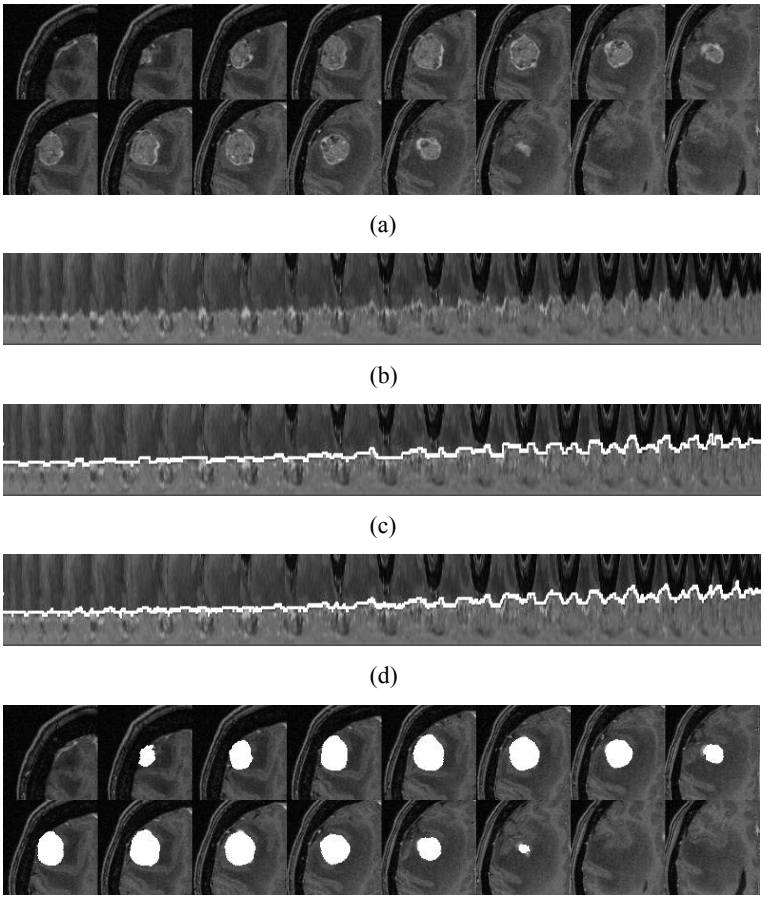


Fig. 2. Illustration of our segmentation method for a solid brain tumor. (a) The VOI of a solid brain tumor, (b) the transformed 2D image of the VOI, (c) the initial outline of the tumor, (d) the final segmentation result in the transformed 2D image, and (e) the reconstructed segmentation result for the tumor in 3D.

The latitude internal cost is defined as the difference in *y* coordinate of an edge candidate and the mean *y* coordinate of its adjacent edge candidates in latitude direction. The sum of the longitude and latitude internal costs constitutes the total internal cost for dynamic programming.

The external cost for an edge candidate depends on its edge strength. We wanted to assign a lower external cost to pixels with stronger edge features. The edge strength for each pixel was determined by the first derivative of intensity along the vertical direction in the transformed 2D image. Because the boundary of tumors generally has a higher intensity than that of background voxels in MRI scans, we retained the positive value of the first derivative to calculate the external cost. The local cost is defined by the weighted sum of the longitude internal cost, the latitude internal cost, and the external cost. In this study, the weighting factors were determined empirically.

3.2.2 Optimal path determination by minimization of cumulative cost

In order to delineate the "optimal" outline of a tumor, we had to determine a "best" path from a large number of paths starting from the first column and ending at the last column of the transformed 2D image. Each path consisted of $4N^2 / \pi$ edge candidates, i.e., it consisted of one and only one pixel on each of the columns. The goal of dynamic programming is to find the optimal path with the lowest cumulative cost, where the cumulative cost of a path is the sum of the local costs of the $4N^2/ \pi$ pixels on the path. The cumulative cost of each path was stored in a cumulative cost matrix. An element of the matrix represented the lowest cumulative cost from the first column to the current element.

The cumulative cost matrix was constructed in two steps. First, the cumulative cost of an element in the first column was initialized with the external local cost only. Then, for an element in other columns, the cumulative cost was calculated by a recursive process[11-13]. A minimum matrix element in the last column represented the final cumulative cost for a path from the first column to the last column of the transformed 2D image. We then traced the path backward from the minimum element on the last column to find a pixel in each column. These pixels were then connected sequentially to form the outline of the nodule.

In this study, we designed a two-phase dynamic programming-based optimization method to search for the optimal path. In the first phase, the dynamic programming algorithm was performed only with the longitude internal cost and the external cost, because the latitude internal cost could not be calculated. The optimal path determined by the first phase was considered as an "initial outline" of a tumor. The initial outline was generally considered quite near the "true" outline of the tumor. Based on the result of the first phase, we estimated the adjacent edge candidates in the latitude direction, and we then used these adjacent edge candidates to calculate the latitude internal cost. Therefore, we could use both longitude and latitude internal costs, and external cost for determining the "optimal" outline in the second phase.

3.3 Volumetry of brain tumors in 3D image space

To obtain the segmentation result in 3D MRI, the "optimal" outline of a tumor in the transformed 2D image was transformed back to 3D image space. Each edge candidate could be transformed back to 3D space by use of the azimuth angle and elevation angle of the corresponding radial line that connected the center of the VOI and the edge candidate. After the 2D to 3D transformation, we obtained a sparse point cloud. From this point cloud, we determined the interior of a tumor by use of a new interpolation method, which simply classified all voxels in the 3D image as a voxel inside a tumor or as that outside a tumor. All of the voxels deemed to be inside a tumor constituted a solid volume for the tumor in 3D image space and the volume of the tumor can be calculated by the number of voxels times the size (volume) of the voxel.

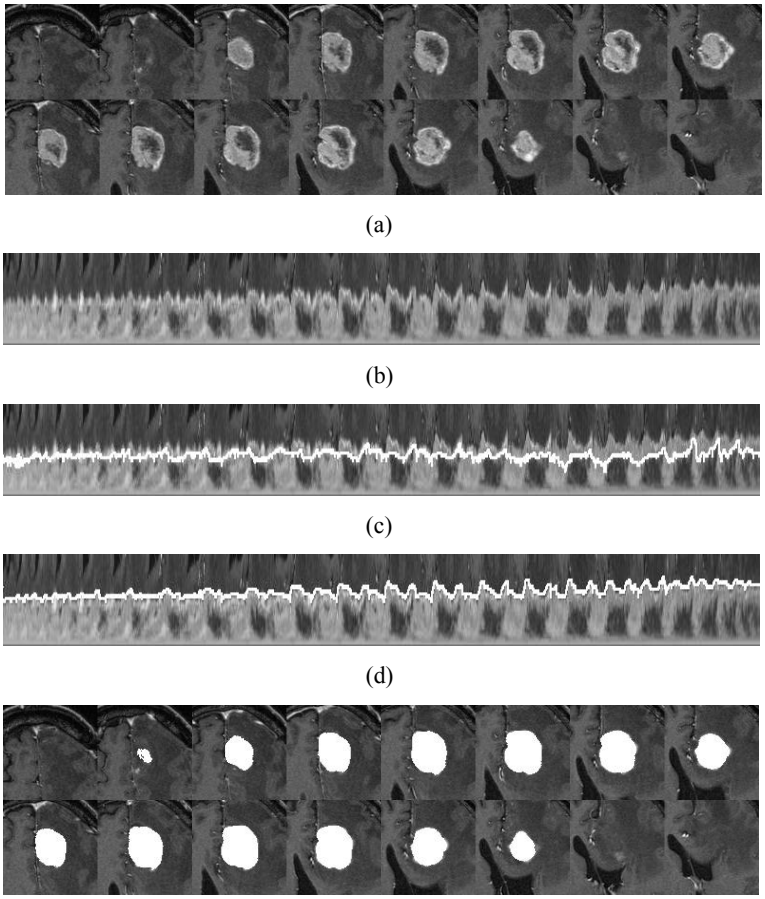
3.4 Evaluation of the volumetry method

To assess the reliability of our proposed volumetry method for brain tumors, we employed as the performance metric the "agreement" of volumes between computerized results and reference standards provided by an expert radiologist. The agreement was defined as one minus the ratio of the absolute difference between the computerized volume and reference standard to the volume of reference standards. The value of the agreement ranged from 0% to 100%, where agreement values of 0% and 100% imply no overlap and a perfect agreement, respectively.

4. RESULTS AND DISCUSSION

Figure 2 shows (a) the VOI of a solid brain tumor, (b) the transformed 2D image of the VOI, (c) the initial outline of the tumor, (d) the final segmentation result in the transformed 2D image, and (e) the reconstructed segmentation result for the tumor in 3D. The segmentation result matched the boundary of the tumor very well and provided a high agreement value of 91.5%. We found that for most of the tumors, there is no significant difference between the initial outline and final segmentation result in the 2D transformed image. However, for some partially solid tumors, there may be a significant difference between the initial outline and the final result. Figures 3 shows (a) the VOI of a partially solid tumor, (b) the transformed 2D image of the VOI, (c) the initial outline of the tumor, (d) the final segmentation result in the transformed 2D image, and (e) the reconstructed segmentation result for the tumor in 3D. It is apparent that the final segmentation result in Fig.3 (d) was improved significantly from the initial outline. Our proposed method provided an agreement value of 83.5% for this partially solid tumor.

Figures 4 shows the segmentation result for another solid tumor with an agreement value of 96.9%, and Fig. 5 shows the segmentation result for another partially solid tumor with an agreement value of 91.4%. We found that the agreement values for partially solid tumors are generally lower than those for solid tumors because of the inhomogeneous intensity inside the tumors.



(a)

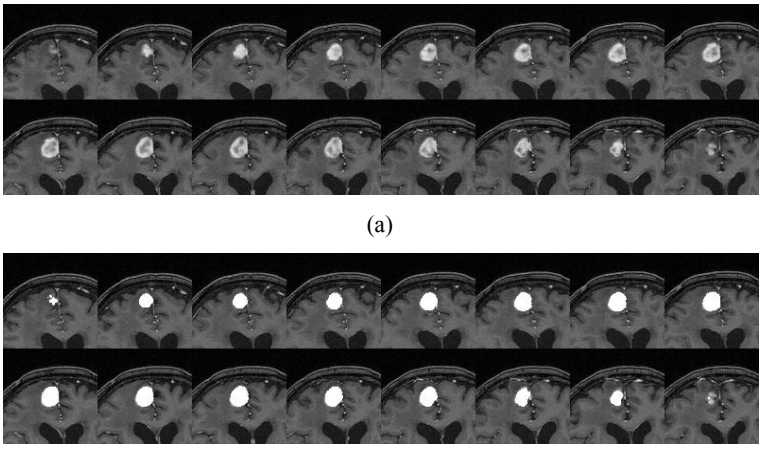
(b)

(c)

(d)

(e)

Fig. 3. Illustration of our method for the segmentation of a partial solid brain tumor. (a) The VOI of the tumor, (b) the transformed 2D image of the VOI, (c) the initial outline of the tumor, (d) the delineated optimal outline in the transformed 2D image, and (e) the reconstructed tumor volume in 3D.



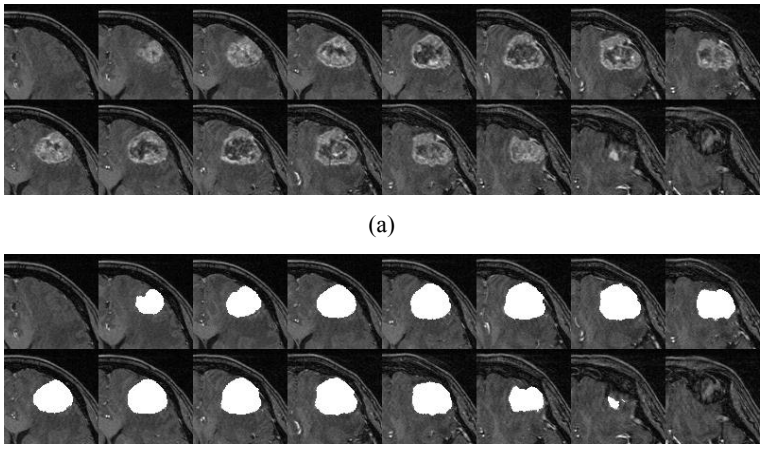
(a)

(b)

Fig. 4. Illustration of our segmentation method for another solid brain tumor. (a) The VOI of the tumor and (b) the reconstructed tumor volume in 3D.

The agreement values for the tumors in our database ranged from 65.8% to 99.6%. The overall mean agreement value was 87.8%. We found that large tumors tend to provide relatively high agreement values, whereas smaller tumors tend to provide lower agreement values. The mean agreement were 85.0%, 88.2%, and 92.6% for tumors with diameters less than 10 mm, between 10 mm and 25 mm, and larger than 25 mm, respectively. Figure 6 shows the relationship between tumor sizes and agreement values for the tumors in our database.

Our volumetry method provided a high performance level with a lower computation cost. On average, our method consumed 21 seconds for the segmentation of a tumor on a Dell personal computer with a CPU clock speed of 3.0 GHz, excluding the time for the selection of the centers of VOIs.



(a)

(b)

Fig. 5. Illustration of our segmentation method for another partially solid brain tumor. (a) The VOI of the tumor and (b) the reconstructed tumor volume in 3D.

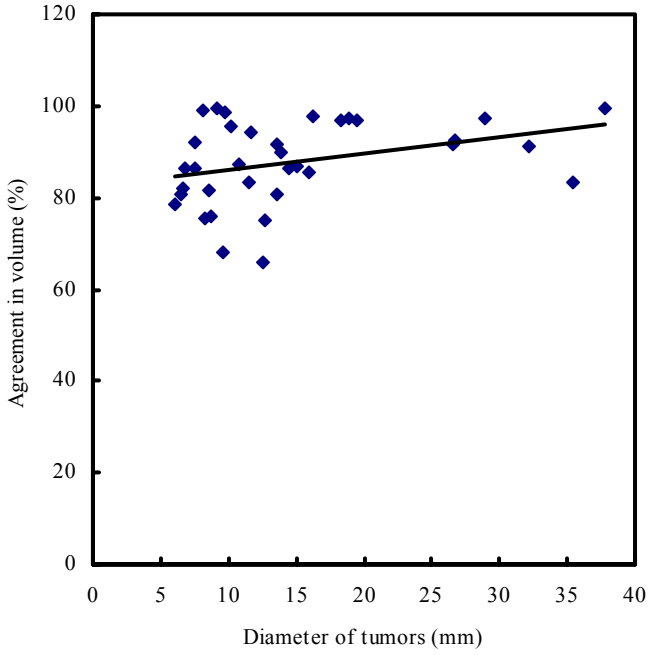


Fig. 6. The relationship between the size of tumors and the agreement values shows the smaller tumors tend to have lower agreement values, whereas the larger tumors tend to have higher agreement values.

5. CONCLUSIONS

In this study, we developed a novel method for the volumetry of brain tumors in 3D MRI. A key contribution of our method is the transformation of 3D images to 2D image space by use of a spiral-scanning technique, which considerably simplifies the volumetry scheme and improves its performance. We also developed a unique 3D reconstruction method for transforming the segmented optimal outline of a tumor in the transformed 2D image into a solid volume of the tumor in 3D image space. Our proposed volumetry method provided a robust and accurate result for both the solid tumors and partially necrotized tumors. This method would be useful for the management of various brain tumors, including evaluating the interval changes in tumor volumes during and after treatment and planning of radiation therapy.

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