A Novel Multi-stage 3D Medical Image Segmentation: Methodology and Validation

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Abstract. In this paper, we present a novel multi-stage algorithm for 3D medical image segmentation that is inspired by an improved Fast Marching method and a morphological reconstruction algorithm. The segmentation procedure consists of three steps: Connectivity Reduction, Hybrid segmentation, and Region recovery. The approach is tested on CT cardiac and MRI brain images, to demonstrate the effectiveness and accuracy of the technique. In order to validate this segmentation algorithm, a novel Radial Distance Based Validation (RDBV) method is proposed that provides a global accuracy (GA) measure. GA is calculated based on Local Radial Distance Errors (LRDE), where measured errors are along radii emitted from points along the skeleton of the object rather than the centroid, in order to accommodate more complicated organ structures. Using this GA measure, our results demonstrate that this multi-stage segmentation is fast and accurate, achieving approximately the same segmentation result as the watershed method, but with a processing speed of 3-5 times faster.

1 Introduction

Medical Segmentation plays a very important role in the field of computer-aided diagnosis and therapy planning, and has been the topic of much research focused on two main approaches: model-based and region-based methods, although these classifications are not mutually exclusive.

The Snake [1], introduced by Kass et al, provides a general model-based solution to the segmentation problem, while at the cost of higher computational complexity. Level Set [2] methods solve region breaking and merging problems. Much effort has focused on reducing the computational time for these algorithms, through the use of approaches such as the Fast Marching method [3]. However, model-based methods are sometimes limited in accuracy. In contrast to model-based methods, region-based methods can achieve more accurate results. Watershed [4] and Morphological Reconstruction [5] are two such methods, both derived from mathematical morphology. Since the methods are pixel-based, they are usually more computationally expensive.

In this paper, we present a multi-stage 3D medical image segmentation algorithm that integrates both the advantages of the Fast Marching method and a Morphological Reconstruction algorithm. To evaluate its performance, we propose a novel Radial Distance Based Validation (RDBV) method, which can quantify both local errors and

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the global accuracy between a segmented result and a gold standard. Its advantages over standard techniques such as Similarity Index [6] are its universality and ability to reflect significant local errors in global accuracy function.

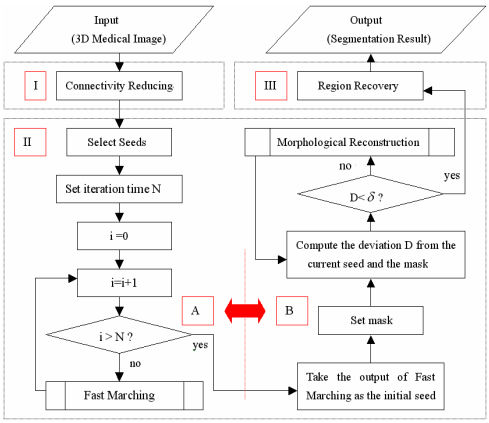


Fig. 1. Flowchart of the multi-stage segmentation method

The rest of the paper is organized as follows: in section 2, an improvement of the traditional Fast Marching method and 3D Morphological Reconstruction algorithm are presented. We describe the multi-stage segmentation strategy in section 3, and focus on the novel validation method RDBV in section 4.

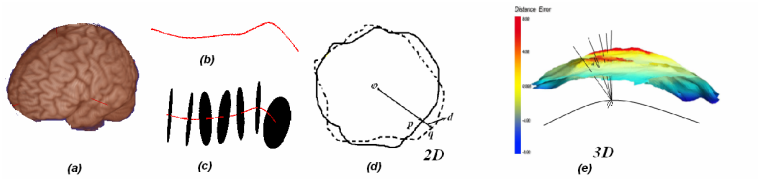


Fig. 2. (a) Origin 3D data. (b) The skeleton computed by distance mapping method. (c) Radius construction. (d) and (e) show the calculation of Local radial distance error (LRDE). Certain radial φq intersects with S and G resulting the intersection points q and p, respectively. d denotes the LRDE along φq . Black curve in (e) represents the skeleton of the object.

2 Improved Fast Marching and 3D Morphological Reconstruction

The Fast Marching (FM) algorithm is a special case of the level-set segmentation method. While the sign of the speed function in general in level-set approaches can be both positive and negative, that in the FM does not change. This restriction makes the FM much more rapid. However, sometimes the traditional FM method leads to overflow of the evolving front into neighboring regions, which is connected with the ROI. To prevent the front propagation from overflowing, we employ the improved FM described in [7] which introduced global information.

Mathematical morphology provides us with many powerful transformations for image analysis. It can efficiently classify particular shapes in an image and reconstruct defined regions via appropriate structuring elements (SE).

Morphological reconstruction (MR) is a typical approach to extract seeded regions, and is defined as:

$$\begin{cases} S_{i+1} = (S_i \oplus k) \cap |m| & (i = 0,1,2\cdots) \quad S_i - S_{i-1} > \delta \\ Stop & \qquad\qquad\qquad\quad S_i - S_{i-1} \le \delta \end{cases} \tag{1}$$

Where $\oplus$ represents a dilation operation, and $|m|$ represents the mask reflecting the edge information in ROI, which is defined via a threshold operation using a histogram analysis. The mask is used to restrict the propagation within the ROI. S denotes the seed when k is the kernel size of dilation operation. δ is the deviation threshold value between |m| and S_i. δ and k are both user defined. Since MR operates on individual pixels, it is sufficiently accurate to recover the ROI.

3 Multi-stage Segmentation Strategy

It is not practical to manually define an initial seed sufficiently close to the final boundary, and thus more computing effort is required in the MR. We introduce here an improved FM method to perform fast propagation from a user-defined seed to the position close to the final boundary, and this is employed as the seed during the MR phase. As shown in Fig.1, the procedure of the proposed multi-stage segmentation method includes three stages:

I. Reduce the connectivity between the ROI and the neighboring tissues.
II. Hybrid segmentation, where in Part A, after we perform the improved FM method to prepare a good initial seed, the MR is employed in Part B.
III. Recover the lost data elements of ROI from stage I.

4 Validation Method

When a new segmentation method is proposed, it is crucial to provide an objective and quantitative analysis of its performance. We propose a novel validation method based on radial distances where the radii are extended from the points along the skeleton of a region (see Fig.2).

4.1 Skeletons and Radial Construction

Several skeleton algorithms, such as manual extraction, topological thinning, distance mapping [8] and so on, can be found in literature. Here, we employ the distance mapping method to construct the object's skeleton, as shown in Fig.2 (b).

From a point φ in the skeleton, we construct sufficient equi-spaced radii in the plane perpendicular to the skeleton as shown in Fig.2 (c). Each radial line intersects the surfaces of the segmented region S and the corresponding ground truth image G. The intersection points are q and p, respectively (see Fig.2 (d)-(e)). We define

$d = \varphi q - \varphi p$ as the local radial distance error (LRDE). If we apply the radial construction method to every point along the skeleton, we obtain LRDE everywhere.

4.2 Framework

Points along the skeleton are numbered in order as $\varphi_0, \varphi_1, \varphi_2 \cdots \varphi_{N-1}$, where N is the number of points. Furthermore, radial lines emitted from the point φ_i are denoted R_{i1}, R_{i2}, R_{i3} …… R_{iM}, where M is the number of radii emitted from φ_i, and the intersection points on the surfaces S and G are presented as q_{i0}, q_{i1}, q_{i2} …… q_{iM} and p_{i0}, p_{i1}, p_{i2} …… p_{iN}, respectively. Thus, the LRDE can be formally defined as:

$$d_{ij} = \varphi_i q_{ij} - \varphi_i p_{ij} \quad (0 \le i \le N-1, 0 \le j \le M-1) \tag{2}$$

Furthermore, the intermediate variable c_{ij} is defined as below:

$$c_{ij} = \left| \frac{d_{ij}}{\varphi_i p_{ij}} \right| \quad (0 \le i \le N-1, 0 \le j \le M-1) \tag{3}$$

c_{ij} represents the fractional under- or over-segmentation along the direction of R_{ij}. We place c_{ij} in one of three categories:

- $0 < c_{ij} \le 1/k$: Local segmentation is considered accurate;
- $1/k < c_{ij} < 2/k$: Local segmentation is acceptable;
- $c_{ij} \ge 2/k$: Local segmentation is unacceptable.

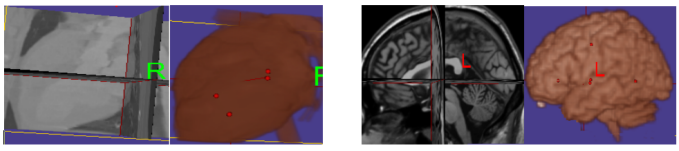
An experienced radiologist considered local segmentation could be considered acceptable for $c_{ij} \le 0.05$, leading to the selection of a value of 20 for k as a constant defining an acceptable segmentation. We introduce the concept of Global Accuracy (GA) to reflect the accuracy of the global segmentation:

$$GA = N.M \left[\sum_{i,j=0}^{N-1,M-1} L_{i,j} \right]^{-1} \quad (0 \le i \le N-1, 0 \le j \le M-1) \tag{4}$$

Where, the target function $L_{i,j}$ is defined as:

$$L_{ij} = \lambda^{c_{ij}k} \quad (0 \le i \le N-1, 0 \le j \le M-1) \tag{5}$$

And, $\lambda = 1.54$ [9].



(a) (b)

Fig. 3. Examples of segmentation results of heart (a) and brain (b) by the proposed method

Since $c_{ij} \le 1/k$ is considered as an accurate segmentation, we can define GA_t, the threshold value of GA, as:

$$GA_t = N.M\left[\sum_{i,j=0}^{N-1,M-1} \lambda^{k\times\frac{1}{k}}\right]^{-1} = 0.65 \ (0 \le i \le N-1, 0 \le j \le M-1) \quad (6)$$

So, $GA \ge GA_t = 0.65$ is considered to be a good segmentation using the RDBV method.

5 Experimental Results

We performed our validation within the "TkSegmentation" software environment, which is based on the Visualization (VTK) and Insight (ITK) toolkits as well as the Python language. To perform the segmentation and validation, the software was implemented on a 2GHz Pentium-4 PC, running on Windows-XP.

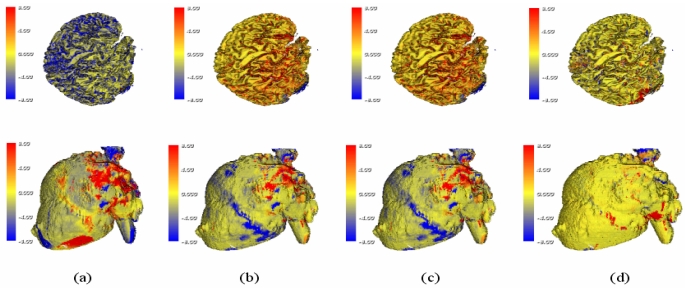


Fig. 4. LRDE distributions in the segmentation results of the FM (a), MR (b), PM (c) and WA (d) on brains and hearts

Table 1. Global Accuracy (GA) measure of the FM, MR, PM and WA on testing Datasets

Datasets	FM	MR	PM	WA
CJH27	0.70	0.82	0.82	0.88
Brain 1	0.68	0.83	0.83	0.88
Brain 2	0.71	0.84	0.84	0.89
Heart1	0.66	0.78	0.78	0.92
Heart2	0.69	0.79	0.79	0.97
Heart3	0.67	0.78	0.79	0.94
Average	0.69	0.81	0.81	0.91

Table 2. The computing time in seconds of FM, MR, PM and WA on testing Datasets

Datasets	FM	MR	PM	WA
CJH27	16.3	188.2	45.8	242.5
Brain 1	16.1	80.6	34.5	131.6
Brain 2	16.4	78.7	31.8	125.2
Heart1	66.9	442.1	120.8	562.6
Heart2	68.7	450.6	116.6	549.3
Heart3	67.4	466.2	137.0	558.7

The simulated datasets employed in our experiments were the standard CJH27 image volume for which "ground truth" is known. CJH27 is a 181×217×181 voxel volume, with isotropic 1 mm^3 voxels. 2 MRI clinical brain volumes (256×256×124) and 3 3D CT canine heart images (512×512×87) were also tested. The "ground truth" of each real clinical dataset was manually defined by an expert radiologist**.** Examples of segmented results using the proposed approach are shown in Fig.3. The FM, MR, Watershed (WA) and our hybrid method (PM) are compared and evaluated with respect to both accuracy and efficiency using the RDBV metric. The results shown in Fig.4 and Table 1-2 reveal that this new multi-stage algorithm achieves superior performance with respect to the other approaches.

6 Conclusion

In this paper we presented a new multi-stage segmentation algorithm integrating the improved FM and MR approaches. Although our approach is still slower than the FM, it offers significantly improved accuracy. In addition, when compared to the MR and watershed methods, it maintained equivalent accuracy at a fraction of the computing cost. Meanwhile, the RDBV method is proposed to offer an improved measure of the segmentation results using both local and global information.

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