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Semi-Automatic Segmentation Methods for 3-D Visualization and Analysis of the Liver

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Abstract. Pre-evaluation of donors prior to surgery of living donated liver transplantation is one of the challenging applications that computer aided systems are needed. The precise measurement of liver volume requires effective segmentation procedures, while three dimensional rendering of the segmented data provides demonstrative information to radiologists and surgeons before surgery. The Insight Toolkit provides effective algorithms for segmentation, which are also optimized for high computational performance and processing time. Furthermore, An ITK pipeline can be combined with a VTK pipeline, so that the result of segmentation can be represented directly in 3-D using VTK. Therefore, there is an on-going trend for developing ITK/VTK based systems. This study presents quantitative and qualitative performance evaluation of two effective ITK algorithms on segmentation of liver from CTA data sets.

Keywords. Liver segmentation, Computed Tomography, Fast Marching, Connected Threshold, Insight Toolkit

Introduction

Liver is one of the most important and complicated organs in the human body. Therefore, analysis of liver using radiographic images is necessary in several occasions including but not limited to diagnosis, planning surgical procedures and treatment follow-ups. One of these procedures is the evaluation of the liver volume of the transplantation donors prior to the hepatic surgery using the images acquired by Computed Tomography Angiography (CTA) [1]. This requires delineation of liver border in each slice image, which is a tedious and expert dependent task if it is done manually. Unfortunately, automatizing this task with computer aided techniques is a very challenging task due to Hounsfield Unit (HU) inhomogeneity after injection of contrast media, partial volume effects, overlapping HU ranges of adjacent organs (i.e. right kidney, spleen, hearth, muscles and fat tissues). Thus, effective segmentation and visualization techniques should be employed for robust segmentation of liver, calculation of its volume and 3-D rendering for further evaluations.

ITK (The Insight Toolkit) [2] is a free toolkit for processing, segmentation and registration of image data. ITK is being developed by three commercial facilities

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(including GE Corporate R&D and Kitware) and three academic institutions (including the University of Utah). Visualization Toolkit (VTK) [3] and ITK is implemented in C++ and they are available for many platforms and has interfaces to Java, Tcl and Python. All algorithms implemented in ITK for processing and segmentation work with two, three, and multi-dimensional data. The algorithms also include linear and non-linear smoothing filter, edge detectors and various regional growth and level-set methods.

Furthermore, an ITK pipeline can be combined with a VTK pipeline, so that the result of segmentation can be represented directly in 3-D using VTK [4]. According to the rapid developments in processors and graphics cards, 3-D visualization of the volume data provides very high additional terms to evaluations in clinical use. As a result, the implementations that are based on ITK and VTK become very popular among medical image research community [5].

This study shows the results of the application of two important ITK segmentation techniques (i.e. Connected Threshold [6] and Fast Marching [7]) to segmentation of liver from CTA data sets. These segmentation algorithms are used with proper pre-processing and post-processing operation through a software developed for medical image analysis research [8]. Then, the results are evaluated quantitatively by performance metrics and qualitatively by expert radiologists.

1. Methods

The segmentation procedure is structured as a three-step procedure. First, pre-processing of the volume data, with the aim to improve the segmentation process (i.e. data reduction, noise suppression) is carried out. In the second step, the actual segmentation is performed to extract one or more objects. In the subsequent post-processing, segmentation results are further processed for pruning. Taking into account the three criteria mentioned above, two methods were selected as segmentation method for parameterization: region growing and active contours (level set method). For both groups, a variety of specific algorithms have been established [2], among which Connected Threshold (see 1.1) and Fast Marching (see 1.2) are used.

1.1. Connected Threshold (CT) Method

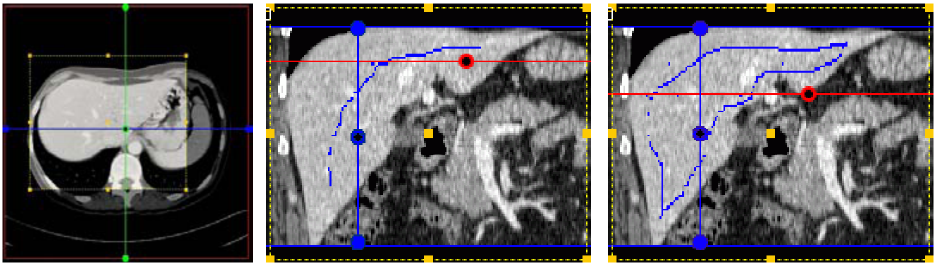
The Connected Threshold (CT) method is universally applicable; there is no restriction on certain medical application areas or certain topologies. It can be used to segment both compact objects (such as the kidney), or long, narrow objects (such as blood vessels). The prerequisite is there should be a difference that distinguishes the object to be segmented from the environment through its HU values. Segmentation for the setting of one or more seed points [6] within the searched object is required. The positioning of the seed points can be arbitrary, which makes the method robust against misplacement. However, the CT method is susceptible to noise. Any noise present should therefore be reduced in a pre-processing by a smoothing filter. The CT algorithm has three free parameters (i.e. lower and upper HU limit and the position of the seed points), which can be determined by a physician without theoretical knowledge about the algorithm. Due to its simple operation, the running time of the algorithm is low even for large volumetric data sets. The CT method works very successfully with objects that have a homogeneous HU value distribution and with contrast-filled vessels. However, depending on the HU value distribution of the object and its environment, leaking may happen. For this case, the Fast Marching method provides more control through additional parameters to control the segmentation result.

1.2. Fast Marching (FM) Method

The Fast Marching (FM) method [7] was chosen because it is supplemented in some way with the CT method. The risk of leakage is significantly lower, but the application is not as wide as CT method: Long, narrow objects - in particular vascular trees - cause problems. Similar to CT method, the set of one or more seed points are required within the object to be segmented. From each seed point, a front propagation launches. The seed points should be placed in the center of the object (Fig. 1.b) to prevent too early slowdown of the uniformly propagating front (i.e. due to high HU value gradients). If two successive fronts overlap, the corresponding regions are merged. In addition to the position of the seed points, the actual FM method has only one additional parameter: the number of iterations. However, it should be noted that although the implementation of the algorithm does not expect the HU value range as the input data, a so-called "velocity field", which contains the velocity of propagation for each voxel position, should be specified. This field is calculated from the HU value gradients in a pre-processing step. The complexity of FM is higher than the CT method, but it can be significantly reduced, if the number of the seed points is increased. Due to the geometric description of the surface, FM method always returns a closed and smooth surface of the segmented object. A spill in the region can only occur when the seed points are placed too close to object boundary (low HU value gradients).

1.3. Application of the Segmentation Methods

Both methods are based on HU values and their gradients. Through interference (such as contrast media) in the volume data, there can be high local HU value fluctuations that negatively affect the segmentation process. It is therefore useful to perform a smoothing in a pre-processing step, which affects the edge steepness as little as possible. Some alternatives are anisotropic diffusion, Gaussian and median filters.



(a) (b) (c)

Figure 1. (a) 2D slice of a VOI determined for reducing data to process. Possible position of the seed points for liver segmentation using the Fast Marching Method: (b) in the center of the liver (more appropriate due to high HU value gradients), (c) close to the border of the liver (low HU value gradients).

In order to reduce memory requirements and to reduce the segmentation time, a volume of interest (VOI, Fig. 1.a) is defined. A further reduction in the memory requirement and the time segmentation can be achieved by subsampling. For the post-processing of the segmentation result, the same filters used for the pre-processing can be employed. It has already been mentioned that the FM method always produce a smooth surface. For the CT method, this is not true, so that a subsequent Gaussian smoothing should be applied to produce a smoother surface.

2. Results

The methods are evaluated on 24 CTA data sets obtained from Dokuz Eylül University Hospital, Radiology Department, Izmir, Turkey. The liver volumes obtained by application of the segmentation methods are quantitatively compared to the manual segmentation, which are delineated by the software tool that is currently used for calculation of the liver volumes of transplantation donor candidates (Fig. 2). The segmentation algorithms (i.e. CT and FM), together with necessary user interaction mechanisms (i.e. insertion of the seed points, VOI selection tools) and necessary pre-processing and post-processing operations (i.e. smoothing filters such as anisotropic diffusion, median, Gaussian etc.) are realized through a software developed for medical image analysis research [8]. Fig. 2 presents three boxplots representing median values for reference, CT and FM volumes. This corresponds to a visual hypothesis test that is analogous to the t test used for means. The line in the middle of each box is the sample median. If the median is not centered in the box, it shows sample skewness.

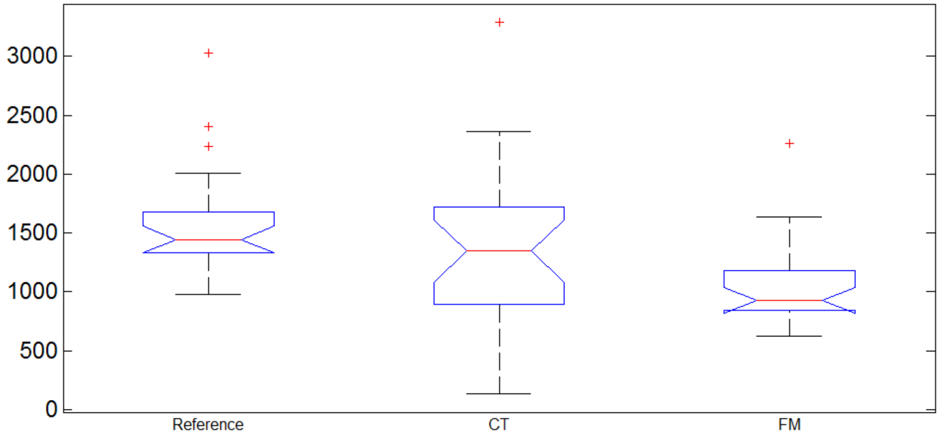
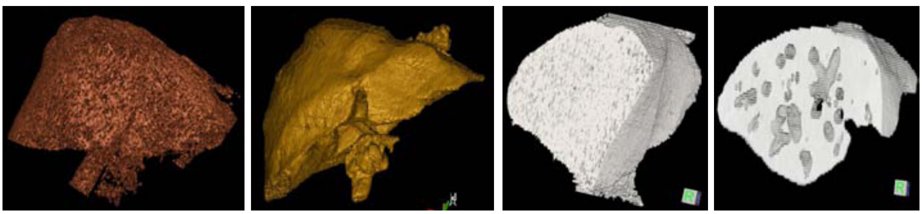


Figure 2. Comparison of the relative deviations from the reference volume for CT and FM methods

There exist significant differences between the results produced by the two segmentation methods. The maximum deviation from the reference volume in the CT method is at 87.52%, while it is 45.18% at the FM method. Thus, it can be concluded that the FM method works more stable than CT. Moreover, the deviation from the reference volume is between 22.39% and 45.18% (difference in percentage: 22.79) for FM method. In comparison, the variation in the CT method is between 0.69% and 87.52% (difference in percentage: 86.83).

The qualitative results show that the segmented data obtained by FM can be visualized for qualitative 3-D visualization of the liver (Fig 3.b), while CT result require significant amount of post-processing (Fig. 3.a). However, these techniques cannot provide enough precision for quantitative analysis. For instance, vessels within the liver are not included in the segmented data when FM is used (Compare Fig 3.c and Fig. 3.d). For this reason, the volume values for the liver cannot be compared with the manually determined values. To be able to use the segmentation results for diagnostic (quantitative) purposes, segmentation process must be extended accordingly (for instance, a morphological post-processing to fill excluded vessels inside the liver parenchyma). It would also be helpful to have additional manual segmentation tools. For instance, if the liver is successfully segmented with some minor mistakes (such as inclusion of the vessels that are too far outside the liver, but collected in the segmentation result), a fast correction can be done using the manual tools. So, there will be no need to re-run the time consuming segmentation procedure including insertion of the seed points, adjustment of the parameters etc.



(a) (b) (c) (d)

Figure 3. Segmentation result using (a) Connected Threshold method, (b) Fast Marching method. Inside of the segmented liver, (c) Manual segmentation, (d) segmentation with the Fast Marching method.

3. Discussion

Based on the results, it can be concluded that the FM method provides more stable results compared to the CT technique, while the results obtained by CT algorithm have higher accuracy. To be able to use the liver segmentation results for diagnostic purposes (i.e. volume measurements), both algorithms need careful selection of pre- and post-processing operations prior to their application.

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