

Temporal Dynamics 4D Level Set Method for Segmentation of MR Renography Images

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Introduction

MR imaging with gadopentetate dimeglumine (Gd-DTPA) can provide a non-invasive method for the measurement of single kidney function. Segmentation is often a prerequisite for quantitative diagnosis [1]. We have developed and tested a novel, fully automatic temporal dynamics 4D level set segmentation method that makes full use of both spatial anatomic structure information as well as contrast kinetic information across all time points.

Methods

Given a 4D image data set $\bar{\mathbf{I}}(\bar{\mathbf{x}}, t)$ with temporal dynamics defining the spatial domain $\Omega = \Omega(\bar{\mathbf{x}})$, a 4D deformable model utilizing temporal vector $\bar{\mathbf{u}}(\bar{\mathbf{x}})$ with associated segmentation energy is used to separate the image into objects and background. In this work, a homogeneity-based energy functional is adapted to segment piecewise constant or piecewise smooth 4D dynamics with each partition of the images. Assuming that in the data, there is an object of representing temporal dynamics of vector $\bar{\mathbf{c}}_1$, and a background with representing temporal dynamics of vector $\bar{\mathbf{c}}_2$, separated by the contours C , the proposed energy functional is defined as:

$$F(C, \bar{\mathbf{c}}_1, \bar{\mathbf{c}}_2) = \mu(\text{length}(C)) + \lambda_1 \int_{\text{inside}(C)} (\bar{\mathbf{u}} - \bar{\mathbf{c}}_1)^T (\bar{\mathbf{u}} - \bar{\mathbf{c}}_1) d\Omega + \lambda_2 \int_{\text{outside}(C)} (\bar{\mathbf{u}} - \bar{\mathbf{c}}_2)^T (\bar{\mathbf{u}} - \bar{\mathbf{c}}_2) d\Omega, \quad (1)$$

where $\mu \geq 0$, $\lambda_1, \lambda_2 \geq 0$ are fixed parameters. The corresponding dynamic equation at each voxel $\bar{\mathbf{u}}(\bar{\mathbf{x}})$ for energy minimization is:

$$\frac{\partial \phi(\bar{\mathbf{x}})}{\partial t} = \mu \text{div} \left(\frac{\nabla \phi(\bar{\mathbf{x}})}{|\nabla \phi(\bar{\mathbf{x}})|} \right) + \lambda_1 (\bar{\mathbf{u}}(\bar{\mathbf{x}}) - \bar{\mathbf{c}}_1)^T (\bar{\mathbf{u}}(\bar{\mathbf{x}}) - \bar{\mathbf{c}}_1) - \lambda_2 (\bar{\mathbf{u}}(\bar{\mathbf{x}}) - \bar{\mathbf{c}}_2)^T (\bar{\mathbf{u}}(\bar{\mathbf{x}}) - \bar{\mathbf{c}}_2). \quad (2)$$

In order to apply temporal dynamics 4D level set to MR renography (MRR), a 3D automated initialization or seeds detection is needed. Segmentation of 3D MRR can be achieved by many approaches, including optimized thresholding, graph cuts, and 3D level set. In this context, the 3D *spatial* level set segmentation method, which perform a minimal partitioning of the image data into piecewise constant objects based on Mumford-Shah functional, are used for its flexibility and efficiency [2].

Dynamic MRR images were acquired on a 1.5T system (Avanto; Siemens, Erlangen, Germany). 3D T1-weighted spoiled gradient echo imaging was performed in the oblique coronal orientation to include the abdominal aorta and both kidneys with TR/TE/flip angle 2.8/1.1/12°; matrix was 161 × 256 × 20, FOV was 425 × 425 × 100mm; voxel size 1.6 × 1.6 × 2.5 mm after interpolation; bandwidth 650 Hz/voxel; and temporal resolution 3 sec. A 4 ml bolus of Gd-DTPA (Magnevist; Berlex Laboratories, Wayne, NJ, USA) was injected after five pre-contrast image acquisitions, followed by 20ml of saline at 2ml/sec. Over 20 min, 36 post-contrast images were acquired. For image processing, all 41 3D data sets were analyzed using proposed method. Cortex, medulla and collecting system were segmented and compared with two reader's manual tracing results. Two experienced individuals collaborated to manually segment each of the 22 kidneys into cortical, medullary and collecting system regions. These observers used an interactive, locally developed Unix-based software package that provides the user with the ability to view and scroll through the 3D data and construct volumes of interest in arbitrary planes. The manual segmentation took on the average of 2.5 hours per kidney. To statistically evaluate the performance of the segmentation method compared to manual labeling, two-sample t-tests ($\alpha = 0.05$) were performed on the volume errors and SI errors for cortex, medulla, and collecting system.

Results

Across 22 kidneys, the volume measurement showed that the discrepancy between the 4D level set method and the expert segmentation was 12.6 ± 8.6 ml, 10.6 ± 4.9 ml, and 2.9 ± 2.1 ml respectively for the cortex, medulla and collecting system. The discrepancy between two experts was 16.3 ± 11.2 ml, 15.9 ± 5.7 ml, and 2.6 ± 1.7 ml. An example of segmented cortex, medulla and collecting system is shown in Fig. 1. On averaged signal intensity versus time across all kidneys shown in Fig.2, there was consistent agreement between enhancement curves derived from two manual segmentations and the 4D level set segmentation. The mean absolute relative errors were $5.3\% \pm 2.2\%$, $4.6\% \pm 3.5\%$, and $3.8\% \pm 2.9\%$ respectively for the cortex, medulla and collecting system. By comparison, the errors between two experts were $5.9\% \pm 2.3\%$, $4.7\% \pm 2.3\%$, and $5.6\% \pm 5.4\%$ correspondingly. The t-test results suggested that the volume errors and SI errors of the proposed segmentation method compared to an expert were statistically comparable to the inter-observer variability for all three renal structures.

Conclusions

In 4D MRR, manual delineation of each 4D dataset typically requires approximately 2.5 hours of a radiologist time at a workstation per case. This remains prohibitively costly and labor-intensive for practical clinical use. In this context, a novel 4D segmentation framework based on a temporal dynamics 4D level set was proposed. It only required less than one minute to automatically segment a 4D data set with more than 40 time points. The error between our method and manual segmentation was statistically comparable to the disparity between two expert observers. The method can be applied to other segmentation problems that are increasingly used in dynamic contrast-enhanced MRI and CT applications.

References [1] V. S. Lee, et. al, AJP Renal Physiol, vol. 292, pp: F1548-F1559, 2007. [2] T. Song, et. al. EMBS pp. 3134-3137, 2006.

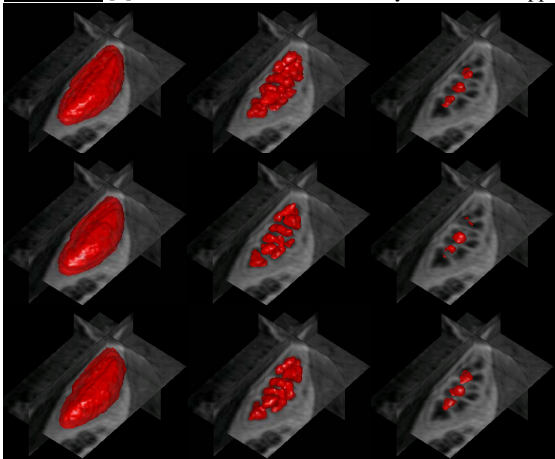


Fig. 1. 3D segmentation results between two experts (first two rows) and our algorithm (3rd row); cortex, medulla, and collecting system are shown in 1st, 2nd, and 3rd columns.

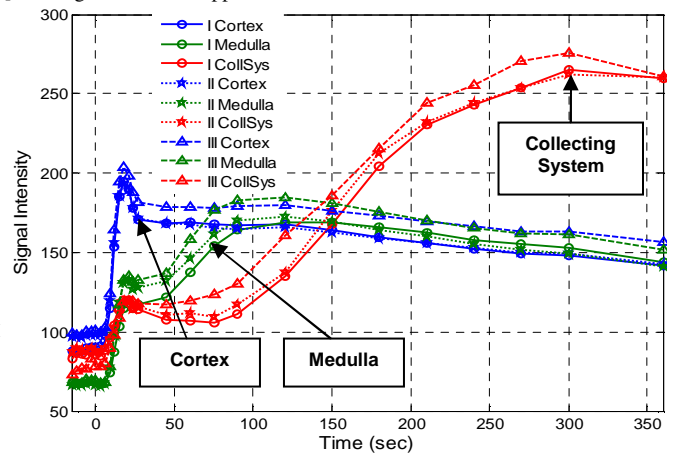


Fig. 2. Circles indicate computer segmented SI (I); stars and triangles indicate manually segmented SIs (II and III).