Registration and Segmentation of Dynamic Three-dimensional MR Renography Based on Fourier Representations and K-Means Clustering

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Introduction

Dynamic contrast-enhanced 3D MR renography has the potential for broad clinical applications. Although high quality images can be acquired, manual registration and segmentation of serially acquired images of the kidney is prohibitively labor-intensive. An effective registration and segmentation algorithm is necessary to process this data in a timely and reliable fashion. Our purpose was to develop automatic registration and segmentation algorithms and to evaluate them on two 4-D MR renography datasets that simulated respiratory motion that are representative of patterns of contrast enhancement in a normal and dysfunctional kidney. In each dataset the spatial transformation, voxel tissue classification, and true signal-time activity were known.

Algorithm

Once the user prepares a cropped volume of the MR data, both registration and segmentation algorithms run as fully automated algorithms. A Fourier transform-based registration method, which relies on edge representations rather than signal intensity values, was extended from 2D[1] to 3D. Edge information is more invariant than intensity values in 4-D MR renography datasets. The rotation and translation can be decoupled in the frequency domain by analyzing the magnitude and phase spectra separately. Let $f(\mathrm{X}), \mathrm{X} \in \mathbf{R}^3$ be a 3D object and let $g(\mathrm{X})$ be a rigidly translated t and rotated R version of $f(\mathrm{X})$. It can be shown that $f(\mathrm{X})$ and $g(\mathrm{X})$ relate as $g(\mathrm{X}) = f\left(R^{-1}\mathrm{X} - t\right), t \in \mathbf{R}^3, R \in \mathbf{R}^{3\times 3}$ and that Fourier transforms are related as $G(\mathrm{K}) = F\left(R^{-1}\mathrm{K}\right)e^{-j2\pi \mathrm{K}^T Rt}$. The translational vector t affects only phase and not magnitude values. Magnitudes are related as $\left|G(\mathrm{K})\right| = \left|F\left(R^{-1}\mathrm{K}\right)\right|$. Rodrigues' rotation formula [2] was used for computing the rotation matrix R. After rotation was corrected, the translational vector t was then calculated by phase correlation. Next, each image was coregistered to the center time frame.

Once the kidney was registered, signal variance along the time dimension was calculated, which was used to extract the kidney from the background based on an automatically selected threshold value. Thus, for every kidney voxel, a vector composed of intensity values from different time frames was used for K-means clustering to segment (or classify) the kidney into three distinct clusters corresponding to the cortex, medulla and collecting system [3].

Methods

Based on a manually registered 4D MR renography data set, a simulated data set was generated by translating and rotating the kidney, representative of typical motion seen with a poorly-compliant patient. Simulated motions included head to feet (HF) translation, left to right (LR) translation, anterior to posterior (AP) translation and rotation (Rot) with respect to three different axes, represented in terms of (α, β, θ), where (α, β) defined the axis of rotation; θ the angle of the rotation along that axis (Table I). Two versions of this data set were generated. In the normal (NL) functioning kidney we simulated concentration-time curves in each renal compartment (cortex, medulla, collecting system) that were representative of normal kidneys with glomerular filtration rate (GFR) 60 ml/min. In the second abnormally (ABN) functioning kidney, we simulated slower uptake and washout of the contrast, representative of GFR=30 ml/min.

Results

Across 18 time frames, the average (±st.dev) error of rotation was 0.50 ± 0.21 degrees for NL and 0.56 ± 0.24 degrees for ABN (Fig 1). Translation errors were effectively zero in HF, LR and AP directions, since the current translation correction was limited to integer voxel accuracy, the upper bound of the error is ± one half of the voxel size,0.75mm (HF), 0.75mm (LR) and 2mm (AP). However, subvoxel translation correction will be studied in the future. Representative segmentation results of NL case are shown in Fig 2. The root-mean-square (RMS) errors in time-signal intensity curves for the NL were 1.7%, 6.9%, and 3.7% corresponding to cortex, medulla and collecting system; for the ABN, the RMS were : 2.6%, 10.9%, and 8.6%, respectively.

Conclusions

An automatic registration and segmentation method has been applied to simulated 4D dynamic renal MR images, with minimal rotational errors and voxel-level translation errors. Resulting errors in signal in renal tissue appears to be within 10%, providing a clinically acceptable level of quantification and accuracy.

References

[1] E. L. W. Giele et al., *JMRI*, vol. 14, pp. 741-749, 2001. [2] R. M. Murray, Z. Li, and S. S. Sastry, *A Mathematical Introduction to Robotic Manipulation*: CRC Press, 1994. [3] A. F. Laine and J. Fan, "Wavelet Packet Analysis for Texture Classification," presented at IAPR Workshop on Machine Vision Applications, 1992.

Table I. Simulated Motion for Each Time Frame (T)

T	Motion	T	Motion	T	Motion
0	Baseline	6	Baseline	12	Baseline
1	LR 1.5mm	7	AP 4mm+(0,90,9) Rot.	13	HF 12mm
2	Baseline	8	Baseline	14	Baseline
3	LR 3mm+(90,0,2) Rot.	9	LR 1.5mm	15	HF 3mm
4	Baseline	10	Baseline	16	HF 9mm
5	HF 3mm+(0,0,6) Rot.	11	AP 4mm	17	HF 3mm

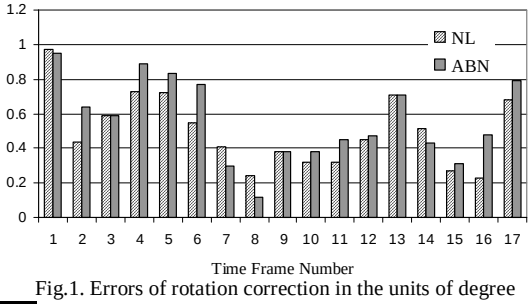

Fig.1. Errors of rotation correction in the units of degree

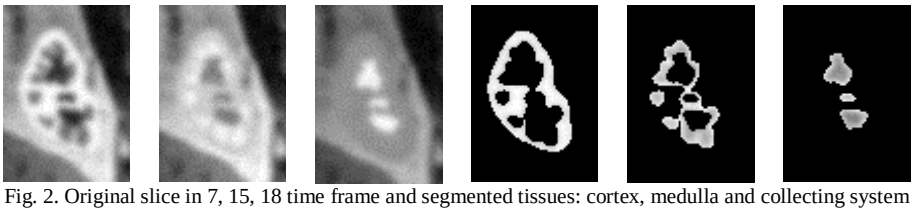

Fig. 2. Original slice in 7, 15, 18 time frame and segmented tissues: cortex, medulla and collecting system