Algorithmic Quantification of Left Ventricle Segmentation in 4D Cardiac Magnetic Resonance Imaging based on Spatio-temporal Continuity

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INTRODUCTION: Accurate, rapid quantification of left ventricular (LV) volumes for calculating ejection fraction (EF) are essential in diagnosis and therapy of heart disease [1]. Manual intervention is often needed for LV segmentation [2-4] due to MR imaging obliquity and the complexity of selecting the basal section. An LV segmentation method is proposed that selects apical and basal LV positions based on spatio-temporal continuity of LV area and shape (Fig.1) and then segments the entire LV at all the cardiac phases using region growing with iteratively decreasing thresholds and spatio-temporal continuous LV areas and shapes.

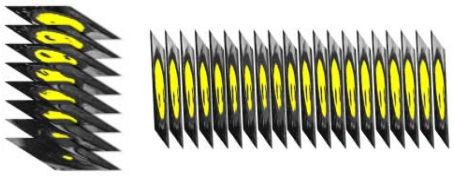

Fig.1 Spatio-temporal continuity of LV area and shape

ALGORITHM: Our algorithmic method for quantitative LV analysis involved the following steps: 1) find LV center at the mid-ventricular slice by subtracting end systole from end diastole and calculating the mass center of Hough Transform space; 2) locate LV center of the remaining slices by calculating the LV region extracted by region growing using the LV center of the near slice as the starting point; 3) denoise the image and enhance endocardial boundaries using an anisotropic diffusion algorithm; 4) extract LV blood region using iteratively decreasing threshold based region growing [3] from mid-ventricle to apex until the area jumps. Jumping areas are estimated by the spatio-temporal continuity according to the following Equation:

$$A(p,s) = A(q,s) * \sum_{i=ms}^{s-1} A(p,i) \Big/ \sum_{i=ms}^{s-1} A(q,i)$$

Here *A (p,s)* is the new estimated area at phase *p* of slice *s*; *A (q,s)* is the no jumping area calculated according to the segmented region at phase *p* which is the closest to *p*; ms is the slice number of LV mid-ventricle. If all the areas jump at this slice, these areas are viewed as zero. LV basal section is defined by the discontinuity of the LV area and the shape. LV region at the basal section are segmented using the region growing constrained by the normal spatio-temporal LV shape.

MATERIAL AND METHODS: Cardiac short axis cine SSFP data at 1.5T (GE Signa EXCITE 14.0) from 38 patients (30 male, mean age 46.7 years ±16.7SD) was analyzed retrospectively with IRB approval and HIPAA compliance. Imaging parameters: TR 3.1-4.1 ms, TE 1.1-1.5 ms, flip angle 60°, matrix 192-224×256, reconstructed to 256×256, receiver bandwidth 62.5-125 kHz, FOV 210-340×280-340, slice thickness and section gap 6-8 mm and 2-4 mm respectively (total 10 mm). The number of images per cardiac cycle was 20-28 depending on the heart rate.

Algorithmic quantification of LV end-diastolic volume (EDV), end-systolic volume (ESV) and EF are compared with manually traced measurements. PTM are excluded from the blood volume in the manual tracing. The basal image positions are defined by the most basal image that encompassed at least 50% myocardium circumferentially [7]. Linear regression and Bland-Altman analysis are used to compare volume estimations between manual tracing and the other automated methods.

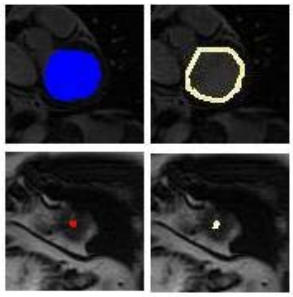

Fig 2: Example of algorithmic segmentation (left column) and manual tracing results (right column) on basal (top row) and apical (bottom row) section

RESULTS: The mean and difference of the algorithmic quantification (AQ) and manual tracing measurement (MTM) in EDV, ESV and EF are summarized in Tables 1. Fig 2 shows one successful segmentation example of algorithmic segmentation and manual tracing results on the apex and base sections, respectively showing good agreement.

DISCUSSION AND CONCLUSION: This algorithmic method based on the spatio-temporal continuity of LV area and shape effectively locates the basal and apical sections and accurately estimates LV cavity areas on all sections. Sometimes there is a limit to define and segment the most basal slice due to the complex structure of basal section, which can be resolved by calculating myocardial length [7]. A blinded study on a larger group of patients is warranted for assessment of performance. In summary, this method is promising for routine clinical evaluation of cardiac diseases with MRI.

Parameters	AQ	MTM	Linear Regression Correlation*	MTM minus AQ**	
				Absolute	Relative (%)
EDV	169.4±61.1(ml)	172.6±58.5(ml)	y = 1.0383x - 9.8278,R^2 = 0.988	3.2±7.1(ml)	2.4±4.8 (%)
ESV	73.9 ±55.0(ml)	74.2±54.8(ml)	y = 0.9981x - 0.2153,R^2=0.9885	0.4±5.9(ml)	-0.2±9.8 (%)
EF	60±13.5 (%)	60.5±14.2 (%)	y = 0.9223x + 4.1299,R^2 = 0.9391	0.6±3.5 (%)	-0.5±6.6 (%)

Table 1: Quantification and Comparison Results of AQ and MTM in 38 Subjects.

Note: All subtraction values are means ± standard deviations of paired differences.

* x = MTM, y = AQ; ** No difference, except end-diastolic volume, are statistically significant (p > 0.05).

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