Semi-Automation of Myocardial Tissue Phase Mapping Segmentation and Analysis

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Target Audience: Radiologists and researchers interested in measuring Left Ventricular wall motion abnormalities.

Purpose: Quantification of regional Left Ventricular (LV) wall motion abnormalities is important for the understanding of the impact of cardiac disease such as coronary artery stenosis or LV dilative or hypertensive cardiomyopathy on regional cardiac function[1,2]. In this context, 2D MRI Tissue Phase Mapping (TPM)[3] allows the quantitative segmental evaluation of myocardial velocities with high resolution and full LV coverage. TPM acquires time-resolved (CINE) magnitude images and and three-directionally velocity encoded phase images (v_x,v_y,v_z) with high temporal resolution. Previous studies have shown the diagnostic value of TPM for the deification of regionally disturbed myocardial function patients with hypertrophy[4], cardiomyopathy[5], after heart transplantation[6], and other cardiac diseases[7,8,9]. However, TPM data analysis requires significant post-processing including the often time-consuming manual segmentation of endo-/epicardial left ventricular (LV) contours which can result in analysis time of 20-30 minutes for typical TPM studies covering basal, midventricular and apical LV locations. As a result, TPM is additionally limited by overseer variability. Due to the limited blood-tissue contrast in the anatomic (magnitude) TPM images compared to standard techniques (CINE SSFP), standard segmentation algorithms that rely on the detection of anatomic boundaries are insufficient for robust and automated segmentation of the LV. It was the aim of this study to develop a novel LV segmentation algorithm for TPM data that includes both anatomic and functional through-time velocity data not used in previously reported segmentation algorithms[10,11]. The aims of this study were to (1) greatly extend and automate the functionality of an in house TPM evaluation tool (2) explore a method of semi-automatic segmentation that uses both magnitude and velocity data through time in conjunction with cluster analysis to create LV endo-/epicardial contours throughout all cardiac phases with minimal user input (3) compare preliminary results of this semi-automated segmentation with those from manual segmentation as the reference standard.

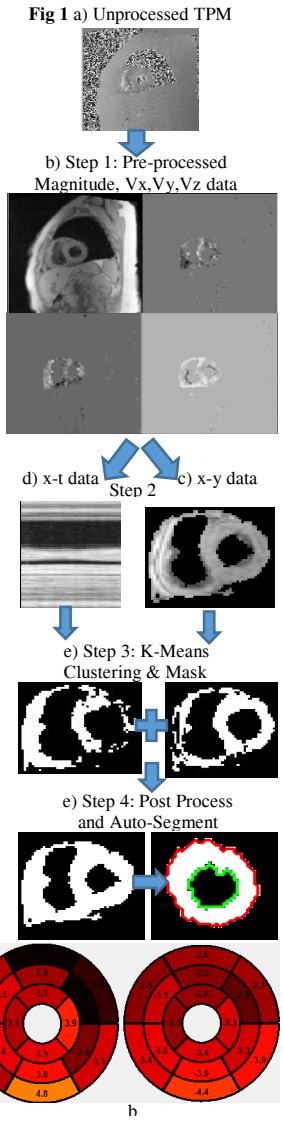

Fig 1 a) Unprocessed TPM

Methods: TPM in the short axis orientation was performed on 4 patients with non-ischemic cardiomyopathy (NICM) on a 1.5 T scanner (MAGNETOM Aera or Avanto, Siemens Medical Systems, Erlangen, Germany). Data were acquired in basal, midventricular and apical locations using a black-blood prepared cine phase-contrast sequence with tri-directional phase encoding in the short axis orientation (venc=25cm/sec, temp res=24msec, spatial res=2.9x2.4mm^2, thickness=8mm). Spatio-temporal imaging acceleration (k-t parallel imaging PEAK GRAPPA) with a net acceleration factor of R_{net} = 3.6 was employed which permitted data acquisition during breath-holding (breath-hold time = 25 heart beats per slice). TPM data was imported into an in-house MATLAB (Mathworks, Natick, MA) tool used for the semi-automatic post processing of PC-MRI data. A 4-step analysis workflow was developed for semi-automation included as illustrated in figure 1. 1) Pre-processing: To acquire an approximate mask of the entire myocardium, noise, velocity standard deviation over time (velSTD), derivative (low pass), and median filters were applied. Static tissue as identified by velSTD was removed and used for eddy current correction of the data (figure 1b). 2) Multi-dimensional re-sampling: In additional to the original shot axis orientation of velocity and magnitude data (x-y stack) another copy was automatically re-sampled in the x-t direction (x-t stack, figure 1 c-d). 3) Feature based cluster analysis: For both x-y and x-t data, k-means clustering was used to separate the myocardium from all other anatomic regions (figure 1e). Several analysis trials were used to identify the optimal image features for cluster analysis: For the x-y stack, absolute velocity (sqrt(v_x^2+v_y^2+v_z^2) and an auto-thresholded version of the magnitude data using Otsu's method to minimize interclass variance of black and white pixels was used[12]. The x-t stack used identical magnitude data but sqrt(v_x^2+v_y^2) and the exponential of the V_z data to better differentiate remaining blood pool pixels through time. 4) Construction of segmentation contours: The x-y and x-t data yield two independent and complimentary masks which were combined to a final mask which was automatically closed (image dilation followed by erosion) and filtered for the largest object (the myocardium). User interaction was required to manually separate the LV from the right ventricle (RV) during a single time frame in diastole, which is then propagated through the rest of the dataset. Finally, the mask is automatically segmented (figure 1e). Further (automated) analysis included the transformation of the acquired three-directional velocities into radial, long-axis, and circumferential velocities as described previously[3]. Myocardial velocities were mapped onto the AHA 16-segment model. For all 16 segments, systolic and diastolic radial and long-axis peak velocities were extracted (Figure 2). The semi-auto segmentations were compared to a reference manually segmented dataset in the same patients.

Figure 2: Examples of AHA bullseye plots output from the TPM Processing a) Peak systolic and b) Peak diastolic LA velocity.

Results: Pre-processing (Figure b) substantially reduced noise and improved later segmentations. The total analysis time for semi-automated segmentation (three slices, base, mid apex) was 3-5 min. Over all basal slices, the algorithm successfully created a contour of the myocardium 90% of the time. In the mid and apex slices the success rate was 79%, and 56% respectively. Bland Altman analysis of the base and mid slices (figure 3) shows strong agreement between both global and regional (individual segments of the cardiac bullseye) data. However, the limits of agreement suggest that the semi-auto method has moderately increased variability.

	Mean Difference	Limits of Agreement	Velocity Range
Global Velocity	5.27x10^{-17} m/s	3.02 m/s	-11.99-8.27 m/s
Regional Vel.	1.54x10^{-16} m/s	2.97 m/s	-18.57-13.54 m/s

Figure 3: Bland Altman analysis of semi auto vs. manual PWV

Discussion: A novel semi-automated TPM segmentation technique utilizing the full anatomic and functional information of TPM data showed moderate agreement with the manual reference standard and warrants further development and analysis. The performance of the technique was weakest in apical slices, when it is difficult for even an expert user to visually discern the epi/endocardial boundaries. The method occasionally fails due to small gaps in the myocardial mask. Small modifications will eliminate this weakness. Selecting two independent clustering algorithms to create a composite mask of the myocardium proved useful as through time data compliments the x-y data when it breaks down during periods of low velocity and SNR. In conclusion, the novel TPM semi-automatic segmentation technique is a promising time reduction step and warrants further investigation.

References: 1. J Am Coll Cardiol 2000;35:1221–1227; 2. Hypertens Res 2007;30:759–766; 3. J Magn Reson Imaging 2006;24:1033-9; 4. Eur Radiol 2013;23:339-47; 5. J Magn Reson Img. 2013;37:119-26; 6. Foll Eur J Cardiothorac Surg 2013: ezt448; 7. J. Magn. Reson. Img. 38: 1054–1062; 8. Circ.: Cardiovasc. Img.; 9. Radiology, 238 (2006), 816-26; 10. Comp. Med Img 29 (2005), 607-16 ; 11. Med Imag Analysis, 15 (2011), 169-84; 12. IEEE Systems,Man, & Cybernetics, Vol. 9, No. 1, 1979