Tracking the left ventricle from under-sampled MR Images

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Introduction: Tracking the left ventricle (LV) from cardiac MR Images has become a standard procedure to diagnose regional left ventricular dysfunctions or to estimate variables such us ejection fraction, ventricular volumes or cardiac output. The acquisition and processing of dynamic cardiac MRI present two major challenges: first, since most of the cardiac MRI protocols require breath-hold during acquisitions, to speed up the acquisition process becomes of great importance. Secondly, tracking/segmentation algorithms need to be robust to noise, pixelation, poorly defined boundaries, and other commonly encountered artefacts.

A recently exploited approach to achieving shorter scan times is to acquire only a portion of the data, and to apply some sort of priorknowledge (or minimisation) based reconstruction algorithm to undo the aliasing of the under-sampled images [1]. Although effective, most of those reconstructing algorithms involve complex or computationally demanding processes. In separate developments, important advances in image segmentation through the application of snake (or active contour) based tracking techniques [2] have been reported that improve robustness to MRI artefacts. However, a combined solution that could face both challenges is yet to be done.

We propose a different approach in which we track the LV directly from under-sampled (and therefore aliased) MRI data sets, without using any reconstruction algorithm (apart from the standard FFT reconstruction). We solve the aliasing issues by introducing a shape descriptor to our snake-based tracking algorithm, so that tracking method converges correctly onto the boundaries of the LV wall. Methods: Six volunteers were scanned using a standard triggered Balanced Fast Field Echo (TR/TE 3.1/1.5 ms, Flip angle 50°, slice thickness 8 mm, in-plane isotropic resolution 2.9 mm, 25 frames) in a Philips Intera 1.5 T, according to the AHA standard of four slices (3 short-axis and 1 long-axis slices of the LV cavity) [3]. Five of the data sets were kept intact for training purposes and one data set was stored in two formats: fully-sampled and as a simulated under-sampled image by taking only 1 every 7 samples of its ky-space data. The fully-sampled and the under-sampled images were independently tracked using an algorithm based on Simplex Mesh Diffusion Snakes (SMDS) [4], in which the endocardium of the LV is segmented from each frame by minimising an energy functional that depends on the image intensities of the processed frame, and on a shape descriptor built from the tracking of the fully-sampled training data sets. Whereas the image intensity part of the energy functional deforms the tracking contour towards the endocardium of the LV, the shape descriptor favours the contour's deformation so that its shape is consistent with what was learnt from the training process. The tracking results were quantitatively evaluated by computing the mean and standard deviation of Euclidean distance of the final contour segmentations of the fully- and under-sampled images (on equivalent frames). Each contour (one contour per frame) was built from 100 control points, and for comparison purposes, results were compared against those obtained from a standard Snake segmentation [5].

Results: As a proof of concept, only the mid-cavity image sequence was analysed in its two versions (fully- and under-sampled). As can be seen in Fig.1a, the reconstructed under-sampled images have strong aliasing artefacts. In particular, the endocardium of the LV has been corrupted by the fold-over of other structures. Fig. 1c (frame 24) shows how the SMDS-based tracking algorithm effectively identifies the LV. However, because of the aliasing artefacts, the boundaries of the LV are not entirely clear, and most of the standard tracking algorithm might fail or converge to an erroneous boundary, which is the case of a traditional Snake segmentation (Fig. 1d). In contrast, the SMDS tracking algorithm can enforce shape consistency through the entire sequence, so that convergence to erroneous locations is substantially reduced. Quantitatively, the mean of the Euclidean distance (between fully and under-sampled SMDS tracking results) ranged from 0.15 to 0.35 pixels, and its standard deviation ranged from 0.1 to 0.2 pixels for all the 25 frames. The same statistics for the traditional Snake algorithm ranged from 0.17 to 1 pixels for the mean and from 0.11 to 0.75 pixels for the standard deviation.

Conclusion: The results show that the shape descriptor introduced in the SMDS-based tracking algorithm considerably reduces erroneous convergences and provides good estimation to LV boundaries in aliased images. Further tests will be required in which the analysis is extended to all the acquired slices, or even in a complete 3D+time fashion, however, the current results suggest that the algorithm can successfully track the LV directly from aliased cardiac MRI data.

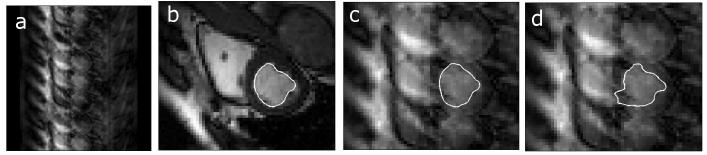


Fig. 1a: Under-sampled MR image of the mid-cavity left ventricle (frame 24) Fig. 1 b,c,d: Magnified view of the tracked LV (frame 24). b) Fullysampled image SMDS tracking. c) Under-sampled image SMDS tracking. d) Under-sampled image Snake tracking. References [1] Tsao et al, MRM 50, 5, 2003. [2] Bardinet et al, ECCV, 317-328, 1996. [3] Cerqueira, et al, "Standardized Myocardial Segmentation and Nomenclature for Tomographic Imaging of the Heart", Circulation 2002, 105, 539-542 [4] Tejos et al, Simultaneous segmentation and registration of MR Images ISMRM 2006. [5] Kass et al, IJCV 1, 321-331, 1987. Grant sponsor: Fondecyt 1060088