

Fully Automatic Cardiac Motion Estimation from Tagged MRI Using Non-Rigid Registration Techniques

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Abstract

Many different techniques have been proposed to compute motion fields on Tagged MR imaging. However, most of them require tags segmentation or endo-epicardial contours segmentation.

Automatic estimation of the myocardial motion field was extracted using a consecutive non-rigid registration algorithm based on a semilocal Bspline parametric model. The sequence was also represented in the Bspline space using this framework to construct the multiresolution pyramid within the optimization process.

Validation was performed on sequences from 5 healthy volunteers comparing the estimated trajectories with the manual tracking provided by an expert. Results were also compared to HARP analysis. Subpixel accuracy was obtained, and results were superior in all cases to HARP analysis.

1. Introduction

Automatic cardiac motion analysis constitutes an important aid for the quantification of the elasticity and contractility properties of the myocardium. Localized regions with movement abnormalities are related to the existence of many different cardiovascular diseases.

Magnetic resonance imaging (CINE-sequences and tagged MRI), is nowadays the reference modality to study the regional myocardial function. Despite the efforts of the medical imaging community, subjective interpretation is still the method of reference in clinical practice. The subjectivity of this approach may induce important disagreements on regional analysis among medical experts and centres, that may be overcome using quantitative methodologies.

The usefulness of MR tagging to assess regional myocardial deformation has been widely demonstrated[1, 2]. Myocardial tagging was first addressed by Zerhouni et al. [3] and Axel and Dougherty in 1989[4]. This technique uses spin tagging concepts to produce noninvasive markers

in the myocardial tissue that persist during at least part of the cardiac cycle. The tagging process is based on modulating the longitudinal magnetization of the tissue right before the sequence of images is acquired. SPatial Modulation of Magnetization (SPAMM) is the most common technique used to produce sinusoidal tag patterns [4]. Different approaches have been developed to compensate for the tag fading using two complementary SPAMM sequences (CSPAMM) [5].

Many different techniques have been proposed to compute motion fields on Tagged MR imaging. Some methods combine image feature extraction (myocardial borders and tags, with deformable and mechanical models[6-9]). The main drawback of these methods is that the computed motion strongly depends on a proper segmentation of the myocardial borders and tags a difficult task on tagged MR sequences due to signal-to-noise ratio the data due to its poor. Prior works using nonrigid registration have also been recently applied to tagged MR studies to compute cardiac motion [10]. However, most of these methods require intensive user interaction, such as supervision of the tags segmentation or of the endo-epicardial contours segmentation.

And automatic and efficient approach has been recently proposed tracking the phase shifts on the modulated SPAMM images (Harmonic phase imaging (HARP) [11]). This method isolates the spectral peaks corresponding to the tag pattern in the frequency domain. Displacement fields are computed automatically spectral optical flow techniques that track the phase tagged in the myocardial tissue.

Our work presents a new approach to estimate motion from Tagged MR sequences using non-rigid registration techniques without requiring any segmentation and providing very good accuracy. The article is organized as follows. In the next section, we present the method used to compute the dense myocardial motion field the imaging procedure and the validation methodology. To end we present the results and the discussion and conclusions in the final section.

2. Methods

Myocardial motion estimation was computed using a non-rigid registration algorithm to obtain inter-frame displacements. The proposed methodology does not require any user interaction or image segmentation, so therefore it is fully automatic. The method is validated with respect to the manual tracking of tag intersections by an expert in data from healthy volunteers. Results are also compared with respect to standard HARP processing.

2.1. Proposed algorithm

Given an image sequence $f(t, \mathbf{x})$, we want to estimate a dense displacement field $\mathbf{g}(t, \mathbf{x})$ that represents the displacement field over the whole sequence. The movement is represented with respect to the first frame of the sequence $t=t_0$. We express $\mathbf{g}_t(\mathbf{x})=\mathbf{g}(t, \mathbf{x})$ as a series of transformations between consecutive pairs of images found through independent non-rigid registration processes.

$$\mathbf{g}_t(\mathbf{x}) = \mathbf{g}'_t(\mathbf{x}_{t-1}) \text{ where } \mathbf{x}_{t-1} = \mathbf{g}_{t-1}(\mathbf{x}) \text{ and } \mathbf{g}_0(\mathbf{x}) = \mathbf{x} \quad (1)$$

where t is the temporal axis in frames (T being the total number of frames) and $\mathbf{x}=(x_1, x_2)$. The non-rigid registration process is formulated as an optimization procedure that minimizes a similitude criterion E to find the best suitable transformation to find the corresponding points from a test image into a reference image. Figure 1 shows the scheme of the independent non-rigid registration processes. E is defined as the sum of squared differences between consecutive frames. The transformation model used in this process \mathbf{g}'_t is defined as a linear combination of Bspline basis functions, located in a rectangular grid [12-14]:

$$\mathbf{g}'_t(\mathbf{x}) = \sum c_j \beta_r(\mathbf{x}/h-j) \quad (2)$$

The scale parameter h determines the space between the grid knots and, therefore, the number of parameters \mathbf{c}_j and the smoothness of the solution.

The optimization strategy encompasses a multiresolution process solved by using a gradient descent method. We generate a continuous version of the discrete image $f(t, \mathbf{x})$ by spline interpolation; providing an excellent framework to find a subpixel solution and to compute the spatial derivatives analytically and, therefore, the criterion gradient. Speed and robustness are guaranteed using a multiresolution approach both in the image and transformation space, creating a pyramid optimal in the L_2 -sense taking advantage of the B-spline representation [15].

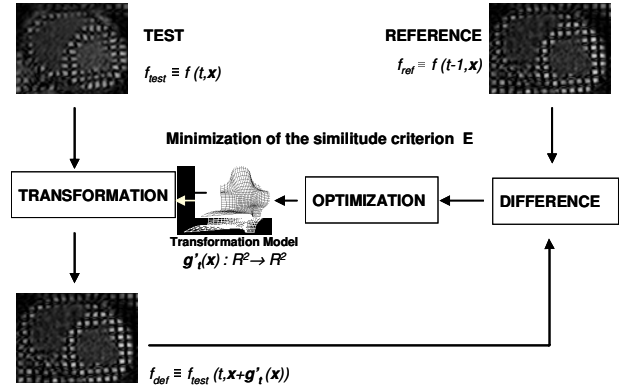


Figure 1: Interframe displacements are obtained applying a non-rigid registration scheme to consecutive pairs of images. This problem is formulated as an optimization process that minimizes a similitude criterion E .

2.2 Imaging

Tagged MR images were acquired using an optimized tagging sequence on a Philips Intera 1.5 T (Philips Medical Systems, The Netherlands) and with a five elements phased-array coil dedicated to cardiac imaging.. Five healthy volunteers were examined acquiring short axis images with a frame rate of 13 frames per cycle. The tagging sequence used was an enhanced version of the free breathing SPAMM sequence provided by the manufacturer for our Philips Intera scanner [16]. The proposed sequence makes use of artesian k-space filling, turbo gradient echo (GE) pulses and both ECG and respiration gating. Main parameters of the sequence are: matrix = 192*192 (phase*frequency), 4 NSA, rectangular FOV = 100%, acquisition percentage = 100%, TE = 1.9 ms, TR = shortest (5.5 ms for 80 bpm), flip angle = 13°, turbo factor = 8, slice thickness = 8 mm, orthogonal grid lines spacing = 8 mm, respiratory synchronization = gating, acquisition time = 1'12'', 13 phases for 80 bpm. The main advantage of this sequence is that the tag contrast is very well maintained through the whole sequence (see figure 2, frame 1 and frame 12) [16].

2.3. Data analysis

All the sequences were analyzed using the Non-rigid registration motion estimation using quadratic Bsplines and $h=1\text{cm}$ knot spacing. HARP analysis [11, 17] was also conducted in all the sequences using the implementation described in [18] as global method. The HARP implementation was tested in an artificial sequence of a short axis image with perfect sinusoidal

modulation confirming the right performance.

In order to set a gold standard tags intersections (24 points for every sequence) were manually tracked by an expert. Estimated motion trajectories computed with the proposed method and with HARP were compared in terms of Euclidean distance. The mean error with respect to the manual tracings along the whole sequence was calculated for every sequence and method.

3. Results

Figure 1 shows the results obtained using the proposed non-rigid registration approach. Green points correspond to the manually tracked expert points and red points to the algorithm outcome. The performance of the method is very good along the whole sequence.

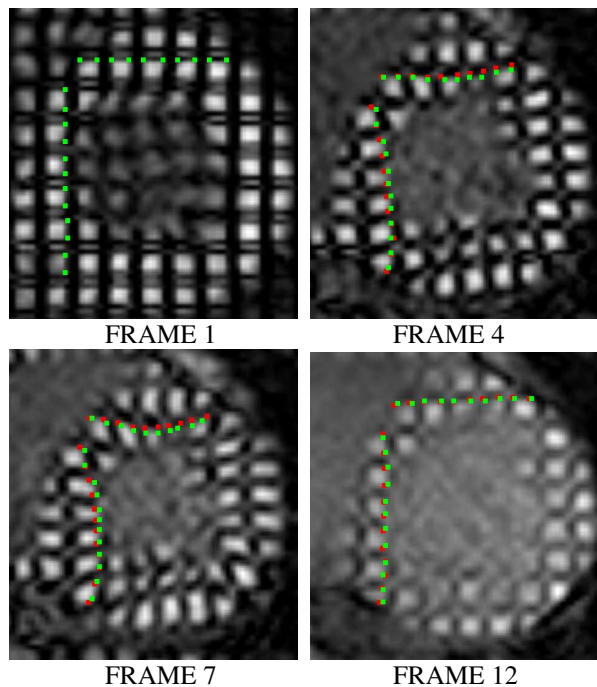


Figure 2: Estimation of points trajectories using the non-rigid registration method versus the expert manual tracking. Manually outlined points shown in green. Non rigid registration results shown in red.

Quantitative results of motion estimations using the proposed approach resulted in a mean error of less than 1mm (~0.76 pixels) for all the analyzed sequences. However, HARP analysis provided worse results in all cases (2.5 pixels ~ 3 mm). Table 1 shows the results in pixels for all the sequences analyzed with both methods.

Table 1: Mean distance errors (in pixels) between the trajectories of the 24 delineated points and the automatically tracked results using the proposed non-rigid registration method and HARP.

Method	S 1	S 2	S 3	S4	S5
Non-rigid registration	0.75	0.81	0.76	0.77	0.71
HARP	2.75	2.60	3.14	1.8	2.45

4. Discussion and conclusions

This work has presented a new approach to compute motion trajectories from Tagged MR imaging without any user interaction using non-rigid registration techniques. In comparison to previous methods [10] proposed interframe displacements are computed using a non-rigid registration method that uses the standard sum of square difference metric. The use of this metric assumes that the interframe time intervals are short in comparison to the T1 tissue recovery [19].

The results of the proposed method have shown very good accuracy along the whole sequence. On the other hand HARP did not provide as good results along the whole sequence. HARP results taking into account only the first few phases were reasonable, and they were worse as tag contrast degraded. As a result the non-rigid registration method showed a more robust behaviour as it considers all the image information and not only the phase information (much more sensitive to artefacts). The semi-local transformation model and the global criterion also set a good framework to balance local transformations with global shape. The multiresolution optimization strategy and the continuous representation of the sequences also contribute to improve robustness.

As a main conclusion we could state that fully automatic Tagged MR image processing is feasible and accurate using non-rigid registration techniques based on the computation interframe displacements. Subpixel accuracy is achieved thanks to the B-spline sequence representation and the robustness of the technique.

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