

Influence of the Temporal Resolution on the Quantification of Displacement Fields in Cardiac Magnetic Resonance Tagged Images

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Abstract

It is difficult to acquire tagged cardiac MR images with a high temporal and spatial resolution using clinical MR scanners. However, if such images are used for quantifying scores based on motion, it is essential a resolution as high as possible. This paper explores the influence of the temporal resolution of a tagged series on the quantification of myocardial dynamic parameters. To such purpose we have designed a SPAMM (Spatial Modulation of Magnetization) sequence allowing acquisition of sequences at simple and double temporal resolution. Sequences are processed to compute myocardial motion by an automatic technique based on the tracking of the harmonic phase of tagged images (the Harmonic Phase Flow, HPF). The results have been compared to manual tracking of myocardial tags. The error in displacement fields for double resolution sequences reduces 17%.

1. Introduction

Several global indicators such as cardiac output, ventricular volume or ejection fraction have been widely used in clinical routine to evaluate heart function [1]. Nevertheless, these indicators are not able to accurately localize injured zones. Regional parameters, such as strains or perfusion, have arisen as more precise indicators for cardiac function assessment [2]. Regional parameters require estimation of the motion that the myocardial tissue undergoes along the cardiac cycle.

Although there are, currently, many medical imaging modalities (echo-cardiography, magnetic resonance) allowing assessment of the overall heart function, they are not well suited for extraction of tissue motion within the myocardial walls. Tagged MR (TMR) [3, 4] is the reference imaging modality for intramural tissue motion visualization. This technique prints a grid-like pattern of saturated magnetization over the myocardium, which, as

it evolves by the underlying motion of tissue, allows visualization of intramural deformation.

A main limitation of current clinical MR scanners is that they do not provide TMR images with, both, a high temporal and spatial resolution. An accurate computation of scores based on the motion extracted from the processing of TMR sequences requires a given (minimum) resolution.

In this paper we explore the impact of the temporal resolution on the accuracy of the displacement field estimated from TMR sequences. In this manner we also evaluate the capability of the acquired sequences for providing series of images valuable for a quantitative analysis of dynamic scores (like strain or ventricular torsion).

We have prepared a standard scanner for TMR series acquisition at simple and double resolution. The tissue deformation (computed with the Harmonic Phase Flow, HPF, in our case) extracted for each simple sequence, S1 and S2, provides two vector fields, V_i (for $i=1, 2$) sampled at the cardiac phases each frame was acquired. The vector field connecting such phases, V , is obtained by applying HPF to the interleaved series. To assess the influence of the temporal resolution, we calculate the displacement field for S1, S2 and the interleaved images with HFP and compare the results with the displacement obtained tracking manually placed points on the myocardium.

We can conclude that if we are to use the image series for quantification, the results will improve in roughly 20% if the temporal resolution doubles.

2. Methods

The displacement fields were calculated for four cases. The images used in all cases were the medial slice from a short axis view. The manual tracking results were obtained by using the tpsDig (SUNY at Stony Brook) software. Six points were placed on the myocardium,

approximately on the centre of each AHA segment (fig 1.). The same points displacements were extracted from the matrices computed with the Harmonic Phase Flow.

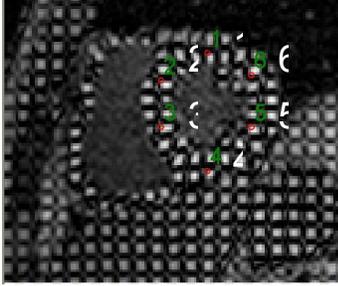


Figure 1 .Manually placed points following the AHA segments

The quadratic error provides our quality measure for quantifying the influence of temporal resolution. It is calculated considering the manually obtained displacements as the golden standard.

Double Acquisition of TMR Sequences

Our images are acquired in a Philips Intera 1.5 T scanner (Philips Medical Systems, The Netherlands), with a SPAMM prepared Turbo Field Echo sequence. The Standard temporal resolution is 13 phases for 80 bpm and the acquisition time is 1'12". This sequence has been prepared by the authors, it is synchronized with both the electrocardiogram and the respiration, and the images are acquired while the patient is breathing freely.

The sequence main parameters 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.

To double this temporal resolution a second series of images is acquired, but introducing a time shift between the first frame and the triggering signal. The time shift corresponds to half of the spacing time between two consecutive frames. We interleave these two acquisitions S1 and S2, and obtain a new series that doubles the temporal resolution of the individual ones, halving the temporal gap between frames.

Harmonic Phase Flow Motion Tracking

There are many techniques (such as FindTags [5] in spatial domain or HARP [6] in Fourier space) addressing computation of LV motion from TMR images. In this paper we use the Harmonic Phase Flow (HPF) method developed by the authors in [7] because it overcomes some of the problems of the above standard techniques:

- It tracks motion at advance stages of the systolic cycle (like HARP).

- It provides continuous vector fields on the image domain.
- It handles local deformation of tissue.

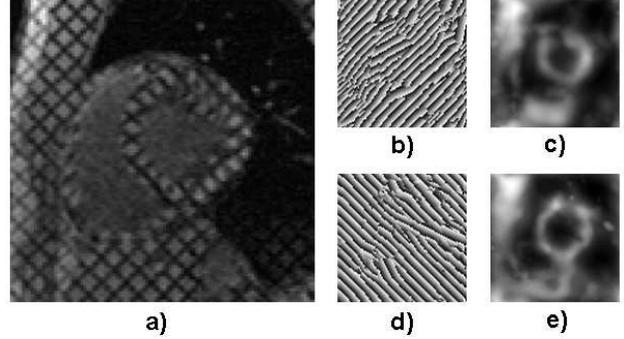


Figure 2 . Given an incoming tagged frame a), two Gabor filter banks are applied to it, leading to a couple of complex images. The wrapped version of their phase is shown in b) and d), while their amplitudes in c) and e).

Let $\{I^t(x, y)\}_{t=0}^T$ denote a TMR sequence (fig.2 a)) and $V^t(x, y)$ the vector field matching frames at times t and $t+1$. The HPF estimation of such vector proceeds in two stages: extraction of a representation space capturing local deformations and feature tracking within a variational framework.

The representation space is two dimensional (see fig.2 b) and d)) and is obtained by assigning to each point the maximum response of two Gabor filter banks (one for each tag direction). The Gabor filters are centered around the main frequency of tags and tuned for each myocardial cut (base and apex). The complex images in the representation space will be noted by (I_1, I_2) and their phase and amplitude by Φ_k and Λ_k , respectively. On one hand, it can be shown [6] that Φ_k (fig.2 b) and d)) is a material property of the tissue that remains constant along the cardiac cycle. Since the brightness constancy constrain is met, classical optical flow [8] can be applied to track both phases. On the other hand, Λ_k (fig.2 b) and d)) provides a measure of the reliability of the phase values detected by the Gabor filter banks.

The variational framework we propose regularizes the deformation field at areas where Λ_k drops. The searched vector field, $V(x, y) = (U(x, y), V(x, y))$ should minimize the energy:

$$\underbrace{\int (1 - (\alpha_1 + \alpha_2)/2)^2 \varepsilon_{reg}^2}_{\text{Regularity}} + \underbrace{\int [\alpha_1^2 \varepsilon_1^2 + \alpha_2^2 \varepsilon_2^2]}_{\text{Matching}} \quad (1)$$

where the matching and the regularizing terms are defined as:

$$\varepsilon_k = \Phi_{kx}\mathcal{U} + \Phi_{ky}\mathcal{V} + \Phi_{kt}$$

$$\varepsilon_{reg} = \|\nabla V\|^2 = \|\nabla\mathcal{U}\|^2 + \|\nabla\mathcal{V}\|^2$$

For Φ_{kx} Φ_{ky} Φ_{kt} the partial derivatives of the k -essim phase Φ_k and the weighting functions α_k 's given by the amplitudes:

$$\alpha_k = \frac{|\Lambda_k|}{\max(|\Lambda_k|)}$$

The solution to the Euler Lagrange equations associated to the functional (1) is obtained by solving the gradient descent scheme:

$$\begin{aligned} \partial\mathcal{U}^t/\partial t(x, y) = & \\ -[(\Phi_x g \Phi_x)\mathcal{U}^t(x, y) + (\Phi_x g \Phi_y)\mathcal{V}^t(x, y) + \Phi_x g \Phi_t & \\ -(1 - \alpha)^2 \Delta\mathcal{U}^t(x, y) + 2(1 - \alpha)\langle \nabla\alpha, \nabla\mathcal{U}^t(x, y) \rangle] & \\ \partial\mathcal{V}^t/\partial t(x, y) = & \\ -[(\Phi_y g \Phi_y)\mathcal{U}^t(x, y) + (\Phi_y g \Phi_x)\mathcal{V}^t(x, y) + \Phi_y g \Phi_t & \\ -(1 - \alpha)^2 \Delta\mathcal{V}^t(x, y) + 2(1 - \alpha)\langle \nabla\alpha, \nabla\mathcal{V}^t(x, y) \rangle] & \end{aligned} \quad (2)$$

where $\langle \cdot, \cdot \rangle$ denotes the scalar product, ∇ and Δ stand for the gradient and Laplacian operators and $g = \text{diag}(\alpha_1^2, \alpha_2^2)$.

The solution to eq. (2) gives our Harmonic Phase Flow. In [7] we prove that it reaches sub-pixel precision in experimental data. Two instances, for basal and apical views, of its performance are shown in figure 3.

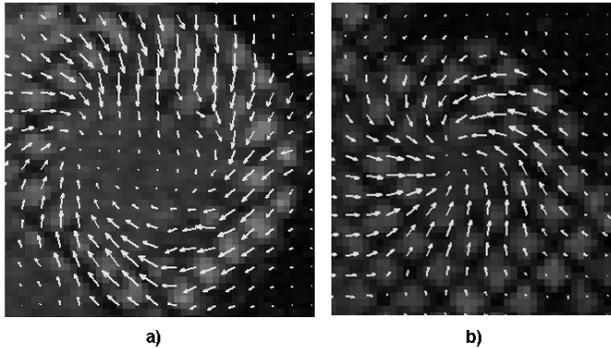


Figure 3. The resultant Harmonic Phase Flow over two analyzed tagged frames, belonging to base a) and apex b).

3. Results

The table below shows the mean quadratic error between the HFP and the manually obtained displacements for each point and for the double (Mean 2 Res) and simple (Mean 1 Res) temporal resolution series.

The mean is calculated using the four sets of images available. The points are numbered as in figure 1.

Point #	Mean 2 Res	Mean 1 Res	Ratio D/S
1	1,16	1,22	0,96
2	1,25	1,06	1,18
3	0,50	0,84	0,59
4	1,09	1,92	0,57
5	0,80	0,97	0,82
6	1,24	1,18	1,05

For points number 2 and 6 the error between the manual and HFP displacements is slightly larger for the double temporal resolution series. For points number 1, 3, 4 and 5 the error is less for the double resolution series.

The quadratic error takes very different values for the diverse segments. Calculating the mean for the quadratic errors for all the segments, we obtain that it is 17% smaller for the interleaved sequence than for S1 or S2 when processed independently.

Point #	Mean 2 Res	Mean 1 Res	Ratio D/S
all	1,00	1,20	0,83

4. Discussion and conclusions

We can conclude that it is important to optimize the MR acquisition sequences in order to obtain the maximum temporal resolution possible for the scanner, if such images are to be used for calculating parameters. In this work we have compared the influence of the temporal resolution for calculating the displacement of some points along a cardiac cycle time. We considered the manually tracked points as the gold standard and compared their displacements with the ones calculated using the HPF method.

The overall result is that the displacements calculated using a double temporal resolution series are 17% better than using a single temporal resolution one. We want to mark the difference between the error for points 2 and 6, which are placed symmetrically on the upper part of the short axis view, and the rest of the points. We can see that the segments move in a different fashion and it affects the parameters quantified from them. We think it is worth to assess the influence of the temporal resolution evaluating other parameters like circumferential or radial strain and analyze the results segment by segment.

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