An Intuitive Validation Technique to Compare Local versus Global Tagged MRI Analysis

J Garcia Barnes[1], J Barajas[1,2], F Carreras[3], S Pujadas[3], P Radeva[1]

[1]Computer Vision Center, Universitat Autonoma de Barcelona, Bellaterra, Spain
[2]CICATA-IPN, Queretaro, Mexico
[3]Hospital de la Sta Creu i St Pau, Barcelona, Spain

Abstract

Myocardium appears as a uniform tissue that seen in convectional Magnetic Resonance Images (MRI) shows just the contractile part of its movement. MR Tagging is a unique imaging technique that prints a grid over the tissue which moves according to the underlying movement of the myocardium revealing the true deformation of the cardiac muscle.

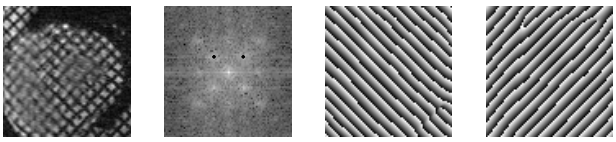
Optical flow techniques based on spectral information estimate tissue displacement by analyzing information encoded in the phase maps which can be obtained using, local (Gabor) and global (HARP) methods. In this paper we compare both in synthetic and real Tagged MR sequences. We conclude that local method is slightly more accurate than the global one. On the other hand, global method is more efficient as it is much faster and less parameters have to be taken into account.

1. Introduction

Cardiovascular diseases have arisen as one of the main causes of mortality during last decades. A complete knowledge of the heart function and how pathologies affect local and global myocardial contractility, would lead to a more accurate diagnosis and prevention. Measure of cardiac motion allows to extract quantitative parameters such as strain, stress, rotation and torsion which contribute to this aim. As the myocardium is a uniform tissue, when it is depicted in conventional MR images, only the contraction of myocardial wall boundaries is appreciated. Nevertheless it is known that there is also a hidden rotational part that gives important information. Tagged MRI is a relatively new technique that prints a grid over the tissue which deforms according to the underlying movement of the myocardial fibers, revealing the true deformation of the cardiac muscle.

Since the appearance of the Tagged MR (TMR) imaging modality in the late 80's ([1], [2]), many analysis techniques have been developed in order to extract information from such amount of raw data. Nevertheless, in this paper we will focus on those that use spectral information to obtain the optical flow (OF) of the sequence. These methods have been shown [3] to be more robust in presence of pixel brightness variation, which is a problem that affects sequences in general, and TMR in particular, due to the so called fading effect that makes tags and tissue to decrease their contrast. This kind of images has also been analyzed by OF methods that apply directly in the spatial domain as in [4], where pixel brightness variation is taken into account to derive the so called variable brightness optical flow (VBOF).

Spectral OF, can be divided in two main categories: local and global ones. The scope of this paper is to compare the performance of these methods over a set of synthetic and real sequences (SS, RS), to determine which of them and for which set of parameters the estimated displacement map (DM) is more accurate. In the case of SS, the real DM is known beforehand thus, comparation becomes trivial. In the case of real sequences, DM is not known and any attempt to validate the OF method, passes through manual landmarking of a "sufficiently large" set of points. In this paper, we also introduce an intuitive means of determining which, of a set of OF methods, performs best and we apply it to real sequences.



a) b) c) d)

Figure 1. a) Frame of a real sequence. b) Its Fourier Transform with two linearly independent harmonic peaks selected. c) and d) Phases of two angle images corresponding to the selected harmonic peaks.

2. Background

According to the tagging equation of the SPAMM (Spatial Modulation of Magnetization) pattern, a Tagged MR image (Fig. 1.a) can be expressed as sum of multiple complex images $\psi = \sum_{k=-K}^{K} \psi_k$ as suggested in [5], where each of the ψ_k is called Angle Image (AI) (Fig. 1.c .d) and whose phase is linearly related to the true motion of the myocardium in a particular direction. As the phase of points is an intrinsic property of the tissue that remains stable during the cardiac cycle, tracking tissue points becomes equivalent to tracking their phases. As each of the ψ_k produces an harmonic peak in the frequency domain (Fig. 1.b), in order to obtain the *kth* AI (ψ_k), its associated harmonic peak needs to be isolated. Depending on the means by which this is done, we will be talking about global or local methods.

To obtain full 2D motion, two angle images (α_1, α_2) coming from two linearly independent harmonic peaks (ψ_1, ψ_2) are required. Now, given any point x in the myocardium at time t, we can associate to it a couple of angle values $(\alpha_1(x,t), \alpha_2(x,t))$. The updated position of x at time $t+1$ is given by a $\tilde{x}$ that fulfils the condition $(\alpha_1(x,t), \alpha_2(x,t))$=$(\alpha_1(\tilde{x}, t+1), \alpha_2(\tilde{x}, t+1))$ [6].

2.1. Global method

Global method (or HARP [5]), retrieves any harmonic peak by applying to it a band-pass filter. This filter has to be wide enough to comprise most of the spectrum spread around the peak while avoiding to overlap its neighbors [5].

In our work we have designed a very simple but effective filter that we call Minimal Shape Filter (MSF), (see Fig. 2.a). Let $U^1 = (u^1, v^1)$ and $U^2 = (u^2, v^2)$ be the coordinates of two linearly independent main peaks (see Fig. 1.b), and let $R = min\{\|U^1\|_2, \|U^2\|_2\}/2$. We define

$$f^i_{MSF}(u,v) = \begin{cases} 1 & \text{if} \quad (u-u^i)^2 + (v-v^i)^2 \leq R, \\ 0 & \text{otherwise.} \end{cases}$$

and the filter for each of the two peaks as $F^i_{MSF} = f^i_{MSF} * G$, where G is an appropriate gaussian that smooths filter borders.

2.2. Local method

In this local approach, AI are not obtained directly as the phase of the response produced by a single filter, but they are constructed assigning to each point, the phase value of the highest response that a tuned filter bank returns. In our case, these filters are Gabor filters.

The Gabor filter was firstly introduced by Daugman in [7], and recently has been used to analyze TMR sequences [8]. It is essentially a Gaussian g modulated by a complex sinusoid s. In 2D, a Gabor filter has the following form in the spatial domain:

$$h(x,y) = g(x',y') \cdot s(x,y),$$

where $g(x',y')$ and $s(x,y)$ are defined as:

$$g(x',y') = \frac{1}{2\pi\sigma_{x'}\sigma_{y'}} \exp\{-\tfrac{1}{2}[(\tfrac{x'}{\sigma_{x'}})^2 + (\tfrac{y'}{\sigma_{y'}})^2]\},$$

$$s(x,y) = \exp[-i2\pi(u^k x + v^k y)].$$

The rotation of the Gaussian is established by:

$$x' = x\cos\theta + y\sin\theta, \quad y' = -x\sin\theta + y\cos\theta.$$

x' and y' represent the spatial coordinates rotated by an angle θ. $\sigma_{x'}$ and $\sigma_{y'}$ are the standard deviations for the Gaussian envelope and they should not coincide necessarily. This allows us to deal with anisotropic envelopes. In fact, an aspect ratio λ and its orientation are defined as:

$$\lambda = \frac{\sigma_{x'}}{\sigma_{y'}}, \quad \phi = \arctan(v^k/u^k)$$

where u^k and v^k represent the 2D frequencies of the complex sinusoid (Fig. 2.b .c .d).

It is well known that the Fourier transform $H(u,v)$ of $h(x,y)$ is a Gaussian centered on (u^k, v^k). Thus, the Gabor filter can be treated as a bandpass filter.

Given the coordinates of a main harmonic peak U^k, we consider a range of neighbor frequencies given by

$$u'^k = \Re\{(u^k + iv^k) \cdot m \cdot \exp(i\Delta\phi)\}$$
$$v'^k = \Im\{(u^k + iv^k) \cdot m \cdot \exp(i\Delta\phi)\}$$

which will define some of the parameters used to create the Gabor Filter Bank (GFB). Others will be independent and will be considered as parameters to vary and determine which maximize the accuracy of the estimated displacement map.

A similar approach to the local analysis of TMR sequences is proposed in [8].

a) b) c) d)

Figure 2. a) MSF filter in the frequency domain. b) c) and d) Real part of three Gabor filters (in the spatial domain) with different orientations and anisotropic envelopes.

3. Correlation measure

The goal of this paper is to compare the performance of different spectral OF methods over TMR sequences. Each of them will provide a dense DM over the myocardium. In the case of SS, the evaluation of its accuracy will be trivial. Nevertheless, in RS we do not know the exact DM thus, if we want to evaluate the accuracy of the estimated DM, we have to develop alternative methods. If we think of optical flow as a field that warps one image into another (usually very similar), we get the key idea to create what we call Correlation Measure (CM). Let us formalize it.

a) b) c) d) e)

Figure 3. a) and b) Two consecutive frames of a real sequence. c) Estimated displacement map between them ($\tilde{D}$). d) Myocardium ROI for first frame (ψ). e) Second frame warpped according to $\tilde{D}$ to match ψ ($\psi_{\tilde{D}}$). Notice that ψ and $\psi_{\tilde{D}}$ show the same structure but fading effect makes the brightness to vary in tag valleys.

Given a sequence of Tagged MR images $\psi(x, y; t)$, suppose that we know the real displacement map among the frames, $D(x, y; t) = (D_x(x, y; t), D_y(x, y; t))$. Suppose also that we know the region of interest that encloses the myocardium and at which we will restrict our calculations, $\Omega_t = \{(x, y) \in \text{Myocardium at time } t\}$. Now, fixed a time t, we deform the frame at $t + \delta t$ according to the displacement map between these two instants,

$$\psi_D(x, y; t) = \psi(x+D_x(x, y; t), y+D_y(x, y; t); t+\delta t)\rfloor_{\Omega_t}$$

Due to the fact that D is the exact displacement map, the two images $\psi(x, y; t)\rfloor_{\Omega_t}$ (for simplifying the notation we notice it by $\psi(x, y; t)$) and $\psi_D(x, y; t)$ are necessarily the same. Thus, any measure applied between them must be zero. In real sequences we do not know D. Instead, we have an approximation $\tilde{D} \approx D$ (see Fig. 3). The objective is to infer how much $\tilde{D}$ differs from D. We can do this by calculating some measure between ψ and $\psi_{\tilde{D}}$.

First of all, we raster-scan points in Ω_t either for ψ and $\psi_{\tilde{D}}$ and we concatenate them in two vectors of the same size V and $\tilde{V}$, respectively. These vectors define two signals (Fig. 4) whose difference depends on the accuracy of $\tilde{D}$ and the previously mentioned fading effect (only in the case of RS). We evaluate their similarity by correlating them:

$$C[\psi_{\tilde{D}}, \psi] = \frac{\sum_{\Omega_t}(\psi_{\tilde{D}} - \bar{\psi}_{\tilde{D}})(\psi - \bar{\psi})}{\sqrt{\left(\sum_{\Omega_t}(\psi_{\tilde{D}} - \bar{\psi}_{\tilde{D}})^2\right)\left(\sum_{\Omega_t}(\psi - \bar{\psi})^2\right)}}$$

where $C \in [-1, 1]$, $C = 1$ when $\psi_{\tilde{D}}$ and ψ match perfectly, $C = 0$ when they are completely different and $C = -1$ when they are opposite. Thus, given $\tilde{D}^1$ and $\tilde{D}^2$, if $C[\psi_{\tilde{D}^1}, \psi] > C[\psi_{\tilde{D}^2}, \psi]$, we assume that $\tilde{D}^1$ is more accurate than $\tilde{D}^2$. Notice that C does not tell us the precision, but only the relative accuracy between the two DM.

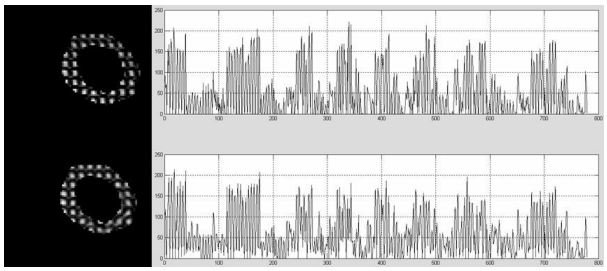
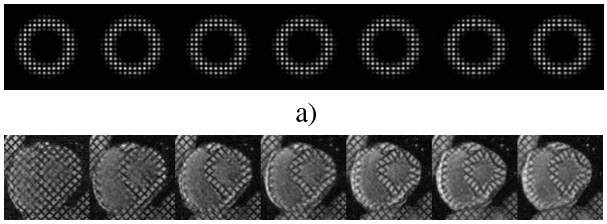


Figure 4. Here we can appreciate one frame and its next, deformed according to the estimated displacement map. On the right, the signals used to calculate correlation error.



a)

b)

Figure 5. a) One of the 4 synthetic sequences, in which we have induced a local displacement by translating the right half of the myocardium. b) Real Sequence.

4. Experiments and results

We performed different experiments over a set of 4 synthetic (Fig. 5.a) and 4 real (Fig. 5.b) sequences of seven frames each one. Real sequences have been obtained using a Siemens Avanto 1.5T MR scanner and belong to three different healthy volunteers. Synthetic sequences have been generated simulating basic deformations such as translation, rotation, scale, shear, eliptication and radial compression over a torus that represents the myocardium and which is marked according to the SPAMM pattern [5]. Local deformation has also been simulated by applying the previous transformations only in a ROI over the myocardium.

Gabor filter bank parameters have been set as following: $m \in [0.9, 1.1]$ and $\Delta\phi \in [-\pi/8, \pi/8]$. For each frequency (u^k, v^k), $\theta = atan(v^k/u^k)$, $\sigma_{x'} = K \cdot P_{u^k,v^k}$ where P_{u^k,v^k} is the period of this frequency and $\sigma_{y'} = \sigma_{x'}/\lambda$. The free parameters we have varied to reach the optimal filter bank, are $K \in [0.25, 1]$ and $\lambda \in [0.5, 2]$.

We have applied both, the global and local methods (varying parameters K and λ), to the synthetic and real sequences. For synthetic sequences, we have taken into account the correlation error (CE), and real error (RE) while for real sequences only CE. In synthetic sequences we have found that parameters $\lambda = 0.65$ and $K = 0.5$, minimize the mean real error (in pixels) with $RE_{GFB} = 0.0557 \pm 0.0689$. At the same time, these parameters minimized the mean correlation error with $CE_{GFB} = 0.9987 \pm 0.0005$. Comparing these results to those obtained by the global method, $RE_{MSF} = 0.0608 \pm 0.0384$ pixels, $CE_{MSF} = 0.9979 \pm 0.0003$, we realize that eventhough local method retrieves more accurate DM, global method also reaches good performance. We have noticed that local method fails mostly at myocardium borders. We have calculated the same error in a ROI inside the myocardium and we have seen that the RE improved in a 46%, $RE_{GFB} = 0.0301 \pm 0.0771$. The CE also improved, $CE_{GFB} = 0.9989 \pm 0.0002$. It is worth to mention that when deformation in the myocardium is extremely local, as the one we have simulated in one of the sequences, where only half a myocardium moves (Fig 5.a), local method clearly improves the global one (see the detail in Fig. 6). In this sequence we obtained $RE_{GFB} = 0.0260 \pm 0.0408$, $CE_{GFB} = 0.9991 \pm 0.0005$, $RE_{MSF} = 0.0639 \pm 0.1527$ and $CE_{MSF} = 0.9970 + 0.0004$. Nevertheless, in practice we never deal with extreme cases like this. For this reason global method reaches good rates of accuracy.

In real sequences, we found that parameters $\lambda = 0.75$ and $K = 0.55$, minimize the mean correlation error with a value $CE_{GFB}(1,2) = 0.9018 \pm 0.0383$, almost similar than the one obtained with the global method, $CE_{MSF} = 0.9012 \pm 0.0352$. Notice that CE is much lower than the observed for real sequences. This fact may be due to the fading effect, which is not present in real sequences.

5. Discussion and conclusions

In this paper we have presented two approaches to spectral optical flow techniques (global and local), to analyze myocardial motion in TMR sequences. We have compared the accuracy of the estimated displacement maps in terms of real and correlation error for synthetic sequences and just CE for real ones. We saw that CE is an intuitive way to evaluate the accuracy of a given DM when no real displacement is available.

Results have shown that local technique gives more precise results in general. Nevertheless, the simplicity of the global method, together with its low cost and high accuracy, makes it to be very well suited for most of the cases, where very high precision is not required, as it could be, for instance, myocardial fiber reconstruction.

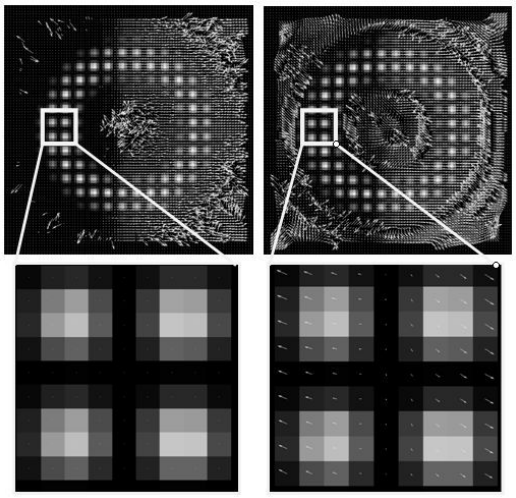


Figure 6. Detail of local displacement detected by local (left) and global (right) method. In this synthetic sequence we have induced translation in the right half of the myocardium.

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