Motion and Deformation Analysis of the Heart using Thin-Plate Splines and Density and Velocity Encoded MR Images *

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Abstract

We have developed a new approach for analyzing the regional and global motion and deformation of the myocardium using density and velocity encoded cardiac MR images. First, the inner and outer wall of the left ventricle muscle are segmented in the density images. A set of homogeneously distributed points on these contours of the myocardium wall is automatically generated and used as a set of landmarks. Based on the velocity information of the MR images, we predict the *evolved* position of these landmarks at time $t' = t + dt$. Secondly, by means of a thin-plate spline interpolation defined by the original landmarks and their evolved counterparts, we create a mapping $\mathbf{F}$ of the landmarks at time t into an evolved (or deformed) set of landmarks at time t'. By using this mapping to warp the original density image at time t into the evolved density image at time t', we can assess the instantaneous deformation and motion of the myocardium avoiding the *off-plane* error introduced by scanning the moving heart with a fixed imaging plane. From the interpolation function we compute the total values of the bending energy of the model and compare them to a measure of the total contraction and rotation of the myocardium obtained from the velocity images. In this manner we provide with a description of the global behaviour of the left ventricle during the cardiac cycle. Finally, the interpolation function provides an ideal tool for visualizing the motion and shape variability of the myocardium by means of a distorted grid that describes the deformation of the cardiac muscle.

1 Introduction

Knowledge of the motion and shape variability of the heart is necessary for the diagnosis and treatment of cardiac related diseases. In particular, the evaluation of the motion, thickening and contraction of the left ventricular wall of the heart (myocardium) plays a key role in the assessment of ischaemia and cardiac malfunction. For this reason, much research has focused on the analysis [1, 2] and modelling [3, 4] of ventricular motion and deformation. Among existing non-invasive imaging techniques, Magnetic Resonance Imaging (MRI) plays a very important role because it allows high-resolution cine imaging of the myocardium. Additionally, MRI allows the measurement of tissue and blood flow velocity.

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The motion and deformation analysis of cardiac cine images is a very difficult task. On the one hand due to the complexity of the cardiac dynamics, it is not sufficient to analyze the myocardium only at the end-systolic and end-diastolic time frames. In order to obtain an accurate and reliable quantitative analysis of the motion and deformation, the entire cardiac cycle has to be covered. On the other hand, nearly all cine imaging techniques use a fixed imaging plane in space and time. However, the heart is undergoing non-rigid deformations in a 3D space. A fixed imaging plane ignores the fact that the heart moves out of the imaging plane during the image acquisition period, thus leading to an *off-plane* error as different times of the cine sequence scan different slices of the heart.

An elegant approach for measuring biological shape variation and deformation has been proposed by Bookstein [5]. His approach is based on using a set of biological landmarks which are identified in the undeformed and deformed object. Using the analogical model of a thin-plate of metal, a thin-plate spline interpolation function is defined for each set of coordinates which warps the original set of landmarks into the deformed one. A common problem is the reliable identification of the corresponding anatomical landmarks in two different images during the cardiac cycle. In the absence of implanted myocardial markers, prominent curvature features could be used as landmarks. However, in normal patients only a small number of curvature features exists and these are very difficult to identify and track over the entire cardiac cycle.

In order to avoid these problems we are analyzing the movement and deformation of the heart at different time frames during the cardiac cycle based only on the density and velocity information at that particular moment in time. This eliminates the need to infer the cardiac motion and deformation from two consecutive time frames which requires tracking of landmark points during the cardiac cycle and introduces off-plane errors into the analysis.

2 Image Acquisition

A standard electrocardiographer synchronized cine Magnetic Resonance Imaging (MRI) technique is used to generate a sequence of 15 tissue density (ρ) tomographic images of the short-axis of the left ventricle (LV), at equally spaced time intervals of approximately 40 ms starting at the beginning of systole and ending at early diastole (we exclude late diastole images since they introduce extra noise in the data when acquired with standard gated MR techniques).

For each of the density images we acquire velocity encoded data of the same anatomical plane of the LV using a phase-sensitive MR imaging technique. The velocity data is obtained in three different images, V_x, V_y and V_z, corresponding to the Cartesian components of the velocity vector field $\mathbf{V}$. Here x and y are aligned with the LV short axis (which is the imaging plane) and z has the direction of the LV long-axis (perpendicular to the imaging plane). In this article we do not make use of V_z.

We must notice that gated MRI techniques generate a single image out of a large number of heartbeats (normally 256) and therefore each image depicts the average behaviour of the heart during these heartbeats. However, the information provided is useful for observing the global dynamics of the heart and we can still refer in a meaningful manner to a particular time of the cine sequence since it belongs to a specific phase of the cardiac cycle.

3 Image Segmentation

The boundary of the myocardium is segmented in the first time frame of the cine sequence using a stochastically optimized geometrically deformable template (GDT) [6]. This approach allows the incorporation of *a-priori* shape information in form of an energy-minimizing deformable template. After segmentation of the first time frame the boundary of the myocardium is tracked using the final shape of the previous time frame as a template for the current time frame. We are using two different templates to segment and track the inner and the outer wall of the myocardium. The segmentation and tracking process is fully automated and requires no user interaction.

4 Landmarks Generation

Once the boundaries of the myocardium have been found we calculate the centre of gravity $\mathbf{C}$ of the myocardium. From this central point we project n radial lines with equal angular spacing. The set of points where the radial lines intersect the inner wall of the myocardium is taken as the landmark positions $P_{in} = \{\mathbf{P}_{in}^1, \cdots, \mathbf{P}_{in}^n\}$ of the inner wall of the myocardium. In the same manner a second set of landmarks P_{out} is produced for the outer wall of the myocardium. This process is also completely automatic.

As mentioned in the introduction any landmark-based motion and deformation analysis depends on the choice of landmarks and their reliable tracking and identification in subsequent frames of a cine sequence. We avoid the necessity of tracking landmark points by using the velocity information at the set of points P_{in} and P_{out} which have been generated from the tessellation of the inner and outer wall of the myocardium in the fashion described above. Figure 1 shows the velocity vectors for each of the points P_{in} and P_{out} after having subtracted from each of them the average translation velocity of the myocardium. The average is computed using the velocities of all pixels that belong to the segmented cardiac muscle on the images. This subtraction has the effect of eliminating from the velocities the contribution of the global translation of the myocardium, and therefore, of highlighting information about the rotation, contraction and deformation.

Let P be the set of landmarks of the inner and outer wall of the myocardium at time t. For each of these points $\mathbf{P}_i = (x_i, y_i)$ we calculate the homologous landmark point in the evolved image at time $t' = t + dt$ as

$$\mathbf{P}_i' = (x_i', y_i') = (x_i + V_x(x_i, y_i)dt,\ y_i + V_y(x_i, y_i)dt) \tag{1}$$

Since the computation of the position of this set of evolved landmarks P' relies on the correctness of the velocity data used, it is desirable to diminish the effect of noise in the velocity images. For this reason we apply an anisotropic diffusion algorithm [7] to the velocity images. When used for a short time (*i. e.* a small number of iterations), this algorithm reduces noise while preserving the internal structure of data, essential for the deformation analysis.

Once these two sets of landmarks have been identified, we can proceed to define a function $\mathbf{F}$ which maps the original landmarks P into the evolved landmarks P'.

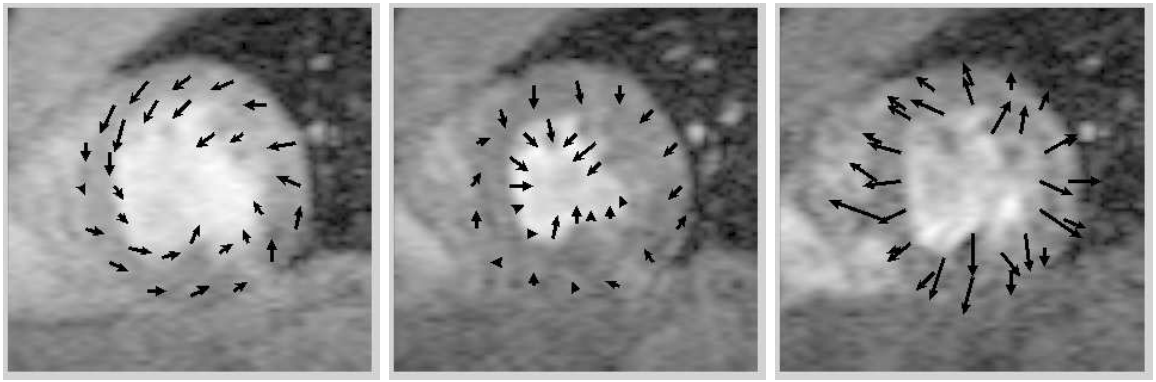

Figure 1: The velocity vectors of the landmarks at three different times during (a) the beginning of the cardiac cycle, (b) the contraction and (c) expansion of the myocardium.

5 Thin-Plate Splines and Deformation Analysis

A thin-plate spline $f(x, y)$ [5] is a smooth function which interpolates a surface that is fixed at the landmark points P_i at a specific height h_i. If one imagines this surface as a thin metal plate, then this plate will take a shape in which it is least bent, *i. e.* it minimizes the quantity

$$\int\int_{\mathbf{R}^2} (\frac{\partial^2 f}{\partial x^2})^2 + 2(\frac{\partial^2 f}{\partial x \partial y})^2 + (\frac{\partial^2 f}{\partial y^2})^2 dxdy \tag{2}$$

This quantity is called the bending energy of the thin-plate spline function. Instead of assuming that f corresponds to a displacement orthogonal to the image plane at the landmarks, one can assume a displacement in the image plane. By using two separate thin-plate spline functions f_x and f_y which model the displacement of the landmarks in the x and y direction we arrive at a vector-valued function $\mathbf{F}$ which maps each point of the image into a new point in the image plane:

$$(x, y) \rightarrow (f_x(x, y),\ f_y(x, y)) \tag{3}$$

A thin-plate spline interpolation function can be written as

$$f(x, y) = a_0 + a_x x + a_y y + \sum_{i=1}^{n} w_i U(|(x, y) - \mathbf{P}_i|) \tag{4}$$

where $U(r) = r^2 \log(r^2)$ is a so-called fundamental solution of the biharmonic equation ($\Delta^2 U = 0$) that satisfies the condition of bending energy minimization. By appropriately choosing a $n \times 2$ matrix $\mathbf{W}$ of the coefficients w_i, the function $\mathbf{F}$ maps $\mathbf{F}(\mathbf{P}_i) = \mathbf{P}'_i$ for all $i = 1, \cdots, n$.

Based on the image I_t at time t and the interpolation function $\mathbf{F}$ we can now predict the evolved image I_{t+dt} at time $t + dt$:

$$I_t(x, y) = I_{t+dt}(x', y') = I_{t+dt}(\mathbf{F}(x, y)) \tag{5}$$

Using this equation it is possible to calculated an evolved (or warped) image based on the velocity field at the inner and outer wall of the myocardium. Because the density and velocity

images are acquired at the same time (or rather at the same phase of the cardiac cycle), the evolved image captures the motion and deformation of the myocardium avoiding the off-plane error.

It can be shown that the transformation $\mathbf{F}$ minimizes the bending energy in eq. (2) and that the value of the bending energy is proportional to $\mathrm{tr}(\mathbf{W}^T\mathbf{Y})$ where $\mathbf{Y}$ is a $n \times 2$ matrix of the evolved landmarks P'. The bending energy of a thin-plate spline is zero only if the coefficients w_i of f are all zero. Moreover, the bending energy is invariant under affine transformations like scaling, rotation and translation. This property makes it particularly suitable to provide a quantitative measure of deformations. On the other hand, the affine part of the transformation (terms corresponding to the coefficients a of equation 4) can be used to obtain 'motion' related information.

In practice, the following points have to be considered when producing the warped images: First, since $\mathbf{F}$ maps pixels in I_t into pixels in I_{t+dt}, it might happen that due to the discretisation of the images different pixels in I_t are mapped into the same pixel in I_{t+dt} and that consequently some pixels in I_{t+dt} are left empty. Since it is not possible to write the inverse transformation $\mathbf{F}^{-1}$ and its numerical approximation is computationally expensive, a linear interpolation of the I_{t+dt} image was applied. Secondly, the function $\mathbf{F}$ does not guaranty to preserve the rectangular shape of the image. Therefore, for the purpose of visualization, each warped image that we show in the figures was generated using a an extra set of landmarks which, fixed under the transformation $\mathbf{F}$, are located at the boundaries of the image (one in each corner and one in the middle of each of the image sides). Finally, the velocity images measure the instantaneous velocity and no information about the acceleration is available. Thus, accurate predictions of the movement of the myocardium can be made only for small time intervals dt.

6 Results and Discussion

The proposed algorithm has been applied to cardiac cine MR images. Some of the results of the image warping at different stages during the cardiac cycle are shown in Figure 2. The grids representing the thin-plate splines which have been used for warping the images are overlayed to help to visualize the deformations.

As we mentioned before, the non-affine part of the transformation $\mathbf{F}$ can be used to express quantitatively the deformation of the myocardium in terms of the local and global bending energy of the transformation. In Figure 3a we show results of the global energy for each phase of the cardiac cycle.

Using the MR velocity images and a polar coordinate system with the origin on the centre of gravity ($\mathbf{C}$) of the myocardium, we computed the average velocity of the myocardium in the radial (V_r) and tangential (V_t) directions, for every phase of the cardiac cycle (Fig. 3b). While the former provides with a description of the contraction (or expansion) of the heart, the latter refers to its global rotation. These quantities describe mainly the rigid body motion of the heart and complement the information provided by the bending energy.

We have presented a new method for analyzing the motion and deformation of the myocardium during the cardiac cycle which combines information from the density and velocity encoded

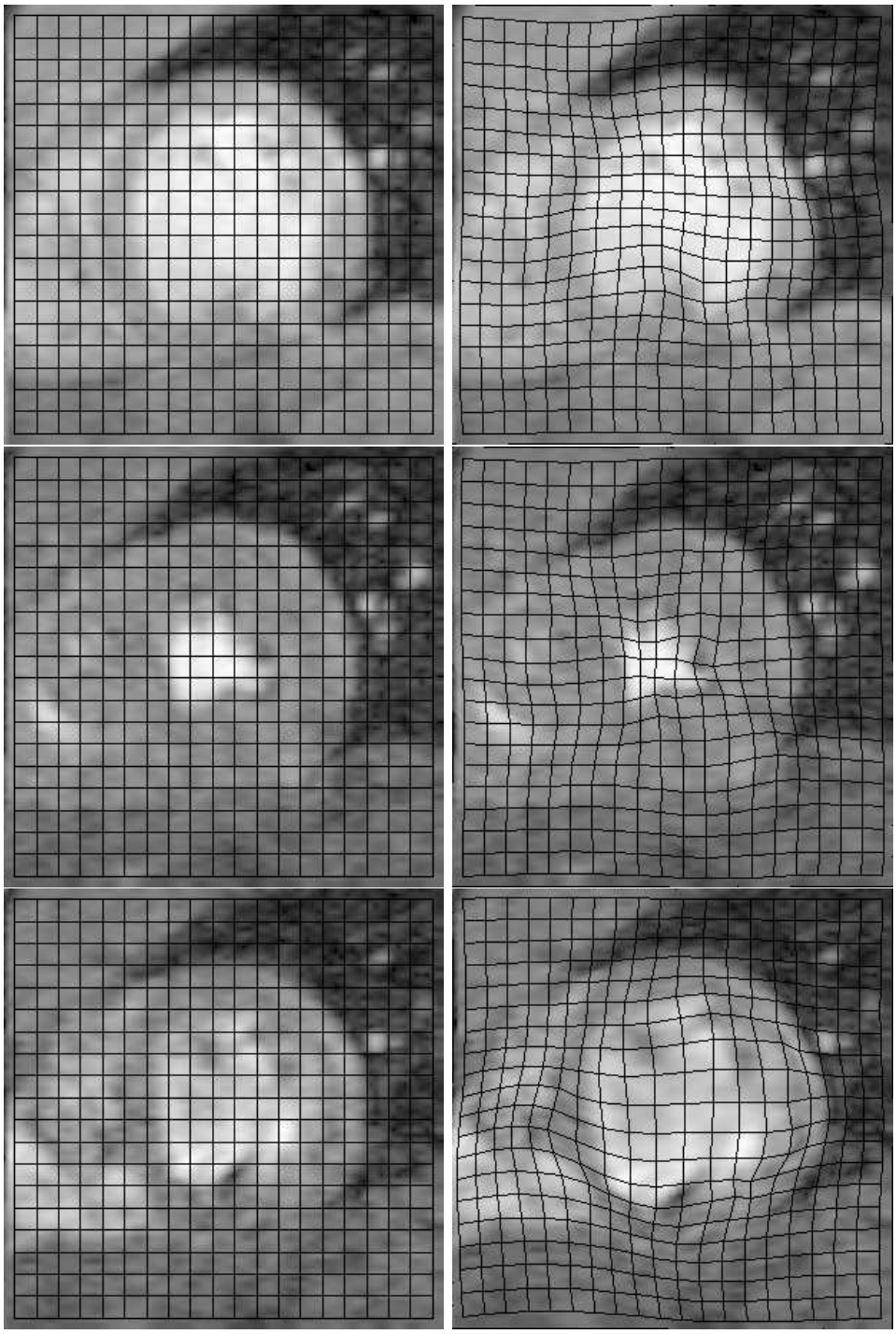

Figure 2: The original and warped MR images of the left ventricle show the deformation of the myocardium and their corresponding bending energy during (a) early systole ($E = 0.031$), (b) end systole ($E = 0.053$) and (c) diastole ($E = 0.133$).

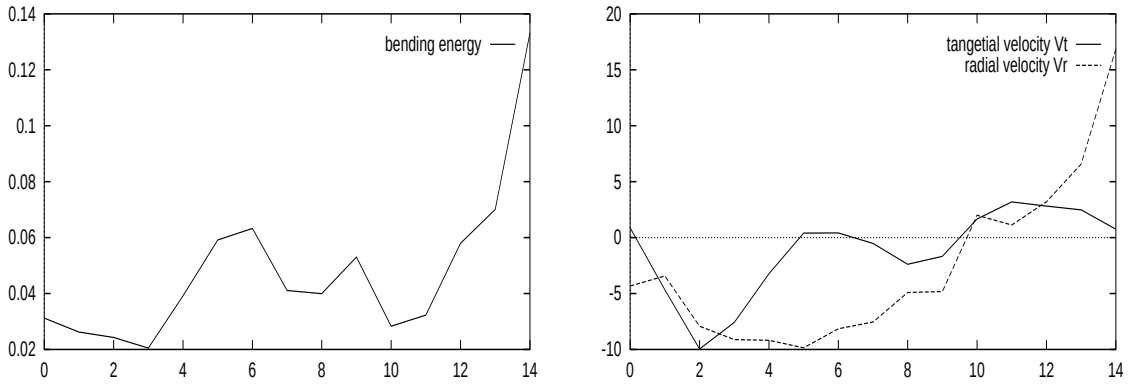

Figure 3: Quantitative description of the global deformation and motion of the myocardium during the cardiac cycle. (a) Bending energy. (b) Average velocity of the contraction (V_r) and of the rotation (V_t). The horizontal axes in both plots represent the phase within the cycle, from systole to diastole.

MR images of a cine sequence. By integrating the density and velocity information we can automatically generate a set of undeformed and deformed landmarks without any off-plane error. The thin-plate spline interpolation function which maps the set of landmarks into the evolved landmarks provides not only a method for evolving the density images according to the the measured velocities but also for the qualitative (in terms of visualization) and quantitative analysis (in terms of bending energy) of the deformation of the myocardium. Although our computations are susceptible to noise in the velocity data, our results show that the proposed method provides an adequate tool for describing the dynamics of the myocardium. Results are discussed in more detail in a forthcoming article where we analyze quantitatively the global and regional characteristic of the dynamics of the heart using thin-plate splines and comparing results to those produced by standard methods.

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