Comparison of Land-Mark-Based and Curve-Based Thin-Plate Warps for Analysis of Left-Ventricular Motion from Tagged MRI

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Abstract. MRI is unique in its ability to non-invasively and selectively alter tissue magnetization, and create tagged patterns within a deforming body such as the heart muscle. The resulting grid patterns define non-invasive tissue markers, providing a mechanism for *in-vivo* measurement of tissue motion and strain. In this paper, we report on objective comparison of thin-plate spline warps in reconstructing true deformations when using homologous land-mark points and when using homologous curves from tagged MR-image sequences of a cardiac motion simulator. In addition, the number of corresponding land-mark points as well as the number of corresponding curves are varied in order to determine the effect on accuracy of reconstructions. Finally, application of the developed techniques to computing LV tissue motion and strain in systole from short-axis tagged images of a porcine model with anterior myocardial infarction (MI) are given.

1 Introduction

Non-invasive techniques for assessing the dynamic behavior of the human heart are invaluable in the diagnosis of heart disease, as abnormalities in the myocardial motion sensitively reflect deficits in blood perfusion [9,17]. MRI is a non-invasive imaging technique that provides superb anatomic information with excellent spatial resolution and soft tissue contrast. In MR tagging, the magnetization property of selective material points in the myocardium are altered in order to create tag grid patterns within a deforming body such as the heart muscle [17,7]. During tissue contractions, the grid patterns move, allowing for visual tracking of the land-mark grid intersections over time. The intrinsic high spatial and temporal resolutions of such myocardial analysis schemes provide unsurpassed information about local contraction and deformation in the heart wall which can be used to derive local strain and deformation indices from different myocardial regions.

A number of researchers have developed different approaches to analysis of tagged MRI data [16,11,10]. An unanswered question is whether more accuracy

is gained in utilizing complete curve-grid information in reconstructing LV deformations, or whether use of tag intersections (i.e., landmarks) alone is sufficient. In this paper, we report on comparisons of land-mark-based and curve-based warps, and describe conditions under which thin-plate reconstructions using complete tag grid information would be preferred. We also apply the reconstruction algorithm to obtain dense strain maps from tagged MRI in a porcine model with anterior MI.

2 Constrained Thin-Plate Spline Warps

Tracking tissue deformations with SPAMM using snake grids provides 2D displacement information at tag intersections and 1D displacement information along other 1D snake points [1,2,3,4]. The displacement measurement from tag lines however are sparse; interpolation is required to reconstruct a dense displacement field from which strain, torsion, and other mechanical indices of function can be computed at all myocardial points.

To proceed more formally, the vector field which warps the *deformed image* into the *undeformed image* is assumed to be C^1 continuous. This smoothness requirement is achieved by minimizing an objective function which combines spatial derivatives of both components of the reconstructed displacements

$$\Phi_1 = \int \int u_{xx}^2 + 2u_{xy}^2 + u_{yy}^2 dx dy + \int \int v_{xx}^2 + 2v_{xy}^2 + v_{yy}^2 dx dy \quad (1)$$

characterizing approximating thin-plate splines. It should be noted that although thin-plate warps have been used in the past for other medical imaging applications ([8]), they have only been utilized to interpolate a warp given homologous landmark points. Assuming 2D tissue motion (as is roughly the case towards the apical end of the heart [13]), two possible physical constraints (in addition to (1)) can be considered:

1. Corresponding homologous land-marks obtained from intersecting horizontal and vertical tag grid lines should come into correspondence after application of the thin-plate warp. The intersection of two tag grid lines are “pulled” towards one another by minimizing

$$\Phi_2 = \sum (u - u_{int})^2 + (v - v_{int})^2 \quad (2)$$

where u_{int} and v_{int} are the x and y components of displacement at tag intersections.

2. Corresponding homologous curves should come into correspondence, that is, any point on a deformed tag in frame n must be warped to lie on its corresponding undeformed tag in frame 0 of the sequence. For a vector field to perform such a warp, $h(u, v)$ of figure 1 must be minimized. Let $\mathbf{P}_1 = \mathbf{P}_1(u, v) = (x, y) + (u, v)$ as in figure 1, and let $\mathbf{P}_2$ be any point on the

undeformed tag line. The following term is then summed over all deformed horizontal and vertical grid points:

$$\Phi_3 = \sum (h(u, v))^2 = \sum \{(\mathbf{P}_1(u, v) - \mathbf{P}_2) \cdot \mathbf{n}\}^2 \quad (3)$$

where the summation is performed on all points (x, y) on the deformed grids.

Fig. 1. Distance of a point P_1 to a straight line can easily be calculated with knowledge of *any* point, P_2 , on the line and the normal vector (left). The residual distance from a *warped point* of a deformed tag line to its corresponding undeformed tag line in frame 0 of the sequence, $h(u, v)$, can similarly be calculated (right).

In order to compare curve-warps with land-mark warps, an objective function maybe formed by a linear combination of the terms in (1), (2), and (3),

$$\Phi = \lambda_1 \Phi_1 + \lambda_2 \Phi_2 + \lambda_3 \Phi_3 \quad (4)$$

where $\lambda_1, \lambda_2, \lambda_3$ are non-negative weights. The following test cases can then considered: **I.** $\{\lambda_1 > 0, \lambda_2 > 0, \lambda_3 = 0\}$, and **II.** $\{\lambda_1 > 0, \lambda_2 = 0, \lambda_3 > 0\}$. Additionally, within each of case **I** (land-mark-based warps) and **II** (curve-based warps), the number of homologous land-mark points/curves may be varied to determine the effect on accuracy of reconstructions. In order to optimize Φ with Conjugate-Gradient Descent, partial derivatives of Φ_1 can be calculated using the computational molecule approach discussed in [14] and also used in [4]. Partial derivatives of (2) can easily be obtained. Finding partial derivatives of Φ_3 is also straightforward:

$$\nabla \Phi_3 = 2 \sum \{(\mathbf{P}_1(u, v) - \mathbf{P}_2) \cdot \mathbf{n}\} \cdot \mathbf{n} \quad (5)$$

As maybe concluded from the last paragraph, minimization of (4) leads to a system of linear equations with full rank under non-trivial deformations. Therefore, (4) is a convex objective function, with a global minimum. It should be

noted that in comparison to [4], in the present article we describe thin-plate techniques which require knowledge of homologous landmark points and/or curves; though with an additional constraint, namely that one set of the homologous curves should be straight. This is a modification of the framework in [4], making the objective function convex, bypassing local minima, and resulting in reduced computational costs.

3 Land-Mark-Based vs. Curve-Based Warps

An environment based on a 13 parameter kinematic model of Arts et al. [6] has been implemented as was described in [15] for simulating a time sequence of tagged MR images at arbitrary orientation. Based on user-selected discretization of the space between 2 concentric shells and by varying the canonical parameters of the model, both a sequence of tagged MR images as well as a “ground truth” vector field of actual material point deformations are available [4]. The parameters of the motion model, referred to as k-parameters, and the transformations to which they correspond are: k_1 : Radially dependent compression, k_2 : Left ventricular torsion, k_3 : Ellipticalization in long-axis (LA) planes, k_4 : Ellipticalization in short-axis (SA) planes, k_5 : Shear in x direction, k_6 : Shear in y direction, k_7 : Shear in z direction, k_8 : Rotation about x-axis, k_9 : Rotation about y-axis, k_{10} : Rotation about z-axis, k_{11} : Translation in x direction, k_{12} : Translation in y direction, and k_{13} : Translation in z direction. For the purposes of comparing 2D displacement field reconstructions, we have used the parameters k_2 , k_4 , k_5 , and k_{10} for generating 2D deformations of the geometric model, based on which simulated tagged images and 2D displacement vector fields of *actual* material points are produced. The error norms used in comparing the ground truth vector field (V_g) with the vector field measured by the warp algorithms (V_m) are: $\varepsilon_{rms} = \sqrt{\frac{1}{N} \sum |V_m - V_g|^2}$ and $\varepsilon_{dist} = \sqrt{\frac{1}{N} \sum (h(u, v))^2}$ where N is the total number of deformed grid points on the myocardial region, the summation in ε_{rms} is performed on entire myocardial regions, and the summation in ε_{dist} is performed on all points (x, y) on the deformed grid (figure 1).

In order to test the accuracy of reconstructions as a function of the number of homologous landmarks and homologous curves, a number of experiments were carried out. The experiments were designed to determine the effect of number of homologous land-mark points vs. number of homologous curves on the accuracy of thin-plate spline reconstruction of deformations. The cardiac simulator was used to generate a sequence of SA tagged images in addition to ground-truth displacement vector fields. The imaging parameters chosen resulted in 7×7 image tag grids. The intersections of the tag lines in the myocardial area yielded all of the available land-mark points, and the tag segments which were in the myocardial region yielded all of the available curves for warping. In order to vary the number of homologous land-marks and curves, the 7×7 grid was subsampled to a 1×1 , 2×2 , 3×3 , 4×4 , and the original 7×7 grid. To compare land-mark based and curve-based warps, for each subsampled grid considered, the intersections of the corresponding grids were used as the land-mark points. The

Fig. 2. Plots of ε_{rms} as a function of number of tag lines used in thin-plate spline reconstruction of deformations. Different plots correspond to different values of k_4 , ellipticalization in short-axis plane.

Fig. 3. Plots of ε_{dist} as a function of number of tag lines used in thin-plate spline reconstruction of deformations. Different plots correspond to different values of k_4 , ellipticalization in short-axis plane.

findings for parameter k_4 (short-axis ellipticalization) are displayed in figures 2 and 3 (plots for k_2 , k_5 , and k_{10} generally follow the same patterns). Please note that for these figures, there are no land-marks for the 1×1 grid, and additionally the results of the 7×7 grid are labeled as case “5” on the x-axis of the plots. For the plots, “1 1 0” corresponds to $\lambda_1 = 1$, $\lambda_2 = 1$, $\lambda_3 = 0$. Similarly, “1 0 1” corresponds to $\lambda_1 = 1$, $\lambda_2 = 0$, $\lambda_3 = 1$, and “1 1 1” corresponds to $\lambda_1 = 1$, $\lambda_2 = 1$, $\lambda_3 = 1$.

The plots indicate that for small deformations, there is no significant difference between using curve-based, and land-mark based warps, but that for larger deformations, there is more graceful degradation of curve-based warps in reconstruction of true deformations in comparison to land-mark based warps. There are also no significant differences between curve-based and land-mark based warps when the number of land-marks/curves increase. In the rest of the article, $\{\lambda_1 = 1, \lambda_2 = 0, \lambda_3 = 1\}$ was used for analysis of the *in-vivo* data.

Fig. 4. Four displacement vector fields for the post-MI study corresponding to 202, 225, 247, and 270 msec after the ECG trigger. Segmental motion of all myocardial points can easily be quantitated and visualized from the location, direction, and length of the displayed vectors. An akinetic area in the lower-right area is indicated.

4 Myocardial Strains

Starting at any time point during the cardiac cycle, the heart's motion is viewed here as a mapping which warps the *deformed* tag configuration into the *undeformed* configuration: $\mathbf{X} = \mathbf{\Gamma}(\mathbf{x})$. Equivalently, with $\mathbf{X} = \mathbf{V}(\mathbf{x}) + \mathbf{x}$, the deformation gradient tensor can be written as $\mathbf{F} = \nabla \mathbf{\Gamma}(\mathbf{x}) = \nabla \mathbf{V}(\mathbf{x}) + \nabla \mathbf{x}$ where $\mathbf{V}$ is the computed displacement vector field. Therefore, assuming little or no through-plane motion, the strain tensor can be computed from spatial derivatives of displacements:

$$\begin{aligned} \mathbf{E} &= \frac{1}{2}(\mathbf{F}^T \mathbf{F} - \mathbf{I}) \\ &= \begin{pmatrix} u_x + \frac{1}{2}(u_x^2 + v_x^2) & \frac{1}{2}(u_y + v_x + u_x u_y + v_x v_y) \\ \frac{1}{2}(u_y + v_x + u_x u_y + v_x v_y) & v_y + \frac{1}{2}(u_y^2 + v_y^2) \end{pmatrix} \end{aligned} \quad (6)$$

Once a displacement vector field is available, the strain of deformation can be computed at all myocardial points within a short-axis slice. Furthermore, the quantity $\mathbf{M}^T \mathbf{E} \mathbf{M}$ will give the value of strain for the direction $\mathbf{M}$.

5 In-Vivo Imaging

A SPAMM pulse sequence was used to collect images from a porcine model of myocardial infarction. The repetition time (TR) of the imaging sequence was approximately 7.1 msec, the echo time (TE) was 2.9 msec, and the rf pulse flip angle was 15 degrees. Other imaging parameters were: field of view = 300mm, data acquisition matrix size = 250×256 (phase encoding by readout), in-plane resolution = $1.2 \times 1.17 \text{ mm}^2$, slice thickness = 7mm, and tag spacing = 7mm.

5.1 Results

Figure 4 shows 4 displacement vector fields ($\mathbf{V}$) computed from grids in tagged short-axis images at 202, 225, 247, and 270 msec after the ECG trigger in a pig after inducing an anterior MI. The magnitude of the motion fields for each of these figures can easily be computed. Although the infarct zone can readily be recognized from the vector fields, these zones more clearly stand out in the vector field magnitude maps [5]. The next pair of figures: figure 5 and figure 6 show the radial and circumferential strains for the post-MI study after application of a median filter for reducing noise. Finally, figure 7 shows the picture of a stained histological slice of the LV roughly corresponding to the position of image slices for the porcine model.

In summary, the areas of the myocardium which lack motion can be recognized from either the magnitude of the displacement vectors or from the patterns of radial and circumferential strain maps. These areas appear to correlate well with the stained tissue.

Fig. 5. This figure shows radial strains for the post MI study (corresponding to the same time points as in figure 4). Notice that the lower-right area consistently has small strain values.

6 Conclusions

We have compared land-mark based and curve-based thin-plate warps for reconstruction of dense displacement vector fields from SPAMM grids. Using the Cardiac Motion Simulator, it was found that for larger deformations, land-mark based warps fail when few homologous land-mark points are available, but that performance gracefully diminishes for curve-based warps when the number of homologous curves are decreased. In addition, preliminary results from application of methods to *in-vivo* data of a porcine model of myocardial infarction were given. Although we have not taken into account motion in the out-of-plane direction, we are encouraged by the in-plane results obtained thusfar.

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Fig. 6. This figure shows circumferential strains for the post MI study (same time points as in figure 4). Once again, the lower-right area consistently has small strain values.

Fig. 7. Stained histological slice of the pig's LV; roughly corresponding to collected short-axis image slice positions. The area in the lower right (between 2 and 7 o'clock locations) of the picture with no dye uptake (bright region) is the infarct zone. Note also the distinct narrowing of the myocardial regions in these areas.

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