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Sparsity and Biomechanics Inspired Integration of Shape and Speckle Tracking for Cardiac Deformation Analysis

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Abstract

Cardiac motion analysis, particularly of the left ventricle (LV), can provide valuable information regarding the functional state of the heart. We propose a strategy of combining shape tracking and speckle tracking based displacements to calculate the dense deformation field of the myocardium.

We introduce the use and effects of l_1 regularization, which induces sparsity, in our integration method. We also introduce regularization to make the dense fields more adhering to cardiac biomechanics. Finally, we motivate the necessity of temporal coherence in the dense fields and demonstrate a way of doing so.

We test our method on ultrasound (US) images acquired from six open-chested canine hearts. Baseline and post-occlusion strain results are presented for an animal, where we were able to detect significant change in the ischemic region. Six sets of strain results were also compared to strains obtained from tagged magnetic resonance (MR) data. Median correlation (with MR-tagging) coefficients of 0.73 and 0.82 were obtained for radial and circumferential strains respectively.

Keywords

Echocardiography; Motion; Shape tracking; Speckle tracking; Radial basis functions; Regularization

1 Introduction

A reliable quantitative and qualitative assessment of the motion behavior can assist in the detection, localization, control and treatment of myocardial injuries. Within this context, echocardiography is a popular and important tool because it is relatively inexpensive and highly portable. It also provides better temporal resolution in comparison to other modalities.

Over the years several shape based tracking methods and speckle based tracking methods have been proposed to calculate dense motion field for the LV and ultimately calculate regional strains. Shape based methods track myocardial boundaries or automatically selected shape and intensity based features which predominantly arise from myocardial boundaries [1,2]. Hence, mid-wall displacements are usually missing or not reliable.

Popular speckle tracking methods can be broadly classified into block-matching algorithms such as Lubinski et al. [3] and non-rigid registration based methods such as Heyde et al. [4]. Speckle tracking methods are better at estimating mid-wall displacements but do not always successfully track the boundaries due to inconsistent speckle patterns at the blood tissue interface.

Compas et al. [5] proposed a method to calculate dense field across the myocardium by integrating displacements from shape and speckle tracking methods using radial basis function (RBF) interpolation. The use of RBFs provided a flexible and simple framework by eliminating the need of complicated grids and meshes to model cardiac geometry. Hence, it provided a simpler mechanism of modeling complex, and sometimes incomplete, cardiac geometries.

In this work, we pose the problem in a Bayesian setting and then present it in a convex optimization format. We use l_1 regularization to tackle noise and also, indirectly, to select features. Drawing inspiration from cardiac biomechanics, we add penalties on divergences and derivatives. We also motivate and demonstrate the need to make motion fields temporally coherent. We test our methods on 2D canine heart images and present appropriate results.

2 Methods

We will first briefly discuss the elementary methods to obtain initial shape and speckle tracking based estimation. Then we will discuss in detail the integration framework where our contribution lies.

2.1 Elementary Motion Estimation Methods

Shape Tracking—We use boundary features derived from an automated level-set segmentation method [6]. Once endocardial and epicardial boundary points are found, a modified Generalized Robust Point Matching (GRPM) algorithm is used to obtain displacement estimates across frames [1].

The algorithm matches two point sets X and Y by solving for a fuzzy correspondence matrix m . The original form was solved using an iterative setup. However, since the objective function was convex, we determined that we could solve this directly using a convex optimization solver [7]. The GRPM formulation allowed us to control the relative weight between minimizing distance between the point sets and minimizing the difference in their shape characteristics such as curvatures. It also allowed us to control the fuzziness (or uniqueness) of the correspondence.

Speckle Tracking—Speckle patterns are inherent to US and, while they seem random in nature, they exhibit some consistency in a small time window. This can be leveraged and a correlation based tracking of local image patches is done.

For a pixel in a given image, a kernel of one speckle length around the pixel, in the complex signal, is correlated with neighboring kernels in the next frame [3]. The peak correlation value is used to determine the matching kernel in the next frame and calculate displacement and confidence measure. The velocity in the echo beam direction is further refined using zero-crossings of the phase of the complex correlation function.

2.2 Integration Framework

Bayesian Viewpoint—For an image frame, the dense displacement is U and the initial shape and speckle tracking displacements are U^{sh} and U^{sp} respectively. Conditioning using Bayes' theorem, and assuming independence between U^{sh} and U^{sp} , we get

$$P(U|U^{\text{sh}}, U^{\text{sp}}) \propto P(U^{\text{sh}}|U)P(U^{\text{sp}}|U)P(U) \quad (1)$$

$P(U)$ captures the assumptions we make about our displacement field as a prior. We assume that U^{sp} and U^{sh} are both normally distributed with respect to U . Taking log on both sides, we get: log

$$\log(P(U|U^{\text{sh}}, U^{\text{sp}})) \propto k_1 - \frac{1}{\sigma_{\text{sh}}^2} \|U^{\text{sh}} - U\|_2^2 - \frac{1}{\sigma_{\text{sp}}^2} \|U^{\text{sp}} - U\|_2^2 + L(P(U)) \quad (2)$$

Here, the σ 's are the standard deviations of the shape and speckle displacements. $L(P(U))$ is the log of the prior distribution on U . We obtain the final dense field by maximizing the log posterior.

RBF Interpolation—An RBF is parametrized by its location $c \in \mathbb{R}^2$ and its width $\sigma \in \mathbb{R}^2$ (in 2D). Hence, during an RBF interpolation process, different resolutions can be captured by altering the width and the number of RBFs. In our case, we place RBFs around the myocardium and use a multi-level scheme, where in each iteration RBFs of different widths and varying quantity are used [8].

For each iteration, first we evaluate the value of all the RBFs for consideration and consolidate them as a design matrix (or a dictionary of bases) H . Then, the displacement

values are expressed as a linear combination of these bases as $U = (U^x, U^y) = (Hw_x, Hw_y)$. Therefore, our goal is to solve for the linear weights $w = (w_x, w_y)$, which we accomplish using an optimization setup:

$$\hat{w}_x, \hat{w}_y = \underset{w_x, w_y}{\operatorname{argmin}} \sum_{i \in A_{sh}} c_i^{sh} ([Hw]_i - U_i^{sh})^2 + \sum_{i \in A_{sp}} c_i^{sp} ([Hw]_i - U_i^{sp})^2 \quad (3)$$

A_{sh} and A_{sp} refer to shape and speckle areas in the myocardium. The confidences of each shape and speckle displacements are c_i^{sp} and c_i^{sh} . The above equation is the RBF parametrized form of Eq. 2, except for the prior part, which we discuss next.

Regularization and Biomechanics—We add the l_1 norm of our linear weights w 's to our objective in Eq. 3 as a prior. This regularization step captures our belief that the interpolation should be smooth and should not overfit our data.

Furthermore, the l_1 norm also induces sparsity on the weights w 's. A large number of w 's will end up becoming zero. This, in essence, is a form of feature selection. Of all the RBFs we consider for interpolation, only a handful will influence our final values. This ultimately allows us to capture varying and appropriate levels of details at different areas of the myocardium.

Next, we add the norm of the divergence of the motion field as a penalty to our in Eq. 3. We do so under the assumption that the cardiac tissue is roughly incompressible and therefore, motion vector field should be roughly divergence free [9]. Finally, we also mildly penalize the norm of the spatial derivatives to discourage jumps and discontinuities in the motion fields. Therefore, we have the following form:

$$\hat{w} = \underset{w}{\operatorname{argmin}} f_{adh}(Hw, U^{sh}, U^{sp}) + \lambda_1 \|w\|_1 + \lambda_2 f_{biom}(U) \quad (4)$$

$$f_{biom}(U) = \|\nabla \cdot U\|_2^2 + \alpha \|\nabla U\|_2^2$$

Here, $U = Hw$, f_{adh} refers to the data adherence terms in Eq. 3. Since we do not want derivatives to be penalized as much as divergences, α is set to be 0.25.

Cross Validation for Parameter Selection—Since regularization is key to our approach, appropriate selection of the regularization parameters $\lambda = [\lambda_1, \lambda_2, \lambda_3]$ is crucial. We use K-fold cross validation (CV) to select our parameters.

Assuming $K = 5$ (without loss of generality), if the value of function f (displacements in our case) is known at n points, then the data is partitioned randomly into 5 sets, each of size $n/5$. From these 5 groups, 4 are chosen randomly and are assigned as the training set X_{train}^k and the remaining one is the test set X_{test}^k . This is done 5 times, hence we have 5 sets of training

and test sets. Corresponding function values are also labeled f_{train}^k and f_{test}^k , where $k \in \{1, 2, \dots, 5\}$.

For a choice of λ , for each k , first solve for w^k , only using the training set:

$$\hat{w}^k = \underset{w^k}{\operatorname{argmin}} \sum_{i=1}^{|X_{\text{train}}|} (f_{\text{train}}^k(x_i) - [Hw^k]_i)^2 + \lambda_1 \|w^k\| + \lambda_2 f_{\text{biom}}(Hw^k) \quad (5)$$

$$\hat{f}^k(x) = H\hat{w}^k$$

where, $x_i \in X_{\text{train}}$.

Next, for all $x \in X_{\text{test}}$, we calculate and accumulate the squared difference between $\hat{f}^k(x)$ and $f_{\text{test}}^k(x)$ as our error in estimation. The set of λ 's yielding the lowest total error value is chosen as the appropriate set of parameters.

Temporal Smoothing—Since strain calculation involves the accumulation of displacement values across time frames, temporal consistency and smoothness is necessary. Once we carry out all our frame-to-frame calculations, we obtain temporal smoothness by doing a spatio-temporal interpolation of our results.

3 Results

Philips iE33 ultrasound system, with the X7-2 probe and a hardware attachment that provided RF data, was used to acquire six open chest canine heart images. For all six canines, baseline and post-occlusion (induced by the occlusion of left anterior descending (LAD) coronary artery) ultrasound images were analyzed (in 2D). However, only three baseline (of three canines) and three post-occlusion (of the three remaining canines) tagged MR images, acquired using 1.5T Sonata MR scanner, were available and analyzed using HARP MR software [10]. The MR derived strains are used as validation of our method. All experiments were conducted in compliance with the Institutional Animal Care and Use Committee policies.

We first present how end-systolic (ES) radial strains have changed from baseline to occlusion condition for one animal in Fig. 2. The median strain value for the entire myocardium has dropped from 14.12 to 9.70. We can also see that the change in strain is most significant in the anterior region, which is expected since the LAD artery was occluded.

In Fig. 3, we compare average radial strain values for each segment, for the entire cardiac cycle (end diastole - end diastole (ED)), between baseline and occlusion conditions of one animal. Confirming with our qualitative analysis for Fig. 2, the anterior region, and to some extent the neighboring regions, goes through the most significant change. We can also see how our post occlusion strains correspond well with our validation MR results.

Next, we compare our strains for the six image sets (for which tagged MR data was available) with tagged MR strains. We compare correlation values of segmental strain plots for the entire cardiac cycle (ED-ED). We also expand our analysis by comparing our results with results from Compas et al. in [5], only shape tracking, only speckle tracking and B-spline non-rigid registration (code obtained from [11]). Box plots illustrating the distribution of correlation values for all the methods, are given in Fig. 4.

The median correlation values for all segmental radial and circumferential strains, obtained from six datasets are displayed in Table 1. We can see that our method performs better than the other methods considered for comparison. Correlations for radial strains are roughly similar for different methods and not very high. However, results for circumferential strains are significantly different for different methods, and high median correlation with MR-tagging was obtained for our method.

4 Conclusions

The use of l_1 regularization, biomechanical constraints and temporal smoothing has allowed us to develop a robust method of estimating dense displacement fields, which we tested on 2D data. Our bayesian inspired framework, which is complemented by the data driven parameter selection for optimization, has added to the stability of our method. The strains generated were in good agreement with MR-tagging based strains.

Our next step is to test the method in 3D. Since 3D data has lower temporal and spatial resolution, and hence, the elementary shape and speckle tracking displacements will possibly be noisier, the use of robust regularization strategy will potentially be of more value. We will also work to expand upon the regularization strategies to make the motion fields biomechanically and temporally more consistent.

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Fig. 1.

(a) Outline with our contribution area highlighted, (b) Speckle (blue) and Shape (red) tracking displacements, RBFs and dense field, (c) Basis selection with sparsity, (d) Path of a point in myocardium - with biomechanical constraints and temporal smoothing (blue, on right) and without (magenta, on left) (Color figure online).

Fig. 2.

Baseline and post-occlusion radial strain values shown across the myocardium for corresponding end systolic (ES) frames (with the anterior region circled).

Fig. 3.

Radial strain values for: Anterior, Anterolateral, Inferolateral, Inferior, Inferoseptal and Anteroseptal regions for ED-ED in (a) Baseline (b) Occlusion (c) Occlusion MR

Fig. 4.

Box plots illustrating the median value and the distribution of correlation (with MR) of segmental strains obtained from different methods.

Table 1

Overall median correlations

	This method	Method in [5]	Shape tracking	Speckle tracking	Registration
Radial	.73	.72	.67	.64	.64
Circumferential	.82	.43	.79	.22	.78