Published in final edited form as:

Magn Reson Imaging. 2015 January ; 33(1): 146–160. doi:10.1016/j.mri.2014.08.007.

Meshless deformable models for 3D cardiac motion and strain analysis from tagged MRI

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Abstract

Tagged magnetic resonance imaging (TMRI) provides a direct and noninvasive way to visualize the in-wall deformation of the myocardium. Due to the through-plane motion, the tracking of 3D trajectories of the material points and the computation of 3D strain field call for the necessity of building 3D cardiac deformable models. The intersections of three stacks of orthogonal tagging planes are material points in the myocardium. With these intersections as control points, 3D motion can be reconstructed with a novel meshless deformable model (MDM). Volumetric MDMs describe an object as point cloud inside the object boundary and the coordinate of each point can be written in parametric functions. A generic heart mesh is registered on the TMRI with polar decomposition. A 3D MDM is generated and deformed with MR image tagging lines. Volumetric MDMs are deformed by calculating the dynamics function and minimizing the local Laplacian coordinates. The similarity transformation of each point is computed by assuming its neighboring points are making the same transformation. The deformation is computed iteratively until the control points match the target positions in the consecutive image frame. The 3D strain field is computed from the 3D displacement field with moving least squares. We demonstrate that MDMs outperformed the finite element method and the spline method with a numerical phantom. Meshless deformable models can track the trajectory of any material point in the myocardium and compute the 3D strain field of any particular area. The experimental results on *in vivo* healthy and patient heart MRI show that the MDM can fully recover the myocardium motion in three dimensions.

Keywords

MRI; Deformable models; Motion tracking; Strain; Cardiac

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1. Introduction

Tagged magnetic resonance imaging (TMRI) is a non-invasive way to track the in-wall *in vivo* myocardium motion during a cardiac cycle. Conventional MRI can only show the boundary of the ventricles. The number of natural occurring landmarks that can be reliably identified on the ventricle boundaries is limited. Axel and Dougherty [1] developed a tagging technique called spatial modulation of magnetization (SPAMM), which can produce saturated parallel planes through entire imaging volume within a few milliseconds compared with other TMRI methods [2–4]. Van der Paardt et al. [5] and Tustison et al. [6] utilize these methods on other organ imaging.

The application of MRI tagging technique on cardiac motion imaging is elaborated and left ventricle circumferential shortening motion scale is measured in different parts of the ventricle wall in paper McVeigh et al. [7]. Cardiac motion of left ventricle of healthy volunteers is tracked on the tagged short axis MRI in paper Sampath and Prince [8]. Two dimensional (2D) motion is validated on a pulse sequence phantom. The motion is combined with long axis image with 2D pathline and the left ventricle strain on short axis MRI is calculated in paper Sampath and Prince [9]. The TMRI of nine canine hearts with ischemia is analyzed and demonstrated that TMRI can detect ischemia of the left ventricle in paper Denisova et al. [10]. The ability of motion tracking of cine phase-contrast magnetic resonance is validated with an in vitro model in paper Drangova et al. [11]. The heart failure could be early diagnosed and prevented with left ventricle dysfunction analysis with MRI. The aortic stiffness and the myocardial strain irregular are found to be highly related in paper Ibrahim et al. [12].

Medical data are obtained from Siemens Magnetic Resonance Imaging machine. Five to six slices of parallel short axis images are captured from the base to the apex with equal intervals. They are put together with three long axis views, four-chamber view, three-chamber view and two-chamber view, as shown in Fig. 1. Three stacks of mutually orthogonal tag planes, two of which are perpendicular to the short axis image planes and one is perpendicular to the long axis, form 2D tag grids in TMRI. As material properties tagging lines deform as the heart contracts and relaxes during a cardiac cycle. Fig. 2 shows the deformation of tag grids in the myocardium during a systole in a short axis TMRI sequence. Myocardium motion in each direction can be quantitatively measured by tracking the tagging lines. Due to the through-plane cardiac motion a fixed image plane in an MRI time sequence does not show the same material points in the myocardium. We extract the deforming tagging lines from TMRI and deform a 3D meshless deformable model (MDM). The 3D MDM reconstructs the motion of the left ventricle. The motion trajectory of each point in the myocardium can be tracked and the myocardium strain can be computed accordingly.

Many research efforts have been dedicated to the heart shape building and cardiac motion reconstruction. Spline interpolation [13–15] and finite element method (FEM) approaches [16,17] have been applied to the heart shape reconstruction. McNerney and Terzopoulos [18] developed an FEM surface model which can track left ventricle deformation. A boundary element model was developed by Yan et al. [19] to extract local shape and motion

property with better time efficiency and comparable quality. Wang et al. [20] derive fiber directions from diffusion tensor MRI, and build a nonlinear FEM model from TMRI based on these material properties. With 16 nonlinear elements, the deformation is computed based on approximated fiber directions.

With the development of the TMRI, not only the heart boundary motion but also the myocardium deformation can be tracked with medical imaging. Harmonic Phase MRI system (HARP) [21–25] automatically segments left ventricle contours and track tagging line deformation with Fourier filtering. Based on HARP, a 3D mesh is developed and the displacement field is interpolated from intersections derived from the 2D HARP [26]. ZHARP [27,28], a system developed from HARP, computes the Eulerian through-plane motion from short axis images. Coupled with multi-slice imaging, it can generate 3D strain from a stack of short axis TMRI with bilinear interpolation. TMRI is filtered with Gabor filters [29,30]. Gabor filters with sinusoidal waves in different directions and Gaussian kernels in different sizes are convolved with the TMRI to extract dark stripes. Robust point matching method (RPM) and deformable model reconstruct the 3D motion of the left ventricle [31].

Deformable models have been proven to be the effective tools for cardiac motion reconstruction. Park et al. [32], Park et al. [33] and Metaxas and Terzopoulos [34] present parameter deformable models to track the left ventricle motion. Haber et al. [35], Haber et al. [36], Park et al. [37], and Park et al. [38] further extend parametric functions to recover the right ventricle (RV) motion and conduct 4D cardiac functional analysis using FEM. The FEM reconstructs a complex shape or motion by representing the volumetric mesh as a number of discrete small elements.

Meshless methods were first introduced to model objects with cracks and surface discontinuities [39] and have been later applied in motion simulation [40,41]. The point based method in these papers simulates the deformation of an object by computing the motion at a set of discrete points inside the object boundary. Müller et al. [41] compute the spatial derivatives of the displacement field with moving least square (MLS) [42] and then compute the elastic and plastic force on the points with the resulting strain energy.

We develop a novel MDM [43,44] for the 3D cardiac motion reconstruction from TMRI. An MDM represents an object with point cloud and iteratively deforms the point cloud with the minimum change of local Laplacian coordinates. The intersections of three stacks of orthogonal tagging planes are material points in the myocardium. They can be used as control points in the meshless model. The MDM will converge when the control points reach the target positions in the consecutive frame. This method avoids time-consuming remeshing procedures [45,46] in FEM when encountering large deformation.

The meshfree method with Galerkin weak form formulation was applied on cardiac deformation from MRI in [47–51]. The Galerkin weak form formulation is an extension of the FEM to deal with large deformation and discontinuity of the materials. The computational cost of Galerkin weak form formulation is higher than FEM. With the same

number of vertices in meshfree method and FEM, the meshfree method is more robust and generates comparable results.

The MDM introduced in this paper reconstructs 3D motion of left ventricle myocardium with tagging line deformation information. The MDM can generate the 3D displacement field and 3D strain tensor in the myocardium with the reconstructed motion, which are demonstrated to be accurate with a 3D numerical phantom. The displacements and strain reconstructed from 3D motion can be projected onto radial, circumferential and longitudinal directions with MDM. Compared with the meshfree method, the novel volumetric meshless deformable method introduced in this paper is easier to implement and very robust. The point cloud in MDMs could be much denser than the mesh vertices in the FEM. The trajectory of any point in the myocardium during the deformation can be computed.

We demonstrated the strength of the MDM as an approach for 3D cardiac motion reconstruction from TMRI by testing its performance on both a numeric phantom and *in vivo* cardiac magnetic resonance images. The experimental results showed a good agreement between our motion reconstruction and the underlying ground truth. The computation of 3D strain field is a difficult task because it is sensitive to the errors of reconstructed displacement field. The computation and analysis of strain field in this paper demonstrates that the 3D motion reconstruction is both accurate and robust. Heart in hypertrophy has weak pumping function. Cardiac model reconstruction shows the different motion and strain of the hypertrophic left ventricle which results in weak blood pumping function compared with a healthy heart. This paper analyzes the motion of the left ventricle of healthy heart and shows the difference between normal and pathological cardiac motion.

The second section of this paper describes volumetric MDMs in the application of cardiac motion reconstruction and strain computation in details. The third section validates the model with a numerical phantom, and compares the MDM with spline methods and finite element methods. The forth section analyzes the medical data with volumetric MDMs quantitatively. The experimental results and analysis from TMRI can be well interpreted by cardiac anatomy and pathology.

2. Volumetric MDMs

Volumetric MDMs represent objects with point cloud and deform the point cloud with control points. Fig. 3 shows the flowchart of the cardiac motion reconstruction from TMRI. A generic left ventricle mesh is registered onto the TMRI data and MDM is automatically initialized on the left ventricle position. The intersection points of three stacks of tagging planes are identified and tracked in a cardiac cycle. The MDMs deform the point cloud by minimizing the Laplacian local coordinates and fitting the control points to their coordinates in the next image time frame. The 3D volumetric motion of the left ventricle myocardium is reconstructed with MDMs following the tagging line information. After the motion is reconstructed from image cues, the 3D displacement field and 3D strain tensors can be calculated. Quantitative plots and charts can be generated with queries for assisting the cardiac disease diagnosis.

2.1. Control point extraction

In TMRI the deformation of tagging planes illustrates the deformation of the myocardium. The intersections of three stacks of orthogonal tagging planes in SPAMM are material points, which can be used as control points for model deformation.

The heart contours in short axis and long axis images are segmented with Metamorph [52], a machine learning based method [53], and deformable models [54,55]. Image landmarks on the heart contour can be detected for model registration. In motion tracking, only tagging line force inside the left ventricle boundary is tracked as image cues of deformation. The automatic tracking of tag intersections was critical in preprocessing TMRI for it provides external force for the MDM. As introduced in Axel et al. [56], Chen et al. [57] and Chen et al. [31], a Gabor filter bank was implemented to generate enhanced phase maps from TMRI and track tagging lines. An RPM module has been integrated into the model evolution to avoid false tracking results caused by through-plane motion and small tag spacing.

The intersections of the three sets of tagging planes are material points in the myocardium. Due to the high complexity of reconstructing 3 stacks of deformable surfaces proposed in Kerwin and Prince [58], we turn the calculation of three tagging plane intersections into a simplified implementation with equivalent results. A set of initially parallel tagging surfaces orthogonal to the long axis, denoted as S , can be reconstructed by the tagging lines in long axis MRI with thin plate splines. The intersections of horizontal and vertical tagging lines in the short axis images are identified. These intersection points from different short axis images are aligned along the long axis direction and interpolated with curves. The interpolated curves intersect with the tagging planes S which are orthogonal to the long axis as in Fig. 4 (right). This implementation avoids fully interpolation of all three stacks of tagging surfaces and the calculation of the intersections of spline curves and a set of tagging surfaces.

2.2. Model registration

The generic model of the left ventricle is built from MR images of a healthy volunteer. The surface mesh was built by a Delaunay triangulation using geodesic distances to preserve the topology of the object better [59,60]. This generic mesh provides an anatomically plausible model for the whole tracking procedure.

To register the model with the image data, we use two sets of landmarks, one set on the image contours and one set on the model surface, as in Fig. 5. Each set of landmarks has 50 points per image slice and 350 points in total. The generic model is sliced into a few contours on the MRI plane locations. High curvature feature points are detected on the contours and other points are computed accordingly [60]. The boundary mesh is fit onto the newly acquired TMRI with two steps. First, we align the generic left ventricle mesh onto the TMRI contours with polar decomposition [61,62]. After the object is globally aligned, we locally deform the model to fit the heart shape in TMRI data. Local fitting is done by Laplacian Surface Editing [63] and Laplacian Surface Optimization [64,65].

Denote the generic model boundary landmarks as p_i , the TMRI contour landmarks as q_i and their centers as $\bar{p}_i$ and $\bar{q}_i$ respectively. Translation between the model and the image data is the difference between $\bar{p}_i$ and $\bar{q}_i$.

$$T = \bar{q}_i - \bar{p}_i \quad (1)$$

Assuming all the points are going on the same similarity transformation, transformation matrix A can be calculated as in Eq. (3). The rotation can be isolated from the rest of the transformation with polar decomposition [66]. Let p_i^0 and q_i^0 be the model-centered coordinates, $p_i^0 = p_i - \bar{p}_i$, and $q_i^0 = q_i - \bar{q}_i$. The error function is the difference between image landmarks and transformed model landmarks. We minimize the error in Eq. (2) by setting its first derivative to zero, and yield Eq. (3).

$$E = \sum \left(A \begin{pmatrix} p_i^0 \end{pmatrix} - q_i^0 \right)^2 \quad (2)$$

$$A = \left(\sum p_i^0 p_i^{0'} \right)^{-1} \left(\sum p_i^0 q_i^{0'} \right) = A_{pp} A_{pq} \quad (3)$$

The rotation matrix can be estimated by decomposing A_{pq} . A_{pq} can be decomposed to a rotation matrix R and a scaling matrix P . R is a unitary matrix and P is a semidefinite Hermite matrix. The singular value decomposition of A_{pq} can be written as $A_{pq} = W \Sigma V'$. W and V are unitary matrices describing rotation of coordinates and Σ is a diagonal matrix describing the stretches in principle orthogonal axes. We have

$$P = V \Sigma V' \quad (4)$$

$$R = W V'$$

The matrix P is always unique. V and Σ can be computed by the Eigen decomposition of $A_{pq}' A_{pq}$ directly based on Eq. (5).

$$P = \sqrt{A_{pq}' A_{pq}} = \sqrt{(V \Sigma W')(W \Sigma V')} = \sqrt{V (\Sigma)^2 V'} \quad (5)$$

$$P^{-1} = V (1/\Sigma) V' \quad (6)$$

If A is invertible, the inverse of P can be calculated by substituting V and Σ into Eq. (6). The rotation matrix of registration can be calculated by substituting Eq. (6) into $R = A_{pq} P^{-1}$. After obtaining translation and rotation, uniform scaling can be computed by comparing the average magnitude of vectors in the object-centered coordinates.

3. Model initialization

After the mesh is registered on the patient data, point cloud inside of the left ventricle boundary is sampled and forms the MDM. The model deforms with the external force provided by control points and fits them to the coordinates in the next time frame. Volumetric MDMs describe an object as point cloud. Points are sampled with equal space inside the object boundary. They do not take each single particle as a unit when computing the interaction and dynamics of the point cloud. As shown as the right side model in Fig. 6, by assuming the neighboring particles are under the same similarity transformation, we can calculate the transformation of each kernel center. The spheroidal kernel of a particle is computed and stored in a hash table during the model initialization to speed up the motion reconstruction [67]. The stiffness of the material can be adjusted with the radius of the kernel. Larger kernels make the model stiffer and small kernels make the model highly deformable. The size of kernel in the cardiac motion reconstruction is comparatively small.

The model-centered coordinates of a point s can be written in the prolate spheroidal coordinate (u, v, w) . (u, v, w) are coordinates in longitudinal, circumferential, and radial

directions. In the left ventricle reconstruction, usually we define $u \in [-\frac{\pi}{2}, \frac{\pi}{6}]$ from the apex to the base of the left ventricle. $v \in [-\pi, \pi)$ is horizontal, starting and ending at the inferior junction of left ventricle and RV. The anterior LV-RV junction winds from anterior base to the inferior apex. The inferior LV-RV junction serves better as landmarks in model registration and myocardium model division. The transmural factor $w \in [0, 1]$ is defined in a way that it equals to 1 on model's epi-surface, and 0 at model's endo-surface. This definition of transmural weights can cope with the thickening of the left ventricle wall in systole. The coordinates of points are computed with the parameters $q = (a_{in}, a_{out}, b_1, t_1, t_2, \tau)$, $i = 1, 2$; $l = 1, 2$.

$$p = f(q, (u, v, w)) \quad (7)$$

where a_{in}, a_{out} are radii of endocardium and epicardium in three directions, b_1 is the magnitude of the bending, b_2 defines the location on the long axis where bending is applied, t_1, t_2 are tapering factors in two short axis directions, and the twisting angle $\phi = \pi \tau(u, v, w) \sin(u)$.

Model is initialized and deformed with the image forces as shown in Fig. 7. The force on the model is transformed from the model coordinate to δq with Jacobian matrix. q is integrated on all the model points. Parameter q is updated as $q = q + \delta q$. The model is recalculated with the updated q . The model keeps deforming until it fits onto the three dimensional intersection points derived in Section 2.1.

The Jacobian matrix $\mathbf{L}$ transforms the derivative on the DICOM coordinates of each point to the derivative on parameters.

$$\mathbf{L} = \mathbf{J}_w \cdot \mathbf{J}_m \quad (8)$$

where $\mathbf{J}_w$ is the Jacobian matrix between DICOM coordinates and model coordinates. $\mathbf{J}_m$ is the coordinate derivative over the model parameters.

The parameter gradient can be updated by integrating the projection of the external force on parameters over the volume. The parameters are updated iteratively and the coordinates of each point can be recalculated at each step [34].

$$\dot{q} = f_q = \int_{\Omega} f_{\text{ext}} \mathbf{L} \quad (9)$$

With the Jacobian matrix and the dynamics function, the model can be deformed globally to fit any patient cardiac TMRI data. The cardiac displacement field and strain field can be easily projected to the prolate spheroidal coordinates. The prolate spheroidal coordinates enable users to divide the cardiac model into 17 sector divisions. The motion and strain of different sector divisions are compared in the analysis section of this paper.

3.1. Local deformation with Laplacian coordinates

The local geometric features of volumetric MDMs can be represented as volumetric Laplacian coordinates. Denote the points in the neighboring area of point p_i , $N_i = \{v_j | \|v_j - v_i\| < h\}$, and degree d_i of the vertex is the number of points in the spheroidal neighboring area N_i . The local volumetric geometry can be described as a set of differentials $\delta_i = \delta_i$. The Laplacian coordinate of point v_j is the difference between point v_j and the average of its neighbors

$$\delta_i = v_i - \frac{1}{d_i} \sum_{j \in N(v_i)} v_j \quad (10)$$

The Laplacian local coordinates describe the relative locations of local points. The error function of volumetric MDMs in Eq. (11) has two terms. The first term is to minimize the change of Laplacian local coordinates. δ_i is the Laplacian local coordinate of the initial neighboring point set. $L(v'_i)$ is the Laplacian local coordinate of deformed neighboring point set. The second term is to minimize the difference between the control points and their target locations.

$$E(V') = \sum_{i=1}^n \|\delta_i - L(v'_i)\|^2 + \sum_{j=1}^m \|v'_j - v_{\text{target}}\|^2 \quad (11)$$

There are n points in the model in total, and m of them are control points which have motion information from TMRI. The heart left ventricle model is deformed with the control points while keeping the local geometry under minimum change. The meshless model is deformed with iterations constrained by the first term of error function 11, with the second term as a stopping criterion, as in algorithm 11. Each iteration has two steps: compute the transformation parameters of each point in the model; and update each point location with the transformation matrix. The iterations repeat until the control points reach the target locations in the consecutive image frame. To calculate the transformation parameters of each

point, we assume its neighboring points in a spheroidal kernel are under the same transformation. The similarity transformation equation can be solved in this way and the transformation matrix parameters of the central point of each kernel can be computed. Then the parameters are substituted into the transformation matrix and the new coordinate of each point is updated.

Algorithm 1. Model deformation algorithm—Algorithm: Given a volumetric MDM and a set of control points. Active points = model points + control points.

Initialize the radius-based kernels of all points with octrees and a hash table.

Loop until the control points converge to the target locations:

1. Calculate the transformation matrix of each point T_i by assuming its neighboring points are under the same similarity transformation;
2. Update the location of each point by $x_i = T_i x'_i$.

The similarity transformation has seven degrees of freedom, three for translation, three for rotation and one for uniform scaling. As long as there are more than seven points in the neighboring area, the transformation equation is solvable. When there is co-linearity or co-planarity in the neighborhood, more points are needed to solve the equation. In general, ten to twenty points in the neighborhood are more than enough to solve the equation.

Transformation matrix T_i can be solved by minimizing the quadratic error in Eq. (12).

$$E(V') = \min_{T_i} \left(\sum_1 \|T_i v_i - v'_i\|^2 + \sum_{j \in N_i} w_j \|T_i v_j - v'_j\|^2 \right) \quad (12)$$

where v_s are the initial coordinates of the points in the neighboring area, and v'_i are current points with the cue points set at the target locations. w_j are weights of the neighboring points in a spheroidal kernel. The deformation works when the weights are in a parachute-shaped distribution in 2D and a Gaussian distribution in 3D, with central points having higher weights.

The class of matrices representing isotropic scales and rotation can be written as $T = s \cdot \exp(H)$, where H is a skew-symmetric matrix. In 3D, skew-symmetric matrices emulate a cross product with a vector h , i.e. $Hx = h \times x$. Drawing upon several other properties of 3×3 skew matrices, one can derive the following representation of the exponential formula above: $T_i = s(\alpha I + \beta H + \gamma \mathbf{h}^T \mathbf{h})$. The first order accuracy of the similarity equation can be approximated as the matrix in Eq. (13).

$$T_i = \begin{pmatrix} s & -h_3 & h_2 & t_x \\ h_3 & s & h_1 & t_y \\ -h_2 & h_1 & s & t_z \\ 0 & 0 & 0 & 1 \end{pmatrix} \quad (13)$$

The transformation parameters $(s_i, \mathbf{h}_i^T, \mathbf{t}_i^T)^T$ can be moved to the right side of the product operator. Eq. (12) can be rewritten as $\|A_i(s_i, \mathbf{h}_i^T, \mathbf{t}_i^T)^T - \mathbf{b}_i\|^2 = 0$, where

$$A_i = \begin{pmatrix} x_{k_1} & 0 & x_{k_3} & -x_{k_2} & 1 & 0 & 0 \\ x_{k_2} & -x_{k_3} & 0 & x_{k_1} & 0 & 1 & 0 \\ x_{k_3} & x_{k_2} & -x_{k_1} & 0 & 0 & 0 & 1 \\ \vdots & & & & & & \end{pmatrix}, \quad (14)$$

$$\mathbf{b}_i = (x'_{k_1} \quad x'_{k_2} \quad x'_{k_3} \quad \cdots)',$$

$$k \in i \cup \text{Neighbor}(i)$$

The matrix A_i has the initial locations V of all points in the neighboring area of v_i and can be computed before the iteration. The vector $\mathbf{b}_i$ has the current points and the expected coordinates of the control points, denote as V' . Once the similarity transformation parameters of each point are calculated by solving the linear system (Eq. (14)), we can update each point coordinate with the transformation matrix. The volumetric point cloud deforms with the external force on the control points iteratively. A model with seven thousand points can deform to its target shape in a few minutes.

3.2. Strain computation

After the motion is reconstructed with volumetric MDMs, a 3D displacement field can be computed by comparing the model in two MRI frames. The strain field of the myocardium during the systole shows the myocardium contraction and blood pumping ability. Strain describes the relative deformation, such as local stretch and compression of the myocardium. The myocardial strain pattern of a patient's heart is different from that of a healthy heart. The strain field of the myocardium could help in detecting scars resulted from cardiac ischemia and infarction.

Given the initial position of a point $\mathbf{x}_0 = (x, y, z)$ in a world coordinate and the displacement $\mathbf{u}(t) = (u_x, u_y, u_z)$ at time t , the current position of the point in the deformed model is $\mathbf{x}(t) = \mathbf{x}_0 + \mathbf{u}(t)$. The Jacobian of this mapping is

$$J = I + \nabla \mathbf{u}^T = \begin{bmatrix} 1+u_{x,x} & u_{x,y} & u_{x,z} \\ u_{y,x} & 1+u_{y,y} & u_{y,z} \\ u_{z,x} & u_{z,y} & 1+u_{z,z} \end{bmatrix} \quad (15)$$

For instance, $u_{x,y}$ is the gradient of the displacement $\mathbf{u}$'s x component on y direction, u_x / y . Given the Jacobian J , the Lagrangian strain tensor ε of the point can be approximated with Green's strain tensor

$$\varepsilon = \frac{1}{2} (J^T J - I) = \frac{1}{2} (\nabla u + \nabla u^T + \nabla u \nabla u^T) \quad (16)$$

The Green's strain tensor is a function of the displacement gradient. With the displacements calculated with parameter functions, we calculate the displacement gradients with the MLS method [42]. As in Fig. 8, the initial spheroidal kernel is deformed to an ellipsoid. The displacement of a neighboring point is estimated as a function of the center point displacement and the displacement gradient, in the first order Taylor expansion as in Eq. (17). As an unknown variable with a uniform value in each kernel, the gradient can be calculated by minimizing the weighted error between the displacements $\mathbf{u}_j$ and the estimated displacements $\tilde{\mathbf{u}}_j$.

$$e = \sum_j (\tilde{\mathbf{u}}_j - \mathbf{u}_j)^2 w_{ij}, \text{ where } \tilde{\mathbf{u}}_j = \mathbf{u}_i + \mathbf{x}_{ij}^T \nabla u|_{x_i} \quad (17)$$

where

$$w_{ij} = \begin{cases} \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{\mathbf{x}_{ij}^T \mathbf{x}_{ij}}{\sigma^2}\right), & x_{ij} \leq d_0 \\ 0, & x_{ij} > d_0 \end{cases} \quad (18)$$

Here x_{ij} is the distance between point j and point i , and d_0 is the radius of each kernel. σ is the standard deviation of the Gaussian kernel, and controls if the density of the kernel is concentrating near the center or comparatively flat. Higher value of σ indicates a kernel with more uniform density.

Components of the displacement gradient ∇u at node i can be computed as (for example, the x component):

$$\nabla \mathbf{u}_x|_i = A^{(-1)} \sum_j (\mathbf{u}_x(j) - \mathbf{u}_x(i)) \mathbf{x}_{ij} w_{ij}, \quad (19)$$

$$\text{where } A = \sum_j \mathbf{x}_{ij} \mathbf{x}_{ij}^T w_{ij}$$

The displacement gradient calculated with formula 19 can be put into the Green's strain tensor (Eq. (16)) for the strain computation. The strain tensor has the strain in x-y-z directions and shear strain. The strain is projected onto radial, circumferential or longitudinal directions of the heart for analysis.

4. Validation on phantom

The ground truth of the *in vivo* cardiac deformation is very hard to access with other medical imaging methods or clinical methods. Tagged MRI is the state-of-art non-invasive medical

imaging method to estimate cardiac deformation. We validated the MDMs with a numeric phantom which enables us to compare results with the ground truth.

The displacement and strain computation of MDMs are validated via a numeric phantom with the similar size of a heart, as shown in Fig. 9. Taking one image slice as an example, the epicardial radius in the reference TMRI frame is 36.13 mm, and is 34.4 mm, 33.0 mm, 31.9 mm and 31.65 mm in the following time frames. The endocardial radius in the reference TMRI frame is 21.78 mm, and is 19.75 mm, 16.65 mm, 14.25 mm and 13.95 mm in the following time frames. The phantom is rotated for 1, 2, 3, 4 degrees on the following frames. The radii of the phantom are the average values of a set of healthy *in-vivo* left ventricle radii in TMRI. We show the phantom at the end of diastole and in the middle of systole, as in Fig. 9.

The phantom is deformed with a MDM formed of 2800 points. The strain is calculated with the MLSs. The deformation is calculated with a meshless kernel having 24 neighboring points. The strain is calculated with an MLS kernel having 12 neighboring points. Table 1 shows the average displacement and displacement variance between consecutive MRI frames. The outer radius contraction and inner radius contraction are calculated with regard to the reference frame. The displacements of MDM points are calculated with the previous frame as reference. The accumulated displacement and error after tracking for a few frames are also listed in Table 1. The errors are computed by comparing with the ground truth. The median and the variance of errors are also shown in Table 1.

The table in Fig. 1 shows the average displacement of each point in the area with regard to the radius contraction. We project the displacement to the radial and tangent directions. The displacement variance is small compared to the average displacement. The displacement errors and the radial displacement errors are three orders of magnitude smaller compared to the displacement magnitude in the second to the fourth frame. From the fourth frame to the fifth frame, the contraction rate is one order of magnitude smaller than the first half of systole. The scale of the displacement errors and the radial displacement errors keeps at the same order of magnitude. The circumferential displacement errors are about two orders of magnitude smaller compared to the displacement magnitude. The results in this table show that both radial displacements and circumferential displacements calculation with MDMs are reliable.

In Fig. 10, the 3D strain field in a 3D phantom [34] is computed and projected to three orthogonal directions, circumferential, radial and tangent longitudinal. Circumferential strain and longitudinal strain are negative. Radial strain is positive due to the left ventricle wall thickening in the systole. The magnitudes of circumferential strain are increasing through the myocardium toward the inside wall. Longitudinal strain is displayed more uniform through the left ventricle myocardium.

Strain tensors computed from a numerical phantom middle ventricle plane are projected into radial strain, the circumferential strain and the shear strain components. The strain ground truth and strain results from the MDM are displayed in Fig. 11. A middle ventricle image plane of the strain phantom is put on the x-y plane and the z axis shows the scalar of the

strain. The average radial strain is 0.13. This indicates that the myocardium is stretched in the radial direction. The average shear strain is -2.5×10^{-4} . The shear strain has very small magnitudes. The torsion around the long axis can be better illustrated with the circumferential displacements by the MDM as in Table 1. The variance of the radial strain and shear strain is both close to zero. The circumferential strain is decreasing from -0.1 at the outer boundary to -0.24 at the inner boundary. This indicates that the myocardium is compressed in the circumferential direction, which agrees with the myocardium fiber direction, with different levels. The strain result of the MDM is shown in the right image of Fig. 11. The average radial strain is 0.124 with variance 0.005. The average shear strain is -0.0015 with variance 0.002. The circumferential strain is decreasing from -0.1 on the outer boundary to -0.2 on the inner boundary. The strain computed with the MDMs has similar pattern and scalar compared with the ground truth.

The estimation of circumferential and radial strain is evaluated with regression plots. In Fig. 12, the circumferential strain has larger magnitudes near endocardium. The regression line fits the data very well, with R^2 equal to 0.695. The errors between the meshless model result and the ground truth have the average value -0.02 . The radial strain is around 0.15. The error of radial strain between the MDM result and the ground truth is 0.0011.

The MDM results are compared to the FEM [61] results and the spline results. The spline model has the same points as the FEM model. The finite element model has 622 tetrahedron elements and 338 vertices. The meshless phantom has 2800 points. Some of them are on the tagging lines which are deformed with spline method and the rest are interpolated. All three methods are deformed with same number of control points, simulated as the intersections of tagging lines. Deformation results in the middle of systole are shown in Fig. 13. In volumetric MDMs and spline methods, errors at the same locations of the finite element mesh vertices are computed and compared. The MDM results have the average error 0.0146 mm, nearly two orders of magnitude less compared to the FEM error 0.9288 mm, and better than the spline method error 0.0189 mm. In this phantom the control points provided by tagging lines are comparatively dense, the meshless method and the spline method outperform the FEM. FEM works well when the external force is only on a small area of the model and the caused deformation is small.

5. Experimental results on TMRI

The datasets are imaged with Siemens Trio MRI system in New York University medical school. This was gradient echo flash imaging, with slice thickness 6 mm, repetition time 40.85 ms, echo time 3.96 ms, tag spacing 6 mm, magnetic field 3 T, image matrix 256×216 , 23 cardiac phase images, field of visualization 280×236 . The images of each time sequence MRI were acquired with electrocardiogram gating.

The experimental results of 3D cardiac motion reconstruction of our method from TMRI on the Siemens TrioTim MRI system are described in this section. The 3D displacement field, which has the 3D displacement of each point in meshless point cloud, is measured on the reconstructed graphical volumetric cardiac model. The 3D displacement field at the end of systole, which has been projected onto circumferential, radial and longitudinal directions are

compared between a healthy heart and a patient heart. The comparison shows difference in global contraction, which causes the weak blood pumping function of the hypertrophic heart. The hypertrophic heart has similar displacement magnitude in the circumferential direction, in which direction that epicardium and endocardium fibers are, compared with the healthy heart. The global motion of left ventricle is illustrated with displacement and rotation analysis. The strain field of different parts of the left ventricle computed from the displacement field is analyzed and compared. The strain fields of a healthy heart and a patient heart are compared and show salient different patterns.

The reconstructed overall motion of a normal heart is shown in Fig. 14. The heart motion in a cardiac cycle is complicated. 3D motion is decomposed into three components corresponding to longitudinal, radial and circumferential directions for visualization. The left ventricle contracts in radial and longitudinal directions as shown in Fig. 14. The circumferential displacements show that the upper half and the lower half of the left ventricle rotate in different directions. Compared to the healthy left ventricle, the hypertrophic left ventricle contracts less in radial and longitudinal directions, and keeps similar degrees of torsion.

To further analyze the motion based on left ventricle anatomy, the left ventricle is divided into 17 sector divisions: 6 sector divisions at the base, 6 sector divisions in the middle ventricle, 4 sector divisions near the apex and the apex, based on the standard of the American Heart Association [68]. The inferior junction between left ventricle and right ventricle has been identified first and serves as a landmark. Viewed from the base clockwise, the 6 sector divisions at the base start from the inferior junction are the basal inferoseptal, basal anteroseptal, basal anterior, basal anterolateral, basal inferolateral, and basal inferior. The 6 sector divisions in the middle ventricle are middle inferoseptal, middle anteroseptal, middle anterior, middle anterolateral, middle inferolateral, and middle inferior. The 4 parts near the apex are the apical septal, apical anterior, apical lateral, and apical inferior. The apex of the left ventricle is isolated as one of the 17 myocardium segments. This division makes it convenient to compare displacements and strain between different parts.

The displacement results of a normal left ventricle with the size about 10 cm long, 3 cm to 3.5 cm short axis radius, and 1.2 cm to 1.3 cm thick of heart wall in middle ventricle are shown in Fig. 16. The scale of contraction and twisting of the left ventricle were analyzed in a cardiac motion time sequence. The contracting displacements and rotation degrees are computed as the average value of all points in a volumetric part of left ventricle. The comparison of displacements and rotation in different parts of left ventricle gives us a quantitative view of the left ventricle motion. The contraction and twisting of the heart are global deformation with almost the same starting time and ending time. The scale of left ventricle motion is plotted in the following figures. The contraction of left ventricle is almost done in the first 40% of time in a cardiac motion cycle started from the end of left ventricle diastole. During the left ventricle contraction the blood with fresh air is pumped from aorta to the artery to the whole human body. During the left ventricle relaxation the blood from left atrium (LA) enters the left ventricle. In the other half of a cardiac cycle which the left ventricle has less motion the right ventricle (RV) contracts and relaxes, pumping blood to the

lung and getting blood from the cardiac veins. The largest movement of the left ventricle we observed is the contraction along the long axis direction. The centroid of the left ventricle moves toward the apex during systole. In Fig. 15, the average longitudinal displacements of the base, the middle ventricle and the area near the apex at the end of systole are 13.85 mm, 8.5 mm, and 3.12 mm respectively. The apex of the left ventricle is nearly keeping in the same spatial coordinates during a cardiac cycle and the base contracts toward the apex. The speed of contraction toward the apex is almost linear with the distance to the apex because the two distances, the distance between the curve of the apex and the curve of the middle ventricle and the distance between the curve of the middle ventricle and the curve of the base, at 0.28 cardiac cycle near the maximum displacement magnitude are almost the same in Fig. 15. The left ventricle base and the left ventricle apex are rotating in different directions during the systole as shown in Fig. 16. Viewed from the left ventricle base the upper half of the left ventricle rotates clockwise for 1.81 degrees in average and the lower half of the left ventricle rotates counter clockwise for 3.69 degrees in average at the end of systole. In the beginning of diastole, the left ventricle is quickly deforming from the twisted state to the relaxed state in about 10% of a cardiac cycle. The rotation back starts and ends earlier than the relaxation in longitudinal and radial directions. A small bounce of left ventricle in the rotation direction at the end of diastole can be observed in Fig. 16.

Compared with other left ventricle motion tracking methods on motion tracking error in the left ventricle systole MDM has less average error. The MDM is compared with mesh based deformable model (DM), FEM, RPM, Gabor filter and Harmonic Phase (HARP) method. The average displacement of myocardium points tracked by MDM in the time sequence of a systole is 0.0, 1.1234, 2.4574, 4.0282, 5.0850, 5.6400, 5.0902 mm. The tracking errors of different methods are shown in Table 2.

Strain tensors are calculated from the cardiac motion at each point with Eqs. (15) and (16). The strain is compared between the epicardium and the endocardium, between middle-ventricle free wall and middle ventricle septum, and between healthy hearts and hypertrophic hearts. The strain computation of left ventricle requires high accuracy of the motion reconstruction. The 3D strain field calculated in this paper further confirms that the 3D displacement of the left ventricle calculated with MDM has reached good accuracy.

In Fig. 21, the strain at the end of systole is projected to 3 orthogonal directions, radial, tangent circumferential and tangent longitudinal. The strain in the middle ventricle short axis image, the three-chamber view and the four-chamber view is calculated and overlaid on the TMRI. The global pattern of the strain matches the numerical phantom results in Fig. 10. The global contraction and local variation are reconstructed by the volumetric MDM. Not only the strain on the TMRI plane can be calculated, strain on an arbitrary oblique plane can be calculated with this MDM. Both the circumferential strain and the longitudinal strain are negative. The longitudinal strain is more uniform compared with the circumferential strain. The circumferential strain has larger magnitude near the endocardium than the strain near the epicardium in a cardiac cycle. The increase of the magnitude of the circumferential strain from the epicardium to endocardium can be observed in Fig. 21.

The strain field computed from TMRI matches the strain pattern in the numerical phantom ground truth shown in Fig. 10. The inner boundary radius of the left ventricle contracts more than the outer boundary radius of the left ventricle. The circumferential strain always has larger magnitude near the endocardium during a cardiac cycle. Divide middle ventricle wall to three layers with different radius, endocardium, middle wall and epicardium, which have different myocardium fiber directions. As in Fig. 17, the average middle ventricle circumferential strain is -0.150 in the endocardium compared to -0.115 in the epicardium at the end of systole, as shown in Fig. 17. The maximum difference of the circumferential strain in the radial direction at the end of systole is 0.035 . Observed from the strain map in Fig. 21 the free wall of the left ventricle has larger strain magnitude compared with the strain of the septum. The average circumferential strain and the average longitudinal strain are nearly double the magnitude at the free wall compared to the strain at the septum at the end of systole, as shown in Fig. 18 (left) and (right). At the end of systole the circumferential strain is -0.275 at the free wall and -0.139 at the septum. The longitudinal strain is -0.257 at the free wall and -0.123 at the septum. This indicates that a major portion of cardiac motion force comes from the myocardium in the free wall of the left ventricle. Radial strain in middle ventricle middle wall is positive. The radial strain pattern could be explained by the fiber direction of myocardium. The myocardium fiber on inner surface and outer surface of left ventricle is more on circumferential direction, while the fiber of middle wall is more on the tangential longitudinal direction. The strain of the *in vivo* left ventricle fits the pattern of the numerical phantom ground truth.

The strain curves in Figs. 17 and 18 almost synchronize with the contraction curve in Fig. 15. The magnitude of the strain reaches its largest value at about 25% of a cardiac cycle. The magnitude of average strain of middle ventricle anterior part of the left ventricle almost reaches 0 at 40% of a cardiac cycle, which is the time that the left ventricle is relaxed in Fig. 15. The magnitude of average strain in middle ventricle free wall, especially the average longitudinal strain, is getting close to 0 between 40% and 50% of a cardiac cycle.

Hypertrophic heart, also called athlete's heart, has thicker heart wall and not as good blood pumping function compared with a healthy heart. The reconstructed motion of a hypertrophic heart is compared with the motion of a healthy heart in a cardiac motion cycle. Both the strain scale and the contraction timing of a hypertrophic heart are different from those of a healthy heart. In Fig. 19, the magnitudes of the circumferential strain and the longitudinal strain in hypertrophic hearts are smaller than those in normal hearts. The average strain magnitude of a hypertrophic heart is about half of the value of healthy hearts at the end of systole. The end of systole of a healthy heart is at the time of 30% of a cardiac cycle. The end of systole of the hypertrophic heart lags about 20% of a cardiac cycle compared with the end of systole shown in healthy heart. Healthy hearts reach the end of systole early in a cardiac cycle. The motion of a hypertrophic heart is much slower. The contraction and relaxation of a hypertrophic left ventricle last for almost a whole cardiac cycle. With less contraction tensivity and slower contraction the heart with hypertrophic cardiomyopathy usually has less efficiency in the blood pumping function.

Volumetric MDMs are the best way to estimate the trajectory of an arbitrary point inside the myocardium. The deformation of a tagging plane, as in Fig. 20, can be tracked with our

model for a whole cardiac cycle and projected onto the image plane at the end of systole. The projections of the deformed tagging plane align very well with the tagging lines in images. This experiment demonstrated that our model can reconstruct the 3D deformation field accurately.

6. Conclusion

A new volumetric MDM for tracking the 3D myocardium motion is presented in this paper. Meshless deformable model tracked the translation, rotation, scaling, twisting, and local deformation of the left ventricle myocardium. Compared to 2D motion analysis, it can easily follow the 3D trajectory of any material point in the left ventricle. The comparison between our results and the numerical phantom ground truth demonstrated the robustness of the model.

The experiments on *in vivo* TMRI data prove that the MDM is robust against motion complexity, image artifacts, and noise. Compared with the similar research on experimental animals [69], our experiments reveal *in vivo* myocardium strain pattern of the left ventricle. The displacement and the strain analysis can be done on any part of the left ventricle myocardium. Quantitative analysis based on the 17 left ventricle sector divisions in the American Heart Association standard shows that the motion features of healthy hearts agree with the heart anatomical features. During the systole the left ventricle contracts globally to pump blood to the aorta. The left ventricle contracts toward the apex of the heart with the apex keeps stable. The upper half of the left ventricle and the lower half of the left ventricle rotate in different directions. The myocardium compressed in both circumferential and longitudinal direction, shown as negative circumferential and longitudinal strain. The circumferential strain has higher magnitude in endocardium compared with the strain in epicardium. The left ventricle middle wall is thickening during the systole because of the contraction of the muscle, shown as positive radial strain. The strain on the lateral side of the free wall has nearly twice the magnitude compared with the strain on the LV-RV septum. The motion of healthy hearts and patient hearts shows salient difference in cardiac motion pattern.

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Fig. 1.

The setting of MR images: five parallel short axis images are placed with equal distance from the base to the apex. Three rotated long axis images are four chamber view, three chamber view and two chamber view.

Fig. 2.
A time sequence of short axis MR images of the middle ventricle from the end of diastole to the end of systole. Two orthogonal tagging planes along long axis direction are viewed on the short axis MRI as dark grids.

Fig. 3.
The flowchart of volumetric MDMs.

Fig. 4. (Left) Calculate the intersections of two sets of tagging lines. (Right) The intersection curves intersect with the tagging surfaces orthogonal to the long axis.

Fig. 5.
(Left) Landmarks on the contours. (Right) Registered model with landmarks on left ventricle and right ventricle endocardium and epicardium.

Fig. 6.
The left is the mesh-based deformable model. The right is the MDM.

Fig. 7.

Flowchart of the model deformation with image force. f_x is the force on the model coordinates. f_q is the force on the parameters. F_q is the integrated force on the parameters. L is calculated from J as in Eq. (8).

Fig. 8.
The strain of a point is computed by the deformation of its neighboring points with the MLS method.

Fig. 9.
A grid tagged numeric phantom contracts in the middle of systole and rotates for 2 degrees.

Fig. 10. The strain fields viewed from top: from left to right are initial model, circumferential strain, longitudinal strain and radial strain. The plane shown with the initial model indicates the location of the strain field in the row. The strain field is plotted on the model at the end of systole.

Fig. 11.

The ground truth of the phantom strain in Fig. 9 is shown in the left image. The strain result of the MDM is shown in the right image.

Fig. 12.
Linear regression plot of radial strain (left) and circumferential strain (right) between the numerical results and the MDM results.

Fig. 13.

The three columns are the deformation with the spline method, the FEM, and the MDM. The MDM results have the average error 0.0146 mm, nearly two orders of magnitude less compared to the FEM error 0.9288 mm, and better than the spline method error 0.0189 mm.

Fig. 14.

The first row is a healthy heart and the second row is a hypertrophic heart. The first column shows the left ventricle shape at the end of diastole. The other columns show the left ventricle at the end of systole. The second to fourth columns show radial displacements, circumferential displacements and longitudinal displacements in model-centered prolate spheroidal coordinates.

Fig. 15.
Comparison of average longitudinal displacements between the base, the middle ventricle and the apex.

Fig. 16.

The rotation angles show that the upper half and lower half of the left ventricle rotate in different directions.

Fig. 17.
Comparison of average circumferential displacements between the middle ventricle endocardium and the middle ventricle epicardium.

Fig. 18. Comparison of (left) average circumferential strain and (right) longitudinal strain between the middle ventricle septum and the middle ventricle free wall.

Fig. 19. The strain of the middle anterior of a healthy heart and hypertrophic heart. (Left) The circumferential strain. (Right) The longitudinal strain.

Fig. 20.
The left image is the tagging plane initialized at the end of diastole; the right image is the deformed tagging plane at the end of systole.

Fig. 21.
The strain at the end of systole is projected to 3 orthogonal directions: radial, tangent circumferential and tangent longitudinal. The strain on the middle ventricle short axis image slice, three-chamber view and four-chamber view is calculated and overlayed on the TMRI. The global pattern of the strain matches the numerical phantom ground truth in Fig. 10. Local geometric variation is reconstructed by the MDM.

Table 1

Displacement results and errors in millimeters of a sequence of contracting TMRI phantom.

Key frame	2	3	4	5	Accumulated
Outer radius contraction	-1.73	-3.13	-4.23	-4.48	-4.48
Inner radius contraction	-2.03	-5.13	-7.53	-7.83	-7.83
Average displacement	1.9324	2.1845	1.7203	0.5077	6.2314
Displacement variance	0.0018	0.1472	0.0814	0.0043	0.4326
Median absolute error	0.0028	0.0017	0.0038	0.0040	0.0294
Error variance	0.0017	0.0160	0.0355	0.0373	0.0523
Average radial displacement	-1.8638	-2.1797	-1.6956	-0.2694	-6.0299
Radial displacement variance	0.0077	0.2432	0.1424	0.0002	0.8142
Radial median absolute error	0.0050	0.0003	0.0009	0.0075	0.0463
Radial error variance	0.0034	0.0147	0.0077	6.5e-5	0.0228
Average tangent displacement	0.5151	0.4825	0.4444	0.4147	1.6579
Tangent displacement variance	0.0053	0.0068	0.0814	0.0080	0.1250
Tangent median absolute error	0.0326	0.0380	0.0300	0.0045	0.0046
Tangent error variance	4e-5	0.002	0.0001	2.6e-5	3.0e-004

The outer radius contraction and inner radius contraction are calculated with the first frame as reference. The displacements of MDM points are calculated with the previous frame as reference.

Table 2
The errors in different cardiac motion tracking methods are compared in an MRI time sequence.

Frame	1	2	3	4	5	6	7
MDM	0.0	0.0044	0.0063	0.0064	0.0075	0.0053	0.0054
Deformable model	0.0	0.0955	0.1807	0.1975	0.2567	0.2056	0.2612
FEM	0.0	0.4234	0.3216	0.4684	0.6452	0.9875	0.6543
RPM	0.0	0.1491	0.1936	0.1921	0.2558	0.3570	0.3677
Gabor filter	0.0	0.0954	0.1978	0.3536	0.5644	0.7192	0.6091
Harmonic phase	0.0	0.1054	0.1655	0.2996	0.4899	0.7120	0.6171

The average displacement of myocardium tracking points is 0.0, 1.1234, 2.4574, 4.0282, 5.0850, 5.6400, and 5.0902 mm.