MESHLESS DEFORMABLE MODELS FOR LV MOTION AND STRAIN COMPUTATION FROM TMRI

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A dissertation submitted to the
Graduate School—New Brunswick
Rutgers, The State University of New Jersey
in partial fulfillment of the requirements
for the degree of
Doctor of Philosophy
Graduate Program in Computer Science

Written under the direction of
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New Brunswick, New Jersey
May, 2011
ABSTRACT OF THE DISSERTATION

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Tagged MRI(TMRI) provides a direct and noninvasive way to reveal the in-wall deformation of the myocardium. Due to the through-plane motion, the 3D trajectories and strain of material points cannot be calculated directly from 2D TMRI images. With the intersections of three orthogonal tagging planes as cue points, we build a meshless volumetric deformable model to track the displacement of every material point in the heart wall. Meshless deformable models describe an object as point clouds inside of the object boundary. Each material point in the object is represented as a parameterized function of its coordinates in the model coordinate system, and the model is deformed by updating these parameters. The similarity transformation of each point is computed by assuming its neighboring points are doing the same transformation. The deformation is computed iteratively when the cue points match the target locations in the consecutive image frame. The 3D strain field is computed from the 3D displacement field with Moving Least Squares (MLS). We validate the performance of meshless deformable models with a numerical phantom and demonstrate that the meshless method outperform the finite element method (FEM). Meshless deformable models can track the trajectories of any material
point in myocardium and compute the 3D strain field of the myocardium. The experimental results on \textit{in vivo} healthy and patient heart data show that the meshless deformable model can fully recover the myocardium motion in 3D.
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Acknowledgements

I want to thank my advisor Dimitris Metaxas for his encouragement and support in my Ph. D. studies. He always encouraged me to pursue progress in career and independent work. He provided a good support for students to concentrate on study and research. I was new to computer vision and medical image analysis when I came to his lab. He taught me about deformable models and topics in medical image analysis, and led me into this research area new to me. He always gives me good directions in research.

I would like to thank Dr. Leon Axel for his consistent support. His group always provides medical image data for our group and explains everything with large patience with us. Each time he visits us he gives us valuable suggestions and insightful comments. The NYU group directed by him shares with us the software Intervu, which provides good segmentation and tagging line tracking results. This software generates the intermediate results for the reconstruction of the cardiac motion.

I would like to thank Ting Chen for his collaboration, getting me start with Intervu and providing valuable suggestions and encouragements in early stage development. I would like to thank Joel Schaerer for that he helped me to get start with visualization toolkit (VTK), both in C and in Python. He shared with me some of the visualization code developed in Medical Imaging Research Center (CREATIS). I would like to thank Zhen Qian for his warm hearted introduction of the cardiac project. He is a close friend of mine and my family. We have been in discussion of many machine learning and statistical methods. He shared with me his Matlab code of finding contour landmarks and basic deformable models. I would like to thank Suejung Huh for her collaboration in the development of meshless deformable models. We used to
work on FEM methods together. She led discussion in the weekly seminar and discussed a paper about MLS in the seminar. I would like to thank Sohae Chuang for always sharing her experience and opinions on cardiac MR image analysis. I would like to thank Viorel Mihalef for his collaboration in the cardiac model reconstruction from the CT data. I would like to thank Shaoting Zhang for sharing his ideas on medical image analysis and the discussion on new visualization techniques.

I would like to thank the other members of my committee: Prof. Vladimire Pavlovic, Prof. Ahmed Elgammal and Prof. Xenios Papademetris and for their advice and help. The computer vision class taught by Prof. Ahmed Elgammal brought me in the image related research area. Prof. Vladimire Pavlovic always provide valuable insights in research projects, seminars, my qualify examination and predefence. Dr. Xenios Papademetris gave me many valuable advices and suggestion for the further improvement of the meshless method and dissertation writing. I would also like to thank Prof. Doug Decarlo for his graphics seminar. In his seminar I read papers about the Laplacian Surface Editing method.

I would like to thank other co-workers in medical image processing and modeling in CBIM, Rui Huang, Jinghao Zhou, and Racheal for their team work and discussion.

I would like to thank my husband and my parents for their understanding and support during my Ph.D. study. They shared lot of housework and help me to take care of my daughter in these years. Thank my dad for the manually segmentation of the left ventricle for the motion reconstruction results of the healthy and patient hearts in this dissertation, and wrote a help for Intvu2 in Chinese.
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Chapter 1

Introduction

1.1 Motivation

Heart disease is the leading cause of morbidity and death in the Western world. In particular, heart failure is a major public health problem, affecting approximately 5 million people in the United States and 22 million people worldwide. The prevention, diagnosis and treatment of patients with heart failure is the largest single expense to medicare. Degree of deterioration of heart function, as reflected in anatomic changes such as remodeling, and reduced measures of global function such as ejection fraction, are correlated with poorer prognosis. In the research on heart diseases such as ischemia and infarction, heart dynamics is of great clinical importance. Imaging and modeling cardiac motion can help for the research and early diagnosis of heart diseases.

The primary function of heart is mechanical pumping. The basic measures of myocardial mechanics are the 3D strains and stresses. The imaging of myocardium motion can help for diagnosing heart diseases such as ischemia and infarction. Usually the infarction area and the myocardium adjacent to ischemia display abnormal motion pattern and systolic strain with small magnitude. The stress and strain analysis can contribute in the research on some cardiac diseases, such as hypertrophy. Abnormal hemodynamic load increases heart wall stress and leads to ventricular hypertrophy, which will alter the chamber geometry and material property and cause the wall stress changing. If this procedure cannot reach equilibrium and the wall stress keeps increasing, heart failure cannot be avoided. In this article, we will compare the 3D
strain field of normal heart and hypertrophic heart quantitatively. The analysis of myocardial
dysfunction also provide information for doctors to make different treatments. A patient with
large loss of regional function would need more immediate aggressive therapy.

Characterization of heart wall motion on a regional level would help to understand cardiac
mechanics or diagnose a cardiac disease. In order to accurately measure heart wall motion,
a number of material points are located and tracked. Previous methods of providing intra-
myocardial markers in the past have included:

1. The implantation of radiopaque markers [1, 2, 3, 4], lead beads [5] or ultrasonic crystals
   [6, 7],

2. Use of naturally occurring landmarks [8, 9, 10, 11]

The invasive nature of the implantation methods do not allow an adequate number of mark-
ers to be implanted for an reconstruction of the LV motion. The implantation methods also pose
potential problems of local myocardium property alteration due to the introduction of foreign
objects. The methods which utilize natural landmarks, such as bifurcations of coronary arter-
ies, do not require surgery. The intra-coronary injection of contrast medium is usually required
in methods using coronary artery features as landmarks. The natural landmarks are inadequate
for cardiac motion reconstruction either.

Compared to conventional MRI in which only heart boundaries can be detected, tagged
MRI [12, 13, 14, 15, 16, 17] can provide visible landmarks inside myocardium non-invasively.
Building a deformable model from tagged MRI can easily give the injection and projection
functions that usually required in cardiac disease diagnosis. It can also recover myocardial
global motions as contraction and twisting, and provide local intramural deformation as well to
reveal any dysfunction of myocardium.

As a comparatively new technique tagged MRI is still under intensive research, and the
imaging quality and resolution has been improved dramatically since it was firstly introduced.
The tagged MRI data we are using now are scanned with Magnetic Resonance Imaging with Spatial Modulation of Magnetization (SPAMM), which was developed by Dr. Leon Axel [12]. The advantages of the SPAMM technique over the others are that a number of material points can be marked in a very short time with a simple procedure, and be tracked during a heart beating cycle in a non-invasive setting, providing temporal correspondence of the material points. The SPAMM technique is to imaging the amplitude of the magnetization varies spatially in a sinusoidal-like fashion. The minima of the sinusoidal-like variation of the magnetization can be viewed as tagging planes, which form dark deformable stripes in the orthogonal images planes. If we continue to image the tissue after the saturation pulse sequence is applied, we can see the tagging lines follow the motion of the underlying tissue. The intersections of three orthogonal tagging planes can be viewed as material points, which are ideal landmarks for volumetric motion reconstruction.

Constructing a volumetric model with higher resolution from 2D TMRI slices can help with the comprehensive understanding of myocardium motion and conducting quantitative analysis on 3D displacement fields and strain fields. A reliable cardiac model has two properties. One is to model local deformations between TMR image slices. The other is to model global motion as contraction and twisting, especially when the TMRI slices are sparsely taken in clinical routine. The meshless deformable model is developed considering these two aspects of requirements. It also avoids time-consuming re-meshing procedure [18, 19] required in FEM, which is used as local deformation method in the cardiac deformable models before. When the size of the finite elements is close to the scale of deformation, the elements tend to degenerate into irregular shape and cause singularity problem in numerical research. As we increasing the resolution of deformable model by incrementally subdividing elements into small size, element degeneration and remeshing become inevitable. With meshless method, the remeshing can be replaced by a simple point resampling procedure with much lower cost.
The displacements of four non-coplanar material points are used to estimate the strain tensor. This method assumes that the strains within a tetrahedron formed by the four points are constant. This assumption makes the method highly depends on the tessellation results. Tetrahedra with irregular shape are less likely to have uniform strain inside. We proposed Moving Least Squares (MLS) approach for strain computation. MLS strain is a by-product of meshless deformable models. The deformation gradient is computed by minimizing estimated displacements and observed displacements in a sphere shaped kernel. The goal of this project is to develop a volumetric model from TMRI, give quantitative analysis of myocardium motion and strain under pathological conditions.

1.2 Tagged MRI

Tagged Magnetic Resonance Imaging (TMRI) is a non-invasive way to track the in vivo myocardial motion during cardiac cycles. Conventional MRI can only shows the boundary of ventricles. The number of natural occurring landmarks that can be reliably identified on ventricle boundaries are limited. Intra-myocardial markers are necessary for tracking intramural motion and estimating regional cardiac function. Myocardial tagging is an MRI technique for quantitative measuring intra-myocardial contractile function. Pai and Axel [20] reviewed some of the progress that has been made in developing imaging methods for tagged cardiac MRI.

MRI technique images the rotation magnetization field generated by large number of hydrogen nuclei in the human body. Without magnetization field, the hydrogen nuclei are rotating in random direction. With a uniform magnetization field. The hydrogen nuclei are aligned in either one of the directions parallel to the magnetic line of force. Radio-frequency pulses can alter the rotation direction of the nuclei. In order to view the different parts of human body or internal organs, the MRI machine puts a gradient magnetization field upon the uniform magnetization field. This would cause the nuclei to rotate in different speeds. The phase difference caused by the different rotation speeds, also viewed as different amount of emitting energy, can
Axel and Dougherty [12, 21, 22] developed a tagging technique called spatial modulation of magnetization (SPAMM), which can produce saturated parallel planes through out the entire imaging volume within a few milliseconds. As shown in Figure 1.1, two 45 degrees radio-frequency pulses and a gradient magnetic field tagged myocardium with magnetization before the heart starts to contract at the heart beating cycle. The magnetization are attached on the myocardium atoms. The deformation of the myocardium can be imaged with the deformed tagging lines. The preimaging pulse sequence consists of a radio-frequency (RF) pulse to produce transverse magnetization, a magnetic field gradient to "wrap" the phase along the direction of the gradient, and a second RF pulse to mix the modulated transverse magnetization with the longitudinal magnetization. Suppose, in the uniform magnetic field, the nuclei rotate along the longitudinal z direction. The first RF pulse rotates the nuclei rotation axis for 45 degrees toward the y axis. The gradient magnetic field makes the rotation axis rotate along z direction with constant speed. The time sequence of the rotating magnetic vector has sine projection on x direction and cosine projection on y direction. The gradient of the modulation magnetic field

Figure 1.1: The SPAMM tagging pulse sequence diagram
along y direction would cause nuclei on the different locations along the y axis have different rotation speeds. The spatial pattern of the nuclei rotation phase along y direction has the same pattern as the temporal sequence, a cosine curve, because they can be viewed as taken at different time spots in the time sequence. So far we have a cosine signal along y direction. To avoid the tag spaces being made twice denser in magnitude reconstruction when taking the absolute values of the signals, the curve is moved above zero on z direction. Another issue is that the magnetic component along z direction is desirable, because the deformation inside the x-y plane will change the inside plane magnetic phase and the longitudinal relaxation time is much longer than the transverse relaxation time. To image the x-y in-plane motion of the myocardium, the second RF pulse further tip the rotated nuclei for 45 degrees toward the y direction. The magnetic field generated by the spin nuclei after the second RF pulse is shown as in 1.2. As $\theta = 45$ in SPAMM technique, the y component and z component are sinusoidal curve with 90 degrees phase different in between. The myocardium will carry the z component of the magnetization for $T_1$, the spin-lattice relaxation time, which almost last for one heart
The starting frame is taken at end of diastole. The seven frame is taken at the end of systole. The first row: frame (1)-(5); the second row: frame (6)-(10); the third row: frame (11)-(15).

The different intensities of the magnetic field cause the different nuclei rotation speeds. The accumulated phase of the nuclei with time can be imaged as different intensities. The resulting images show periodic stripes due to the modulation. Motion between the time of striping and image formation is directly demonstrated as a corresponding displacement of the stripes. Consider one sequence of pulses. The minima of the sinusoidal variation of the magnetization are parallel planes, which displayed as stripe-like darker tags in relatively brighter myocardium on the image planes orthogonal to the tag planes. When two sequences of pulses are excited in orthogonal directions, grid tags are shown on the image planes orthogonal to both tag planes. Tags are material properties so that they deform as the heart contracts and relaxes during the cardiac cycle. Myocardial motion in one direction can be quantitatively measured by tracking the deformation of tags that are initially in the perpendicular direction. In Figure 1.3, we can observe that tag grids deform with myocardium during systole and diastole.

The other techniques computing displacement and strain from MRI [23], such as simulated-echo acquisition mode (STEAM) and displacement encoding with simulated echo (DENSE),
send two 90-degree RF pulses and a gradient magnetic field in the beginning of a sequence, and send RF pulse and magnetic field after a time interval for date acquisition. The DENSE system can generate displacement field directly from phase difference caused by motion over time, which can possibly be used as the ground truth of TMRI analysis.

For heart study, usually tags are created in three sets of mutually orthogonal tag planes, two of which are perpendicular to the short axis (SA) image planes and one to the long axis (LA), to form 2D tag grids in the myocardium for both views of the heart, as shown in Figure 1.4.

![Figure 1.4: The setting of MR Images: 5 SA parallel images are placed with equal space from apex to base. 3 rotated LA images are taken with 60 degree angles in between. (a)LA view (b) SA view](image)

Figure 1.5 illustrates the relation between material points in myocardium which created by tagged MRI, and tagged MR image data points we observed. Two orthogonal tag planes are in direction $n_1$ and direction $n_2$ are initialized in $t_1$ and deform into another shape in $t_2$. The projections on $t_2$ can be seen on the image plane as dotted lines. Their intersection line $l$ deforms from $l(t_1)$ to $l(t_2)$. A material point initially located at $M(t_1)$ moves to the location $M(t_2)$, where no image plane passes. What we can see on the TMRI is the intersection of two tagging lines $S(t_2)$. It indicated the point where the intersection line $l$ passes through. With two sets of tagging lines on SA images, we can identify intersection line of two orthogonal tag planes such as $l$. The displacement component alone LA direction can be recovered from the LA images. Tag planes orthogonal to LA project to LA images as tagging lines. By reconstructing and
deforming these tag planes, the intersection of all three orthogonal tag planes can be traced as the points where these tag planes intersected by $l$.

Using appropriate mathematical approaches, we can retrieve 2D displacement fields in these image planes by tracking the deformation of tag grids. Compared to the conventional MRI which can only capture the global cardiac function measurements such as the ventricular volumes, tagged MRI can be utilized to recover local heart wall motion within the myocardium and derive potentially critical clinical information such as local torsion, shearing, and strain.

### 1.3 Related Work

Intensive research effort has been put on medical image based cardiac motion reconstruction and strain analysis since the MRI technology developed. Both surface models and volumetric models have been developed to reconstruct motion from medical images.

McInerney and Terzopoulos [24] developed a 3D Finite Element (FEM) surface model deformed by balloon force which can track large deformation of LV. They applied it to CT volume...
images and reconstruct motion of a cardiac cycle. Yale’s group approaches this problem by shape-based estimation. The contours of the LV in the image data are segmented and the local patches on each surface are tracked by their principle curvatures. A deformation framework based on continuum mechanics are developed for building surface displacement field. Compared to McInerney’s work, their method can provide quantitative analysis and indicate shear motion in the contour tangent direction. Their work includes FEM based approach [25, 26, 27] and BEM based approach [28] and Bspline based approach [29]. Shape-based FEM can achieve higher tracking accuracy while shape-based BEM can achieve acceptable accuracy with higher time efficiency.

Volumetric motion model reconstruction are mostly on tagged MRI. The imaging processing and tag tracking are not trivial issues in TMRI data analysis. Heart contours can be segmented by many methods that integrating statistical estimation and image information together. Montillo and Metaxas [30, 31] segments the epicardial and endocardial surfaces by combining gray scale morphology and 2D active geometry and integrating the image preparation step into data analysis. Xiaolei Huang et al. developed deformable shape and texture models Metamorph [32, 33], which deforms contours with free form deformation (FFD) while considering the edge information and region information in images at the same time. Her method [33] integrates the shape and appearance prior information in the contour deformable models. Junzhou Huang et al. [34] proposed a tag seperation method based on the Discrete Cosine Transformation and Wavelet Transformation. Qian et al. [35] developed a learning based segmentation method which train a Adaboost classifier with Gabor features. Tagging lines are tracked with multiple approaches. Zhu et al. [36] developed a subject-specific dynamical model (SSDM) that simultaneously handles temporal dynamics and inter-subject variability. Their dynamic prediction algorithm can progressively identify the specific motion patterns of a new cardiac sequence based on the shapes observed in past frames. They apply the statistical prediction and constraint method on the real-time three-dimensional echocardiography myocardial border.
tracking with the near-constant volume assumption [37]. Guttman et al. [38] tracked tagging lines by matching a template of expected profile to the dark lines in the image using a least squares estimate. Gupta et al. were trying to track tagging lines with variable brightness optical flow [39] and bandpass optical flow [40] and cope with the tag fading problem. Denney [41] proposed a method with maximum-likelihood estimate and a maximum a posteriori (MAP) hypothesis test to identify the myocardial tags without prior knowledge of the myocardial contours. As introduced in Chen et al. [42, 43, 44], a Gabor filters bank was implemented to generate corresponding phase maps for TMRI images [45]. A Robust Point Matching (RPM) module has been integrated into the approach to avoid false tracking results caused by through-plane motion and irregular tag spacing. The difficulty of tag tracking lies on the confusion caused by the dark heart boundaries and the tagging line occlusion came from myocardium through-plane motion.

Spline models have been used to reconstruct volumetric motion of the LV and the RV. In the work of Huang and Amini [46], Öztürk and McVeigh [47], the deformation is modeled with B-spline tensor product in Cartesian space. In Declerck et al [48] and O’Dell et al [49], the deformation is also modeled using Legendre polynomials or B-splines, but in a particular polar geometry. Denny and McVeigh [50] gave a discrete finite difference analysis method to reconstruct displacement and strain. Denny and McVeigh [50] and O’Dell et al [49] model the backward transformation, which deforms a tag line on each TMRI time frame back to its location at reference time. Declerck et al [48] and Öztürk and McVeigh [47] proposed a computation of forward transformation to calculate the displacements of material points over the sequence. Chandrashekara et al [51] present a nonrigid registration algorithm based on a cylindrical free-form deformation (FFD) model and the optimization of a cost function based on normalized mutual information (NMI). Histace et al [52] add an original diffusion preprocessing to the B-spline model, which significantly increased the robustness of the detection and the follow-up of the grid tags. They [53] also compare two active contour modeling and
draw the conclusion that image domain methods performs better than the frequency domain 
methods. In the above methods, displacements normal to three orthogonal tagging planes are 
calculated separately and grouped together with Splines. Another approach is to measure all 
three components of the motion at tag sheet intersections (Kerwin and Prince [54]; Pan et al. 
[55]).

FEM models are also used on volumetric motion reconstruction. Young [56, 57] built a 
cubic polynomial model driven by FEM, fit it to the human TMRI data, and gave qualitative 
motion fields and strain field. Guccione et al. conducted FEA of the LV in the beating dog 
heart [58].

Deformable models have been used for the cardiac motion reconstruction from tagged MRI 
for a long time. Park et al. [59, 60, 61] presented deformable models combining spatially 
varying parameter functions to track the left ventricle (LV) motion. The parameterized model 
provides a robust basis for generating reasonable deformation between sparse TMRI slices. 
Compared to spline models only based on interpolation, a locally deformable parameterized 
model allows motion reconstruction in higher resolution with less affection by noise or arti-
facts. Haber et al. [62, 63, 64] and Park et al.[65, 66] further extended parameter functions 
to recover the right ventricle (RV) motion and conduct 4D cardiac functional analysis using 
FEM. Hu et al. [67, 68] heuristically converge the stress field with deformable models and 
expectation maximization (EM) algorithm. The stress results showed the gradual variation of 
transmural myocardium fiber directions which fit anatomic facts. Qian and Liu [69] developed 
a tensor-based classification framework that better conserves the spatio-temporal structure of 
the myocardial deformation pattern than conventional vector-based algorithms.

Meshfree methods based on continuum mechanics has been introduced in book [70]. The 
deformation is calculated with base functions. It has been first developed for simulating the 
cracks in deformations and discontinuity of materials, and has larger complexity than FEM. 
The method has been applied for body tracking in computer vision [71]. The method has
been applied for cardiac motion analysis and solving cardiac electrical propagation [72, 73].

Our meshless deformable model replaces meshes with point clouds comes from the meshfree method and Müller’s paper [74]. This paper simulates the combination of elastic and plastic deformation with a physics based meshless approach. The combination of the meshless idea and deformable models [75] is published in CVPR’2008 [76]. We further developed the method with the insight provided by Laplacian surface editing [77, 78] and Local Scale-Invariant Features (SIFT) [79]. The application of meshless deformable models on left ventricle motion and strain analysis is published in MICCAI’2008 [80].
Chapter 2

Cardiac 3D Motion Reconstruction Preprocessing

2.1 2D Contour Segmentation

The segmentation of cardiac ventricle boundary is a very difficult task in tagged MRI. The dark tagging lines on the bright myocardium make it difficult for the edge based segmentation methods. The region or texture based segmentation methods are hard to separate the heart and surrounding tissues. Motion detection based methods can capture most of the heart area while keeping many noises due to the breathing and movement of patients. The results of motion detection based methods are not able to separate the endocardium surface and the blood pool because the blood pool also changes the intensity during the heart beating cycles.

Most of methods for the boundary segmentation in tagged MRI need the preprocessing to remove the tagging lines first. One way is to remove it with fourier filtering, as in Harmonic phase (HARP) analysis [81, 82]. The filtering will blur the boundary. Thresholding the magnitude image will give the bright heart region and muscle region. Thresholding is not accurate enough for segmentation due to the blur. Metamorph [32] segments the heart boundary with free form deformation (FFD) and a close initialization. It also utilizes the statistic information of the intensities. The boundaries can also be segmented with active contour models [83]. A good initialization is important in the active contour models or FFD, especially at the boundary between myocardium and the surrounding muscle. A semi-automatic method Intervu are developed in NYU. A few key frames of accurate boundaries with manual correction can be used for correcting the boundaries in the rest frames with spline methods. Gabor filtering banks are
2.2 2D Tagging Line Tracking

The most wildly used method in tagging line tracking is Harmonic phase (HARP) analysis. It has been developed into an automatic cardiac strain analysis software for clinical usage. Gabor filters are another method for extracting tagging line information. These two methods are both processing tagging line information with image processing filters. We can track tagging lines directly on the TMRI with active contour models.

2.2.1 HARP

Harmonic phase (HARP) analysis [81, 82] is a method for automatic segmenting heart contour and generating phase images. Velocity maps, circumferential and radial strain can be measured with the phase images. Theoretically, the displacement of every point in one direction is illustrated in the phase image itself. In practice, the displacements in the phase images are traced with optical flow method, which is not a very robust method.

Consider the tagged cardiac images shown in Figure 2.1, showing the same slice at the reference time and later in the middle of systole. These images have two-dimensional Fourier transforms that have collections of spectral peaks. Harmonic peaks are the high intensity spots in the frequency domain. They correspond to the frequency of repeated patterns in the image texture. Denote the image intensity in one direction as function $f(x)$, with fourier transform

$$F(a) = \int_{-\infty}^{+\infty} f(x)e^{-2\pi i a x} dx.$$  \hspace{1cm} (2.1)

Setting $a = a + T$ is equal to setting $x = x - T$. Because the integration is from negative infinite to positive infinite, the integration interval has not been changed. From calculation we have $F(a + T) = F(a)$. If the image has repeated pattern, a point and the points with periods away are mapped to the same spots in the frequency domain. Since multiple times of the period
can also be taken as a period, there are harmonic peaks with equally spaced intervals. The peak nearest the DC component corresponds to the smallest period. It is possible to isolate a single peak in each image and take the inverse Fourier transform of just the spectral contents within this single peak, yielding a harmonic image. A harmonic image has magnitude and phase images. The magnitude images can be used for heart contour segmentation. In the phase images as shown in Figure 2.1, the intensity of each point keeps constant during a heart beating cycle. The "sawtooth" appearance fits the repeated pattern of tagging lines. Mathematically, the phase of harmonic images is linearly related to the tissue motion in a direction orthogonal to the tagging lines.

As an minimally-interactive method, HARP can achieve acceptable 2D displacement and strain analysis. HARP's results are not accurate enough for 3D motion reconstruction for two reasons. The first is that the magnitude images are blurred due to the filtering process, therefore the segmentation of the cardiac contour is inaccurate because of the loss of resolution. The threshold of the magnitude images is hard to determine automatically. The second is that the phase images are difficult to recovered near the end of systole because the tagging lines are bent in different directions. In the frequency image on the right of the second row of Figure 2.1, we notice that the high intensity area is distributed around the peak in the frequency image at the end of diastole shown on the left. If we only isolate a single peak in one direction, the deformation of the tagging lines are underestimated in the recovered phase images. If we isolate a larger area in the frequency image, the recovered phase images will easily have branches. In healthy hearts beating with normal forces, the bending of tagging lines will cause unneglectable error in HARP results.

Optical flow[84] is a method measuring the displacements on consecutive image frames in a image sequence by assuming the lighting condition does not change over time. Tagged MRI has comparatively dense temporal resolution, and there is no lighting condition change in phase images. Let the image brightness at the point \((x, y)\) in the image plane at time \(t\) be denoted by
The brightness of a particular point in the pattern is constant, so that

\[
\frac{dE}{dt} = 0
\]  (2.2)

Using the chain rule for differentiation we see that

\[
\frac{\partial E}{\partial x} \frac{dx}{dt} + \frac{\partial E}{\partial y} \frac{dy}{dt} + \frac{\partial E}{\partial t} = 0
\]  (2.3)

Denote the velocity along x direction and y direction as \( u \) and \( v \),

\[
Err_b^2 = E_x u + E_y v + E_t = 0
\]  (2.4)

where we can also write it in another way,

\[(E_x, E_y), (u, v) = -E_t\]  (2.5)

Thus the component of the movement in the direction of the brightness gradient \((E_x, E_y)\) equals

\[-\frac{E_t}{\sqrt{E_x^2 + E_y^2}}\].

Taking an image sequence as a 3D pixel volume, \( E_x, E_y, E_t \) can be easily represented with a 8 pixel cube. We take the total error as a sum of two parts: the constraint on the minimum lightening change in Equation 2.4; and the smooth constraint on the velocity flow

\[
Err_c^2 = \nabla^2 u + \nabla^2 v.
\]

Using the calculus of variation we obtain an iterative solution

\[
\begin{align*}
\tilde{u}^{n+1} &= \tilde{v}^n - E_x[E_x \tilde{v}^n + E_y \tilde{v}^n + E_t]/(\alpha^2 + E_x^2 + E_y^2) \\
\tilde{v}^{n+1} &= \tilde{v}^n - E_y[E_x \tilde{v}^n + E_y \tilde{v}^n + E_t]/(\alpha^2 + E_x^2 + E_y^2)
\end{align*}
\]  (2.7)

The smooth constraint on the velocity flow in Equation 2.6 further underestimates the magnitude of displacement fields in HARP results. Observed from Figure 2.2, the optical flow method is not robust on high gradient area such as the big phase change from the -180 degree to the 180 degree. When normalizing the velocity, the large magnitude of \( \sqrt{E_x^2 + E_y^2} \) makes the velocity very small. Even we set contraction and rotation to very small values, we still notice the opposite tracking direction at the lower right part of the phantom near the high gradient.
area. The other problem is that if we only keep the myocardium part of the phase image, there is large difference between the phase image and the blood pool texture. The tracking results near the endocardium would be inaccurate.

### 2.2.2 Active Contour Models

Active contour models, also called snake [85, 86], is an energy-minimizing spline guided by external constraint forces and influenced by image forces. The active contour models have been wildly used in image segmentation. We use active contour models to track the tagging line deformation directly on the TMRI. The tagging lines are automatically initialized with manually selected area of interest and automatically alignments. The intervals between tagging lines can be automatically determined with fourier filtering described in the previous subsection.

As shown in Figure 2.3, the tagging lines in the previous time frame are taken as the initial tagging lines in the next time frame. The first step is to search along tagging line normal direction to find the darkest point with two constraints. One constraint is that the length of tagging line can only have small changes. The other constraint is that the ratio between distances of two sets of neighboring consecutive tagging lines are keeping as unchanged as possible. This constraint is like putting short springs with same elastic coefficients between tagging lines. Point energy is a combination of image intensity information and two constraints. The point along normal direction with smallest energy is selected as the point location in the new tagging line.

The tagging lines are further deformed with active contour models. The image intensity gradients are taken as the external forces.

Active contour models represent a spline point sets as $v(s) = (x(s), y(s))$, we can write its energy functional as

$$E_{snake} = \int_0^1 (E_{int}(v(s)) + E_{image}(v(s)) + E_{con}(v(s))) ds \quad (2.8)$$

where $E_{int}$ represent the internal energy of the spline, $E_{image}$ gives rise to the image forces,
\( E_{\text{con}} \) includes the manual interaction forces and the adjusting forces of neighboring tagging lines. The internal spline energy can be written as

\[
E_{\text{int}} = (\alpha |v_s(s)|^2 + \beta |v_{ss}(s)|^2)/2
\]  

(2.9)

The spline energy is composed of a first-order term making the contour smooth, and a second-order term making the contour less curvature. The image forces we used are the gradient of the intensity. The external forces come from the manual interaction. The interactional force is inverse proportional to the distance between the mouse clicked point and points on the tagging lines. The adjusting force tends to put the tagging line in the middle of two neighboring tagging lines. Let \( E_{\text{ext}} = E_{\text{image}} + E_{\text{con}} \). The derivative of the external energy is the external forces.

The external forces include the image intensity gradient forces and the constraint forces. Radial contraction in the first half of the systole is significant. The distance map inside of the left ventricle blood pool provides the constraint forces. This constraint makes sure the tagging lines inside the blood pool are centralized during the systole, and the elastic springs between tagging lines would not cause errors. During the diastole, the left ventricle myocardium is relaxed and recovered to the reference state. The displacement field of the tagging lines are proportional to the constraint forces during diastole. The following Euler equations can be generated by minimizing the energy functional of equation,

\[
\alpha x_{ss} + \beta x_{ssss} + \partial E_{\text{ext}}/\partial x = 0
\]
\[
\alpha y_{ss} + \beta y_{ssss} + \partial E_{\text{ext}}/\partial y = 0
\]

(2.10)

Approximating the derivatives with finite differences, the first and second derivative of \( v(s) \) can be written as linear functions of neighboring points. The coefficients of \( v(s) \) is a sparse matrix that can be precomputed before calculating \( v(s) \) iteratively. From

\[
Ax + f_x(x, y) = 0
\]
\[
Ay + f_y(x, y) = 0
\]

(2.11)
The Euler equation is solved by setting the right-hand side as a small step.

\[ A x_t + f_x(x_{t-1}, y_{t-1}) = -\gamma (x_t - x_{t-1}) \]
\[ A y_t + f_y(x_{t-1}, y_{t-1}) = -\gamma (y_t - y_{t-1}) \]  

Equation 2.13 can be solved by matrix inversion

\[ x_t = (A + \gamma I)^{-1} (\gamma x_{t-1} - f_x(x_{t-1}, y_{t-1})) \]
\[ y_t = (A + \gamma I)^{-1} (\gamma y_{t-1} - f_y(x_{t-1}, y_{t-1})) \]  

The method is implicit with respect to the internal forces, so it can solve very rigid snakes with large step sizes. Adding the spatial-temporal constraints as constraint forces in the active contour models may be a duplicate and does not yield more accurate results. If the external forces become large, the explicit Euler steps of the external forces will require much smaller step sizes. With active shape models, we automatically track tagging lines in a heart beating cycle first.

We manually correct the errors may be caused by the following reasons: tagging lines are out of image planes due to the through plane motion. Grid tags bring in confusion and cause one line shift when there is comparatively large rotation. Large movement of tagging lines in the consecutive TMRI frames or too small intervals between tagging lines near the end of systole. After the tagging lines have deformed for a few time frames, the myocardium area with large deformation will be blurred and tagging lines are hard to located. Tracking results in middle ventricle SA TMRI slices are very accurate. Tracking results in SA TMRI slices near the apex are less accurate due to the rotation and blur. The out-of-plane of the left ventricle due to the through-plane motion in base SA TMRI would cause confusion in the tagging line tracking.

The 2D displacement and strain fields can easily be computed with 2D meshless deformable models, which are similar to 3D meshless deformable models we will introduced in Chapter 4.
2.3 Tagging Line Intersection Tracking with Scale-invariant Feature

The intersections of tagging lines are detected as Scale Invariant Features [87] [88]. The local maxima and minima of a cascade filtered images are identified as feature points. These feature points on low-contrast area and on the edge are rejected. The local area textures around a feature, the gradient magnitudes and orientations at image points in the neighboring region, are computed as feature descriptions. Features on different image time frames are mapped by finding one with the most similar feature description and the shortest distance.

2.3.1 Feature Point Detection

The local maxima and minima in the scale-normalized Difference of Gaussian produce the most stable image features compared to some other possible image functions, such as the gradient, Harris corner function [89]. Scale-normalized Gaussian is the image convolved with variable-scale Gaussian. With an input image, $I(x,y)$,

$$G(x, y, \sigma) = G_0(x, y, \sigma) * I(x, y), \quad (2.14)$$

where $*$ is the convolution operation in x and y directions, and

$$G_0(x, y, \sigma) = \frac{1}{2\pi\sigma^2}e^{-(x^2+y^2)/2\sigma^2}. \quad (2.15)$$

The convolved image is blurred and have the smaller size compared to the original one. The blurred image is normalized to the original size and the difference between them are the Difference of Gaussian $\sigma^2\nabla^2 G$.

$$DoG(x, y, \sigma) = (G_0(x, y, k\sigma) - G_0(x, y, \sigma)) * I(x, y)$$

$$= G(x, y, k\sigma) - G(x, y, \sigma) \quad (2.16)$$

The Laplacian can be approximated by the Difference of Gaussian with different variance.
scale at $k\sigma$ and $\sigma$:

$$\sigma \nabla^2 G = \frac{\partial G}{\partial \sigma} \approx \frac{G(x, y, k\sigma) - G(x, y, \sigma)}{k\sigma - \sigma} \quad (2.17)$$

and therefore,

$$\text{DoG}(x, y, \sigma) = G(x, y, k\sigma) - G(x, y, \sigma) \approx (k - 1)\sigma^2 \nabla^2 G \quad (2.18)$$

The original image convolve with Gaussians of an increased variance multiplying a constant factor $k = \sqrt{2}$ each level. This produce a stack of 5 images from clear, to blurred. Adjacent image scales are subtracted to produce the Difference-of-Gaussian images. In order to detect the local maxima and minima of $\text{DoG}(x, y, s)$, each sample point is compared to its eight neighbors in the current image and nine neighbors in the scale above and below. It is selected only if it is larger or smaller than all of its neighbors. The cost of this check is low because that most sample points will be eliminated with a few comparisons. Maxima and minima are detected by comparing each point in the stack with its 26 neighbors in $3 \times 3 \times 3$ regions. Once a complete stack has been processed, we resample the Gaussian image that has twice the initial value of $\sigma$, which is the third image in the previous stack before the normalization. The features are detected from a few stacks with different sizes.

Once the extrema of $\pm 1$ sample spacing in each dimension are detected, the extrema to sub-pixel / sub-scale accuracy are interpolated with the Taylor expansion up to the quadratic terms.

$$D(\hat{x}) = D + \frac{\partial D^T}{\partial x} \hat{x} + \frac{1}{2} \hat{x}^T \frac{\partial^2 D^T}{\partial x^2} \hat{x} \quad (2.19)$$

where $D$ is the difference of Gaussian and its derivatives are evaluated at its sample points. $\hat{x} = (x, y, \sigma)$ is the offset from the sample point and the unknown variable to calculate. The derivative on the extreme is zero. The estimated offset is

$$\hat{x} = -\frac{\partial^2 D^T}{\partial x^2}^{-1} \frac{\partial D^T}{\partial x} \quad (2.20)$$

The $\hat{x}$ is calculated by solving the linear system $\frac{\partial^2 D^T}{\partial x^2} \hat{x} = \frac{\partial D^T}{\partial x}$ with gauss method. If the offset $\hat{x}$ is larger than 0.5 in a dimension, the interpolated offset are closer to its neighbor in
that direction. The sample point is changed to that neighbor and the offset is computed with regard to the neighbor. The final offset $\hat{x}$ is added to the sample point to get the extremum with sub-pixel /sub-scale accuracy. The feature locations with the sub-pixel accuracy is calculated in cardiac MRI with the heart area of size 120 pixel × 120 pixel.

### 2.3.2 Feature Point Selection

Two types of feature points are eliminated to achieve higher robustness. The first type includes feature points with low contrast, which tend to be noise. A threshold was set on the difference of gaussian. In tagging line intersection detection, all extrema with a value of $|D(\hat{x})|$ less than 0.01 were discarded assuming the intensity is ranged in $[0, 1]$.

$$
D(\hat{x}) = D + \frac{1}{2} \frac{\partial D^T}{\partial \hat{x}} \hat{x}
$$

(2.21)

The Difference of Gaussian at feature point with the sub-pixel accuracy is interpolated with equation 2.21, which is derived by substituting equation 2.20 to 2.19.

The second type of features to be removed are point along edges, because the locations of feature points along edges are difficult to determine. The difference of Gaussian function will have a strong response along edges, indicated by a large principle curvature. If the curvature in the perpendicular direction is small, the feature point is hard to located along the edge. The principle curvatures can be computed from a $2 \times 2$ Hessian matrix,

$$
H = \begin{pmatrix}
D_{xx} & D_{xy} \\
D_{xy} & D_{yy}
\end{pmatrix}
$$

(2.22)

The derivatives are estimated by taking differences of neighboring sample points. Because we are interested in the ration between eigenvalues of the Heissen matrix, which are principle curvatures. Denote the large eigenvalue as $\alpha$ and the small one as $\beta$. The trace of the Heissian matrix is the sum of its eigenvalues. The determinant of the Heissian matrix is the product of eigenvalues.
\[ Tr(H) = D_{xx} + D_{yy} = \alpha + \beta \]  
\[ Det(H) = D_{xx}D_{yy} - D_{xy}^2 = \alpha \beta \]  

Let \( \gamma \) be the ratio between the large eigenvalue and the small eigenvalue, so that \( \alpha = \gamma \beta \).

\[ \frac{Tr(H)^2}{Det(H)} = \frac{(\alpha + \beta)^2}{\alpha \beta} = \frac{(\gamma \beta + \beta)^2}{\gamma \beta^2} = \frac{(\gamma + 1)^2}{\gamma} \]  

The ratio in equation 2.24 only depends on the ratio of eigen values. The quantity \((r + 1)^2/r\) is minimum when two eigenvalues are equal and increases with \(\gamma\). Its threshold can be set by setting the threshold of \(\gamma\). In this application the threshold of \(\gamma\) is set as 10.

A heart wall mask is generated with left ventricle contours. Feature points outside of the heart wall are removed.

### 2.3.3 Feature Point Matching

The local texture around the feature point is described as discrete statistical information of the gradient magnitudes and orientations of its neighboring points. Firstly, for each feature point \((x, y)\) at scale \(s\), the gradient magnitude \(m(x, y)\) and orientation \(\theta(x, y)\) is precomputed using pixel differences:

\[
m(x, y) = \sqrt{(D(x+1,y,s) - D(x-1,y,s))^2 + (D(x,y+1,s) - D(x,y-1,s))^2}
\]

\[
\theta(x, y) = \tan^{-1}((D(x,y+1,s) - D(x,y-1,s))/(D(x+1,y,s) - D(x-1,y,s)))
\]

The gaussian weighted gradient orientation in the neighborhood is put into 36 bins covering the 360 degree range of orientations. The gaussian window size is proportional to the exponential of the scale in the subscale accuracy. The peak in the orientation histogram is taken as the keypoint orientation. The gradient orientations of neighboring points are rotated relative to the feature point orientation in order to achieve orientation invariance. A descriptor of a feature point divides the neighborhood into \(4 \times 4\) regions and the gradient orientation into 8 bins.
4 \times 4 \times 8 \text{ results in 128 bins in total. The gaussian weighted gradient magnitude in each region is added into the region bin with the gradient orientation. The texture descriptor of each feature point is a histogram of the gradient magnitude, represented as a vector. The texture descriptor and the location of a point is combined as a descriptor of a feature point. The feature points in the consecutive frames are matched with nearest neighbor method.}

In the grid tagging images, similar gradient patterns repeat in many areas. This gradient histogram descriptor is combined with location descriptor to get better matching results. Assumption of the normalized gradient histogram and feature location makes acceptable features. The matching pairs are further selected. Based on the assumption that displacements in local areas are similar, displacements in a 70 degree sector around a feature is selected as neighbors. Displacements in a sector are projected to the radial and tangent directions and fit with gaussian distributions. Only matching features with displacements in the truncated gaussian distribution are selected. When the median displacement is not very small and in the opposite direction of a pair of features, this matching is removed. The procedure repeats until no matching pairs are removed. In general case, two iterations would get good results.

2.3.4 Validation on a Phantom

Taken one image slice as an example, the epicardial radius in the reference TMRI frame is 36.13mm, and is 34.4mm, 33.0mm, 31.9mm in the following frames. The endocardial radius in the reference TMRI frame is 21.78mm, and is 19.75mm, 16.65mm, 14.25mm in the following frames. A phantom is built with sinusoid wave with frequency 0.18, which similar to MRI tags. The phantom is rotated with 1, 2, 3 degrees on the following frames. The radiiuses of the phantom are obtained from a healthy heart in-vivo TMRI. Displacements automatically tracked with scale invariant features are listed in table 5.3 in millimeters. The variance of the displacements and median square errors are also listed. The outer radius contraction and inner radius contraction is calculated with the first frame as reference. The other displacements are
2.3.5 Preliminary Experimental Results

The features points on the short axis (SA) tagged MRI are tracked with scale-invariant features, shown in Figure 2.10. Tagging lines tracked with active contour models and adjusted manually are taken as ground truth. The displacement of each detected scale-invariant feature point is bilinear interpolated by the displacements of four intersections around it in the ground truth. Displacement results in pixel are projected to radial and tangent directions. Displacements between the reference frame and frame 1, and between frame1 and frame2 are plotted as this. SIFT results are close to the "ground truth". Figure 2.12 Some of scale-invariant features are not on the intersections. As shown in Figure 2.11, the number of automatically detected paired SIFT features are comparable to the number of intersections. The number of scale-invariant features decreases when the left ventricle contracts, mostly because the tagged MRI become blurred after large deformation.

2.4 3D Tagging Plane Intersections Motion Reconstruction

The intersections of the three tagging planes are material points in myocardium. Because the high complexity of reconstructing 3 deformable planes and the projection method proposed in [54], we turn the calculation of three tagging plane intersections into a simpler implementation with equivalent results. A tagging surface can be reconstructed by tagging lines in MRI with thin plate splines.

The thin plate spline method construct a smooth surface fitting the given control points. Given control point set \((x_i, y_i)\). The energy function of the TPS is

\[
E = \sum_{i=1}^{K} \| y_i - f(x_i) \|^2 + \lambda \int \int \left[ (\frac{\partial^2 f}{\partial x^2})^2 + 2(\frac{\partial^2 f}{\partial x \partial y})^2 + (\frac{\partial^2 f}{\partial y^2})^2 \right] dx dy
\]  

(2.26)
The first term is to make sure the surface closest to the control points. The second term is to make the surface as smooth as possible. The surface function which would minimize was defined by the following function

\[ f(x, y) = P(X) + \sum_{i=1}^{K} \phi(\| z - x_i \|) \cdot c_i \]  

(2.27)

where \( \phi(r) \) is a radius based function. It could be \( \phi(r) = r^2 \log(r) \) for 2-dimensional data and \( \phi(r) = r^3 \) for 3-dimensional data. Once we know control points, \( \phi(\| z - x_i \|) \) can be calculated for each location in the surface grid, denote it as \( \Phi \). The task is to compute the unknown coefficients \( c \) and \( d \). \( P(X) \) is a polynomial function of \( X \). For example, when \( X \) is 2D, the \( d_0 + d_1 \cdot x + d_2 \cdot y \) defines a regression plane fits the points best. The latter part is for local deformation. Substituting equation 2.27 to equation 2.26, we get energy function as

\[ E_{tps}(d, c) = \| Y - Xd - \Phi c \|^2 + \lambda \text{trace}(c^T \Phi c) \]  

(2.28)

A nice property of the TPS is that it can always be decomposed into a global affine component controlled by \( d \), and a local non-affine component controlled by \( c \). The smoothness term solely depends on the non-affine components. The separation of the affine and non-affine warping space is done through QR decomposition.

\[ X = [Q_1|Q_2](R0)^T \]  

(2.29)

where \( Q_1 \) and \( Q_2 \) are \( K \times (D + 1) \) and \( K \times (K - D - 1) \) orthogonal matrices, corresponding the \( R \) and 0 respectively. The matrix \( R \) is upper triangular. The local deformation only depends on \( Q_2 \). With the QR decomposition in place, we have the energy function

\[ E_{tps}(\gamma, c) = \| Q_2^T Y - Q_2^T \Phi Q_2 \gamma \|^2 + \| Q_1^T Y - Rd - Q_1^T \Phi Q_2 \gamma \|^2 + \lambda \text{trace}(\gamma^T Q_2^T \Phi Q_2 \gamma) \]  

(2.30)
Setting $c = Q_2\gamma$. The least-squares energy function in the last equation can be first minimized w.r.t. $\gamma$ and then w.r.t. $d$. We have $X^Tc = 0$ for the least-squares part. The solution of $c$ and $d$ of the least-square part is

$$
\hat{c} = Q_2(Q_2^T\Phi Q_2 + \lambda I_{(k-D-1)})^{-1}Q_2^TY
$$

$$
\hat{d} = R^{-1}Q_1^T(Y - \Phi \hat{c})
$$

The minimum value of the TPS smoothing energy obtained at the optimum $(\hat{c}, \hat{d})$ is

$$
E_{bending} = \lambda [Q_2(Q_2^T\Phi Q_2 + \lambda I_{(k-D-1)})^{-1}Q_2^TYY^T]
$$

The smoothing parameter can be added into $\Phi$ matrix and the form of the solution is unchanged in equation 2.31.

We calculate the intersections of horizontal and vertical tagging lines in sagittal images first. These intersection points are aligned along the long axis direction and interpolated with cubic splines. The intersection lines intersect with the set of parallel tagging planes, which are orthogonal to the long axis. This implementation avoids fully interpolation all three tagging surfaces, and simplifies the problem of calculating the intersections of lines and surfaces.

Calculating the intersections of curves and surfaces can be viewed as calculating intersections of lines and planes in the small neighborhood of the intersections. The interpolated curve can be represented by a set of points and short lines connecting these points. We find the short line that intersects with the surface first. Then we project the two ends of the line $P$, $Q$ to the surface as $P'$, $Q'$, as in Figure 2.14 (b). Since the curve is almost normal to the surface, the projection points are located very close to the intersection $O$. And a small area of the surface is close to a plane. Thus the intersection of $PQ$ and $P'Q'$, denoted as $O'$, is very close to the real intersection $O$. The location of $O'$ is taken as the location of $O$ in this paper.
Figure 2.1: Automatic segmentation and phase extraction of left ventricle of a patient with cardiac hypertrophy disease. The left column shows the LV at the end of diastole. The right column shows the LV at about 1/6 cardiac beating cycle. The first row shows TMRI; the second row shows the frequency domain of fourier transform; the third row shows the magnitude image; the forth row shows the phase image with a segmentation on LV.
Figure 2.2: Optical flow tracking results. Optical flow tracking methods are tested on phase images from the numerical phantom. The numerical phantom contracts from radius 47.5mm to 46.25mm, and rotates for 1 degree. The phantom with grid tagging lines and their phase images with period in one direction. The second row shows the optical flow tracking results of the upper-left and lower-right corner.
Figure 2.3: The tagging line initialization method

Figure 2.4: Tagging line tracking errors. Rotation near the LV apex and large displacement between two frames cause the lose track of tagging lines. The blur of tagging lines also cause the error. The large deformation of long axis image cause the lose track of tagging lines.
Figure 2.5: Automatic horizontal tagging line tracking results. The first image is the automatically initialized tagging lines. The contraction of left ventricle almost finished at the first half of the heart beating cycle. The tracking results are very close to the ground truth.

Figure 2.6: Automatic vertical tagging line tracking results. The first image is the automatically initialized tagging lines. The contraction of left ventricle almost finished at the first half of the heart beating cycle. The tracking results are very close to the ground truth.
Figure 2.7: In each stack, the initial tagged short axis MRI is repeatedly convolved with Gaussians to produce the scale space images shown on the left. Adjacent Gaussian images are subtracted to produce the difference-of-Gaussian images on the right. Each stack down-samples the image with a factor of 2 with Gaussian image.

<table>
<thead>
<tr>
<th>key frame</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>outer radius contraction</td>
<td>-1.8922</td>
<td>-3.4234</td>
<td>-4.6266</td>
</tr>
<tr>
<td>inner radius contraction</td>
<td>-2.2203</td>
<td>-5.6109</td>
<td>-8.2359</td>
</tr>
<tr>
<td>mean feature displacement</td>
<td>2.1127</td>
<td>2.6295</td>
<td>2.3104</td>
</tr>
<tr>
<td>feature displacement variance</td>
<td>0.0690</td>
<td>0.4436</td>
<td>0.5092</td>
</tr>
<tr>
<td>mean square error</td>
<td>0.3428</td>
<td>0.5074</td>
<td>0.5680</td>
</tr>
</tbody>
</table>

Figure 2.8: Displacement results in millimeter and errors of a sequence of contracting TMRI phantom. The outer radius contraction and inner radius contraction is calculated with the first frames reference. The other displacements are calculated with the previous frame as reference.
Figure 2.9: (a) The deformation of the first frame (b) second frame (c) third frame. The green points are initial locations; the red points are deformed location; the yellow points are the ground truth. The displacements and the errors are shown in table 5.3.
Figure 2.10: (a) The deformation of 9 frames tagged MRI. The green points are initial locations; the red points are deformed location; the yellow points are the ground truth. The displacements and the errors are shown in table 5.3. The features points and matching pairs are more than those at the end of the systole. In the area with comparatively large deformation, the tagging lines are blur and feature points are harder to be detected.
<table>
<thead>
<tr>
<th>Time frame</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of SIFT features</td>
<td>71</td>
<td>70</td>
<td>69</td>
<td>65</td>
<td>53</td>
<td>55</td>
<td>61</td>
<td>54</td>
</tr>
<tr>
<td>Number of intersections</td>
<td>70</td>
<td>70</td>
<td>67</td>
<td>70</td>
<td>65</td>
<td>67</td>
<td>68</td>
<td>75</td>
</tr>
</tbody>
</table>

Figure 2.11: Comparison on feature point numbers. The in-wall intersections are taken as control points in deformation. The number of automatically detected paired SIFT features are comparable to the number of intersections. Some of scale-invariant features are not on the intersections.

Figure 2.12: Displacement results in pixel are projected to radial and tangent directions. Tagging lines tracked with active contour models and adjusted manually are taken as ground truth. Displacements between the reference frame and frame 1, and between frame1 and frame2 are plotted as this. SIFT results are close to the "ground truth".

Algorithm:

1. Calculate the intersections of horizontal and vertical tagging lines in the sagittal images, as in Figure 2.14 (a).

2. For each intersection point in one image, find the nearest point in the neighboring sagittal slices, connect them with a cubic spline.

3. Build surfaces with tagging lines orthogonal to the LA using thin plate splines

4. The curves resulted from step 2 intersect with the surfaces built in step 3. Calculate their intersections, as in Figure 2.14.

Figure 2.13: The algorithm of calculating the intersection of the three tagging surfaces
Figure 2.14: (a) Calculate the intersections of two sets of tagging lines (b) Calculate the intersection of a curve and a surface (c) The intersection curves intersect with the tagging surfaces orthogonal to the LA
Chapter 3

Physics based Approaches

In Metaheless Deformable Models, an object under study is interpreted as particles with parameterized representation. The deformation of the object, viewed as the movement of point clouds, is reconstructed globally and locally using the Lagrange equation. In meshless methods, each particle and its neighboring particles are grouped with a radius based function. The global deformation of an object is described by the parameterized functions and can be obtained by integrating the global motion contribution at each point over the volume during a small time interval. The velocity is calculated at each point using the Lagrange equation. The elasticity of the object is simulated by adding the internal force term, which is derived from local strain energy, into the Lagrange equation. We use an iterative framework to recursively estimate the global and local deformation in order to reconstruct the dense 3D motion in the LV myocardium.

3.1 Lagrangian Formulation

The coordinates of points in the world coordinate system are transformed into a model-centered coordinate system as \( x = c + Rp \), where \( c \) is the world coordinates of the model centroid, and \( R \) is the rotation matrix. In this paper, we will focus on the deformation part of the model. Some deformation is shared by the whole object and can be described by parameterized functions. The model uses an ellipsoid as the base function and global deformation such as non-uniform scaling, tapering, bending, twisting. \( x \) as the displacement of a structure, \( \dot{x} \) is the velocity, and
Figure 3.1: The flowchart of the motion reconstruction.

\( f_{\text{ext}} \) is the external force. The dynamics equation can be rewritten as

\[
D \dot{x} = f_{\text{ext}} + f_{\text{int}}
\]

(3.1)

In this paper we define the damping matrix \( D \) be diagonal and constant over time. The internal force is only considered in local deformation.

The velocity of a point in world coordinates can be calculated as

\[
\dot{x} = \dot{c} + \dot{R}p + R\dot{p}
\]

\[
= \dot{c} + B\dot{\theta} + R\dot{s} + R\dot{d}
\]

(3.2)

where \( B = \partial(Rp)/\partial \theta_i \), \( \theta \) is the rotation coordinate of the model, and \( \dot{s} = [\partial s/\partial q_s]\dot{q}_s = J\dot{q}_s \). \( J \) is the Jacobian of the model-centered coordinates with respect to the global deformation parameters at each point.

Equation 3.2 can be written in the form

\[
\dot{x} = [I \ B \ RJ]\dot{q} = L\dot{q}
\]

(3.3)

where \( J = (J_1, \ldots, J_n), q = (c, \theta, s, d) \), and \( n \) is the number of points in the object. We can omit the local deformation \( d \) in the stimation of global parameters so that the velocity of the global variables \( q_g = (c, \theta, s) \) can be calculated by combining formula 3.14 and formula 3.15.

\[
\dot{q}_g = f_{q_g} = \int_\Omega f_{\text{ext}}L
\]

(3.4)
The external forces $f_{ext}$ on global parameters are integrated over the volume

$$f_{q_g} = \int_\Omega f_{ext}L = (f_c, f_\theta, f_s) \quad (3.5)$$

where

$$f_c = \int_\Omega f_{ext} \quad (3.6)$$

$$f_\theta = \int_\Omega f_{ext}B \quad (3.7)$$

$$f_s = \int_\Omega f_{ext}RJ \quad (3.8)$$

The integration over the volume can be interpreted as the sum of the integrals over each point in the volume.

### 3.2 Global Deformation

The model-centered coordinates of a point $s$ can be written in the prolate spheroidal coordinate $(u, v, w)$, and calculated with equations 3.10 to 3.13. In the LV reconstruction, usually we define $u \in [-\frac{\pi}{2}, \frac{\pi}{2}]$ from apex to the base of the LV. $v \in [-\pi, \pi]$ is horizontal, starting and ending at the inferior junction of LV and RV. 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 LV wall in systole. The location of points are computed with the parameters $q = (a_{in_k}, a_{out_k}, b_i, t_l, \tau), k = 1, 2, 3, b = 1, 2; l = 1, 2$.

$$p = s(q, (u, v, w)) \quad (3.9)$$

$$r = \begin{pmatrix} a_{out1}w + (1 - w)a_{in1} \\ a_{out2}w + (1 - w)a_{in2} \\ a_{out2}w + (1 - w)a_{in2} \end{pmatrix} \quad (3.10)$$
\begin{equation}
    e = \begin{pmatrix}
        r_1 \cos(u) \cos(v) \\
        r_2 \cos(u) \sin(v) \\
        r_3 \sin(u)
    \end{pmatrix}
\end{equation}

\begin{equation}
    m = \begin{pmatrix}
        (1 + t_1 \sin(u)) e_1 + b_1 \cos(e_3 + b_2 \pi) \\
        (1 + t_2 \sin(u)) e_2 \\
        e_3
    \end{pmatrix}
\end{equation}

\begin{equation}
    s = \begin{pmatrix}
        m_1 \cos(\varphi) - m_2 \sin(\varphi) \\
        m_1 \sin(\varphi) + m_2 \cos(\varphi) \\
        m_3
    \end{pmatrix}
\end{equation}

where \(a_{in1}, a_{in2}, a_{in3}, a_{out1}, a_{out2}, a_{out3}\) are radiiues 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 \(\varphi = \pi \tau(u, v, w) \sin(u)\). Variables \(r, e, m\) are intermediate variables, and can be interpreted as parameterized functions of other variables.

The Lagrangian equation for the model is

\begin{equation}
    \ddot{u} = f_{\text{ext}} + f_{\text{int}}
\end{equation}

where \(u\) is the displacement of myocardium, \(\dot{u}\) is the velocity, \(f_{\text{ext}}\) is the external force and \(f_{\text{int}}\) is the internal force.

The velocity of a point in DICOM coordinates can be calculated as

\begin{equation}
    \dot{u} = L \dot{q}
\end{equation}

where \(L\) is the Jacobian matrix between point coordinates and parameters. The Jacobian of the heart-centered coordinates w.r.t. the parameters is

\begin{equation}
    J_m = \partial s/\partial q = (\partial s/\partial a, \partial s/\partial b, \partial s/\partial r, \partial s/\partial \tau)
\end{equation}
\[ \frac{\partial s}{\partial a} = \frac{\partial s}{\partial m} \cdot \frac{\partial m}{\partial e} \cdot \frac{\partial e}{\partial r} \cdot \frac{\partial r}{\partial a} \quad (3.17) \]

\[ \frac{\partial s}{\partial t} = \frac{\partial s}{\partial m} \cdot \frac{\partial m}{\partial t} \quad (3.18) \]

\[ \frac{\partial s}{\partial b} = \frac{\partial s}{\partial m} \cdot \frac{\partial m}{\partial b} \quad (3.19) \]

\[ \frac{\partial s}{\partial \tau} = \frac{\partial s}{\partial \phi} \cdot \frac{\partial \phi}{\partial \tau} \quad (3.20) \]

The Jacobian matrix \( L \) transforms the derivative on the DICOM coordinates of each point to the derivative on parameters.

\[ L = J_w \cdot J_m \quad (3.21) \]

where \( J_w \) is the Jacobian matrix between DICOM coordinates and model coordinates. The deduction of \( J_w \) can be found in [75]. \( J_m \) is calculated in equation 3.16.

With the Lagrangian equation, the Jacobian matrix can be moved to the right side and the velocity of the variables \( q \) can be calculated. The finite difference of the parameters can be calculated by integrating the external forces \( f_{ext} \) on parameters over the volume.

\[ \dot{q} = f_q = \int_{\Omega} f_{ext} L \quad (3.22) \]

Replacing the velocity in the Lagrangian equation (3.14) with the velocity of parameters in equation (3.15), we can update the parameters using an explicit iterative scheme

\[ q_{t+1} = q_t + (f_q) dt \quad (3.23) \]

3.3 Local Deformation with Finite Elements Method

The internal forces \( f_{int} \) in equation 3.14 can be calculated with Finite Element Methods (FEM). With new point locations calculated with updated global parameters, we can get the displacement of each point. With the displacements, strain, stress and stress force on each point can be calculated. Stress forces are taken as the internal forces of the model.
In our physics based cardiac deformable models, the heart is modelled as a mesh with tetrahedron shaped elements. With a linear approach, the stiffness matrix indicates the linear function which can generate the stress forces from displacements. In each element, the world coordinates can be transformed to the a coordinate system with the four nodes of the tetrahedron as the base.

\[
\begin{bmatrix}
1 \\
x \\
y \\
z
\end{bmatrix} =
\begin{bmatrix}
1 & 1 & 1 & 1 \\
x_1 & x_2 & x_3 & x_4 \\
y_1 & y_2 & y_3 & y_4 \\
z_1 & z_2 & z_3 & z_4
\end{bmatrix}
\begin{bmatrix}
\zeta_1 \\
\zeta_2 \\
\zeta_3 \\
\zeta_4
\end{bmatrix} = X_0 \zeta
\]

The linear coefficients \( \zeta \) can be calculated by inverting this relation \( \zeta = X_0^{-1} x \). \( X_0^{-1} \) can be written as a matrix of linear functions of \( x \). The partial derivative of \( x \) over \( \zeta \) and the partial derivative of \( \zeta \) over \( x \) can also be calculated accordingly.

The displacement of any point can be interpreted with the displacements of tetrahedron’s four nodes using the same transformation coefficients \( \zeta \).

\[
\begin{bmatrix}
u_x \\
u_y \\
u_z
\end{bmatrix} =
\begin{bmatrix}
u_{x1} & \quad u_{x2} & \quad u_{x3} & \quad u_{x4} \\
u_{y1} & \quad u_{y2} & \quad u_{y3} & \quad u_{y4} \\
u_{z1} & \quad u_{z2} & \quad u_{z3} & \quad u_{z4}
\end{bmatrix}
\begin{bmatrix}
\zeta_1 \\
\zeta_2 \\
\zeta_3 \\
\zeta_4
\end{bmatrix} = U_0 \zeta
\]

The strain field within the element is strongly connected to the displacement by the strain-displacement equations. A 3D strain tensor has six independent components, and can be arranged into a 6-component strain vector. Based on the definition,
The column of $B$ can must be reshuffled based on the settings of $u$.

Assuming the material is linearly elastic and no initial strains are considered, the constitutive equation may be expressed as
\[
\sigma = E e
\]  
(3.27)

where the elasticity matrix $E$ is symmetric. For an isotropic material of elastic modulus $E$ and Poisson’s ratio $\nu$, the foregoing relation
\[
\begin{bmatrix}
\sigma_{xx} \\
\sigma_{yy} \\
\sigma_{zz} \\
\sigma_{yz} \\
\sigma_{zx} \\
\sigma_{xy}
\end{bmatrix} = \frac{E}{(1+\nu)(1-2\nu)} \begin{bmatrix}
1-\nu & \nu & \nu & 0 & 0 & 0 \\
\nu & 1-\nu & \nu & 0 & 0 & 0 \\
\nu & \nu & 1-\nu & 0 & 0 & 0 \\
0 & 0 & 0 & 1/2 - \nu & 0 & 0 \\
0 & 0 & 0 & 0 & 1/2 - \nu & 0 \\
0 & 0 & 0 & 0 & 0 & 1/2 - \nu
\end{bmatrix} \begin{bmatrix}
e_{xx} \\
e_{yy} \\
e_{zz} \\
2e_{xy} \\
2e_{yz} \\
2e_{zx}
\end{bmatrix}
\]  
(3.28)

Introducing $e = Bu$ and $\sigma = Ee$ into the strain energy functional restricted to the element volume and rendering the resulting algebraic form stationary with respect to the node displacements $u^e$, we get the usual expression for the element stiffness matrix as the following. Assuming that the elastic moduli are constant inside the element, the integration over the volume can be written as the multiplication of the volume
\[
K^e = \int_{V^e} B^T E B dV = Volume B^T E B
\]  
(3.29)
The stress forces can be taken as internal forces, written as

\[ f_{int} = -Ku \]  

(3.30)

The dynamics of the physics based deformable models can be implemented by putting the \( f_{int} \) into the equation 3.14.
Chapter 4

Meshless Deformable Models

4.1 Model Registration

The generic model of the LV is built from MR images obtained from a healthy volunteer. The image information is obtained by manual segmentation with validation of experts. The surface mesh was built by a Delaunay triangulation using geodesic distances, to preserve the topology of the object better [90]. This generic mesh provides an anatomically plausible model for the whole tracking procedure.

Figure 4.1: (a) Landmarks on the contour (b) Registered model with landmarks on LV, RV endocardium and epicardium

To register the model with the image data, we use a set of landmarks, 50 landmarks per slice and 350 landmarks in total, on the contours defined by different curvatures [91]. The high curvature points on the septum in the right ventricle are detected. Two points on the left ventricle contour and two points on the periphery closest to these two highest curvature points on the right ventricle contour are located. The other feature points are marked with even intervals on the contours. We slice the model to get the same plane as the image plane location. Landmarks are detected with the same method on the contour of each slice.
The boundary mesh is fit onto the patient’s TMRI at two steps. First, we assume the object is doing the similarity transformation, calculating the translation, rotation and uniform scaling. After the object is globally aligned, we locally deform the model to fit the patient heart shape in TMRI. The translation of the object is the difference between the centers of two objects. Denote the generic model boundary landmarks as \( p_i \) and the TMRI contour landmarks as \( q_i \). Translation is

\[
T = \overline{q_i} - \overline{p_i}
\]  

(4.1)

We calculate the rotation of source landmarks and destination landmarks with polar decomposition [92, 93, 94]. Assume all the points are going on the same transformation \( A \). Let \( p_i^0 \) be the coordinates in the model-centered coordinates and \( q_i^0 \) be in the heart-centered coordinates. \( p_i^0 = p_i - \overline{p_i} \), and \( q_i^0 = q_i - \overline{q_i} \). The error is the difference of the image landmarks and the transformation of model landmarks. We minimize the error in equation 4.2 by setting its first derivative to zero, and yield equation 4.3.

\[
E = \sum (A(p_i^0) - q_i^0)^2
\]

(4.2)

\[
A = \left( \sum p_i^0 p_i^0 \right)^{-1} \left( \sum p_i^0 q_i^0 \right) = A_{pp} A_{pq}
\]

(4.3)

The first part of the transformation matrix \( A \) is a symmetric matrix, which is the sum of the vector \( p \) times \( p' \). It only has the information of scaling, and no information of rotation. The rotation matrix can be isolated from the second part of the transformation matrix \( A \). Intuitively, the polar decomposition \( A = RP \) separates \( A \) into a component that stretches the space along a set of orthogonal axes, represented by \( P \), and a rotation \( R \). \( R \) is a unitary rotation matrix and \( P \) is a positive-semidefinite Hermitian matrix. If \( A \) is invertible, then the matrix \( R \) is given by \( R = AP^{-1} \). In terms of the singular value decomposition of \( A_{pq} \), \( A_{pq} = W \Sigma V' \), we have

\[
P = V \Sigma V'
\]

(4.4)

\[
R = W V'
\]
The matrix $P$ is always unique,

$$
P = \sqrt{A' A} = \sqrt{(V \Sigma W')(W \Sigma V')} = \sqrt{V (\Sigma) V'}^T \tag{4.5}
$$

$V$ and $W$ are unitary rotation matrix. $V$ and $\Sigma$ can be deprived with Eigen decomposition of $A'_{pq} A_{pq}$. $\Sigma$ is a diagonal matrix with eigen values’ square root on the diagonal. $\Sigma$ encode the stretch along each orthogonal axis.

$$
P^{-1} = V (1/\Sigma) V' \tag{4.6}
$$

The rotation matrix of two sets of points can be calculated by substituting equation 4.6 into $R = A_{pq} P^{-1}$.

After getting translation and rotation, scaling can be easily deduced by comparing the average distance of landmarks and object center. Local fitting is done by Laplacian Surface Editing and Optimization [77, 95]. We introduced Meshless Volume Editing with the insight provided by Laplacian surface editing[77] and Local Scale-Invariant Features (SIFT) [79].

### 4.2 Model Deformation

The task of model deformation is to calculate the deformation of the rest free points given a set of control points with known motion. Meshless deformable models describe an object as point clouds in model centered coordinates inside of the object boundary. It does not take each single particle as a unit when computing the dynamics of the particle clouds and the interaction of points. As shown as the right model in Figure 4.4, a particle and its neighboring particles are grouped into a sphere shaped kernel. The local geometry can be represented as volumetric Laplacian coordinates. Denote the points in the sphere shaped kernel as neighborhood of point $p_i$, $N_i = v_j | \| v_j - v_i \| < h$ and the degree $d_i$ of the vertex is the number of elements in $N_i$. The local volumetric geometry can be described as a set of differentials $\Delta = \delta_i$. The Laplacian coordinate $i$ will be represented by the difference between point $v_i$ and the weighted average of its neighbors.
\[ \delta_i = v_i - \sum w(i, j) \times v_j \] (4.7)

The weights are distributed in each kernel in parachute shaped functions. The method is not sensitive to kernel parameters. The weights we used in our model is shown in equation 4.8.

Figure 4.2: The left is the mesh-based deformable model. The right is the meshless deformable model. They are both in prolate spheroidal coordinates and the global deformations are both controlled by parameterized functions. In stead of mesh elements, points are grouped with radius based kernels in meshless deformable models.

\[
W(r, h) = \begin{cases} 
\frac{1}{h^3} (h^2 - r^2) & \text{if } r < h \\
0 & \text{otherwise}
\end{cases}
\] (4.8)

where \( r \) is the distance to the center particle and \( h \) is the current support radius of the kernel. The kernel weights are normalized by dividing by constant \( \int W(|x - x_0|, h)dx \), the weights of the discrete neighboring particles are \( w(i, j) = W(i, j)/\sum W(i, j) \). The neighborhood of a particle is found by octrees. As the meshless deformable models are initialized with uniformly distributed point clouds, the space inside of the bounding box of the object is divided into equally spaced cubes. Neighbors are searched inside the same cube of the particle and neighboring cubes. The neighborhood of a particle is computed and stored in a hash table to speed up the motion reconstruction [96]. During the motion estimation, the stiffness of the materials can be adjusted by varying the kernel size.

Let \( A \) be the adjacency matrix for neighboring points and \( W = \text{diag}(w_{11}, ..., w_{kk}) \) be the
weight matrix in a kernel. $\Delta = LV$, where $L = I - WA$. The matrix $L$ is commonly considered as the Laplacian operator of a kernel with connectivity $A$. Laplacian coordinates are invariant under translation, but sensitive to linear transforms. $L$ has rank $k - 1$, which means the motion of points can be recovered from $\Delta$ by fixing one vertex and solve a linear system.

Since the relative location of local points is encoded in Laplacian coordinates $\Delta$, Meshless deformable models set the control points at the desired location and solve the remaining points by keeping the Laplacian coordinates to the minimum change. We put the least square errors of the control points and the lease square errors of the Laplacian coordinates together in the error term 4.9. The second term only constraint cue points. It indicates that the algorithm stops when the cue points match the target locations.

$$E(V') = \sum_{i=1}^{n} ||\delta_i - L(V'_i)||^2 + \sum_{i=1}^{m} ||v'_i - v_{\text{target}}||^2 \quad (4.9)$$

The main idea of meshless deformable models is to assume that each particle in a kernel is going on the same similarity transformation. This assumption can keep the object with least deformation while fitting the control points, so that avoids artifacts in the deformation. The similarity transformation matrix has seven degrees of freedom. To solve the equation and get the translation and rotation parameters, each kernel should have at least 7 points. Colinearity and coplanarity will reduce the useful information in the transformation computation. If there is Colinearity or coplanarity in the neighbors, we need more points for solving the equation. The equation is guaranteed to be solvable with enough number of points because the density of point cloud is adjustable.

Similarity transformation $T_i$ on each point and can be written as a linear function of $x$. The idea to minimize the first term in equation 4.9 is similar to the Expectation Minimization (EM) algorithm in machine learning, and the dynamics in the deformable models. One step is to calculate the parameters based on current states. The other step is to update the states with new parameters. The first term of the equation guarantees the minimum local deformation and
density smoothness in the model. The second term of the equation can be used as a stopping criteria. We iterate two steps for minimizing the first term in loops:

- **Step 1.** Assume we know the transformed location of each point and points in each kernel are doing the same transformation, calculate the similarity transformation matrix \( T_i \) for each kernel. The initial locations in all iterations are the initial locations of all points before the transformation. The transformed locations are current points after setting the control points at the target location.

- **Step 2.** Calculate the new location of each point with the transformation matrix \( T_i \).

Deformation at each step may not be large enough to deform the control points to the desired locations while keeping the density smoothness of volume. This goal can be achieved with multiple iterations.

\( T_i \) can be solved by minimizing the quadratic error function 4.10.

\[
E(V') = \min_{T_i} \left( \|T_i v_i - v'_i\|^2 + \sum_{j \in N_i} w_j \|T_i v_j - v'_j\|^2 \right) \tag{4.10}
\]

where \( v_i \)s are the initial locations of the points in the neighborhood, and \( v'_i \) are current points with the cue points set at the target locations.

The similarity transformation matrix has 1 degree of freedom for uniform scaling, 3 degrees of freedom for rotation, and 3 degrees of freedom for translation. The translation can be isolated by comparing the centers of two point sets. The rest transformation should be a linear function of isotropic scales and rotations. The class of matrices representing isotropic scales and rotation can be written as \( T = s \exp(H) \), where \( H \) is a skew-symmetric matrix. In 3D, skew-symmetric matrices emulate a cross product with a vector, i.e. \( Hx = h \times x \). Drawing upon several other properties of \( 3 \times 3 \) skew matrices (see Appendix A), one can derive the following representation of the exponential above:

\[
s \cdot \exp(H) = s(\alpha I + \beta H + \gamma h^T h) \tag{4.11}
\]
In 2D the matrices of class \( \text{sexp}(H) \) can be completely characterized with the linear expression. In 3D, there is a quadratic term. As a linear approximation of the class of constrained transformations, we use the first accuracy part of Equation 4.11 without the quadratic term. The linear approximation of the transformed vector reaches the tangent line of the rotation arc. Therefore only when the rotation angle \( \theta \) is very small, the approximation is close to the ground truth.

\[
T_i = \begin{pmatrix}
  s_i & -h_3 & h_2 & t_x \\
  h_3 & s_i & h_1 & t_y \\
  -h_2 & h_1 & s_i & t_z \\
  0 & 0 & 0 & 1
\end{pmatrix}
\]

(4.12)

Vector \((s_i, h_i^T, t_i^T)^T\) are unknown variables in \(T_i\). We want to solve the transformation equation and get these unknown variables.

\[
T_i V_i = s V_i + \beta H V_i + t_i \\
= s V_i + h_1 \times V_i + t_i \\
= s V_i - V_i \times h_1 + I t_i
\]

(4.13)

The first term for each point in equation (4.9) can be rewritten as \( ||A_i(s_i, h_i^T, t_i^T)^T - b_i||^2 \).
where

$$A_i = \begin{pmatrix}
    x_{k1} & 0 & x_{k3} & -x_{k2} & 1 & 0 & 0 \\
    x_{k2} & -x_{k3} & 0 & x_{k1} & 0 & 1 & 0 \\
    x_{k3} & x_{k2} & -x_{k1} & 0 & 0 & 0 & 1 \\
    \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots
\end{pmatrix},$$

$$b_i = \begin{pmatrix}
    x'_{k1} \\
    x'_{k2} \\
    x'_{k3} \\
    \vdots
\end{pmatrix},$$

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

(4.14)

Similar with finite element method, the deformation of each point is calculated iteratively.

Because in each iteration, the similarity transformation of a point is assumed to be very small.

We minimize the error $$||A_i((s_i, h_i^T, t_i^T)T - b_i)||^2$$ with the following algorithm.

**Algorithm:** Given a set of model points and a set of cue points. Active points = Model points + Cue points. Initialize the radius based kernels of all points with octrees and a hash table. We deform model points at each iteration and reset the cue points fixing at the target locations. Loop until the cue points converge to the target locations:

1. Reset the cue points to their target locations.
2. Calculate the deformation of each active point by assuming its neighboring points are going on the same rigid transformation.
   (a) Calculate the parameters in the transformation matrix by solving $$(s_i, h_i^T, t_i^T)$$ from $A_i((s_i, h_i^T, t_i^T)T = b_i$;
   (b) Update the location of each point $x_i = T_i x'_i$.

Figure 4.3: Model deformation algorithm

The volumetric point clouds deform with the external forces on the cue points iteratively. The initialization of the radius based kernels takes some time. After initialization, a model with seven thousand points will deform to its target shape in a few seconds.

Meshless deformable models has the advantage of the FEM, that the forces on one small local area can be propagated to the other areas. They do not need as many control points as in the spline model. In the cardiac deformation project, due to the through-plane motion we
only use the in-wall intersections as the control points. The spline model results tend to have artifacts near the left ventricle boundary and at the base area which has less image information. Meshless deformable models do not have this problem because they keep the minimum change at the area lack of image information while preserve the local geometric smoothness of the object.

Compare to the FEM, meshless deformable models do not have the element degeneration problem when the deformation is large compared to the element size. Dense points can be sampled inside the object boundary, so that displacements or strain can be calculated accurately in the fine level. The dense models are still very stable with large deformation.

4.3 Strain Computation

The strain represents the response of the myocardial tissue to the combination of external and internal forces it experiences, and is independent of the average local displacement. Strain is the fractional change in length of a material element within the wall. It is a higher order quantity (a tensor) than more familiar vector quantities such as the local displacement, and it depends on the orientation of the element being considered.

In deformable model dynamics, the internal forces in the meshless deformable model is to keep the shape deformation with least artifacts. It can be calculated as the gradient of the strain energy [74, 76]. The strain can be used for calculating the stress of myocardium with assumed material properties[67]. The strain analysis can also help doctors for early diagnosis of heart dysfunction. With the displacements calculated with parameterized functions, we calculate the displacement gradients with moving least squares (MLS) [97]) method. As in Figure 4.4, 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 equation 4.15. As an unknown variable with a uniform value in each kernel, the gradient can be calculated by minimizing the weighted error between
the observed displacements and the displacements estimated.

\[ e = \sum_j (\tilde{u}_j - u_j)^2 w_{ij}, \text{ where } \tilde{u}_j = u_i + x^T_{ij} \nabla u_i \]  

(4.15)

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

\[ \nabla u_x|_i = A^{(-1)} \sum_j (u_x(j) - u_x(i)) x_{ij} w_{ij}, \]

where \( A = \sum_j x_{ij} x^T_{ij} w_{ij} \)  

(4.16)

In finite element methods, element quality degeneration will cause the singularity problem in dynamic equations. In meshless volume models, points are grouped in spheroid kernels, which has the smallest possibility to be co-planar compared to elements in tetrahedron or cube shapes.

Given the initial position of a point \( x_0 = (x, y, z) \) in a world coordinate and the displacement \( u(t) = (u_x, u_y, u_z) \) at time \( t \), the current position of the point in the deformed model is \( x(t) = x_0 + u(t) \). The Jacobian of this mapping is

\[ J = I + \nabla u^T = \begin{bmatrix} 1 + u_{x,x} & u_{x,y} & u_{x,z} \\ u_{y,x} & 1 + u_{y,y} & u_{y,z} \\ u_{z,x} & u_{z,y} & 1 + u_{z,z} \end{bmatrix} \]

(4.17)

Given the Jacobian \( J \), the Lagrangian strain tensor \( \varepsilon \) of the point is

\[ \varepsilon = \frac{1}{2} (J^T J - I) = \frac{1}{2} (\nabla u + \nabla u^T + \nabla u \nabla u^T) \]

(4.18)

4.4 Visualization

In this dissertation, the computation of 3D cue points are done with MATLAB, the meshless deformable model is implemented with C++ and visualized with the Visualization Toolkit (VTK). VTK is an open-source, freely available software system for 3D computer graphics, image processing and visualization. VTK consists of a C++ class library and several interpreted interface
layers. VTK supports a wide variety of visualization algorithms including: scalar, vector, tensor, texture, and volumetric methods; and advanced modeling techniques such as: implicit modeling, polygon reduction, mesh smoothing, cutting, contouring, and Delaunay triangulation. VTK is written on the graphics library OPENGL. VTK provides a pipeline that enables users to visualize the model easily. The tagged MR images, meshless deformable model mesh and cue points can be displayed in the same window. The deformation per frame can be updated after calculation and the animation of the model can be generated.

The tagged MR images are scanned and saved as DICOM files. The DICOM information gives the location of the upper left corner of the image, the orientation of the image and the pixel spacing of the image. The 3D coordinates of each point in 2D images can be computed with \( \text{cor}_3 = \text{cor}_2 \times \text{spacing} \times \text{orientation} + \text{origin} \). With VTK, we visualize a plane and map the MR image onto the plane as texture. Points are visualized with spheres. The meshless deformable model can be visualized as its boundary mesh or point clouds.

The user interface is implemented with Qt4. The user can select "Load images" in the menu to load TMRI. If some of images are not required to be viewed in the window, they can be removed from the scene. The removed images can be added back if the user want to see them in some particular frames. The images for display and hidden images can be swapped.

Figure 4.4: The strain of a point is computed by the deformation of its neighboring points with moving least square (MLS) method.
with buttons. The user can select "Load LV mesh" in the menu to load the boundary mesh and click "Generate Model" in the menu to generate a volumetric meshless deformable model. It generates the initial model which fits the LV boundary at the end of diastole. The cue points can be loaded by the item "Load intersections" in the menu. The user can deform the initial model with the cue points by clicking the button "Meshless Deform". After the deformed models in all frames have been computed, the user can drag the slider under the displaying window to view the model in different time of a heart beating cycle. The button "Divide Sectors" and "Compute Strain" can divide the LV into 17 sectors and compute the strain tensor of them.

Figure 4.5: User interface of the cardiac motion tracking system with meshless deformable models.
Chapter 5

Validation on Phantoms

The ground truth of the in-vivo cardiac deformation is very hard to access with medical imaging methods or clinical methods. Tagged MRI is the state of art non-invasive medical imaging method to estimate the cardiac deformation. We validate the meshless deformable models with numeric phantoms and the results on the numeric phantoms as the ground truth.

5.1 2D Phantoms

![Figure 5.1: A grid tagged phantom image contracts in the middle of systole and rotates 2 degrees. The epicardial radius contracts from 36.13mm to 33.00mm. The endocardial radius contracts from 21.78mm to 16.65mm. We deform the phantom with meshless deformable models and calculate the strain with MLS.](image)

The displacement and strain computation of meshless deformable models are validated via a 2D numeric phantom, as shown in Figure 5.1. A 2D meshless deformable model has similar implementation as the 3D meshless deformable model. The epicardial radius in the reference TMRI frame is 36.13mm, and is 34.4mm, 33.0mm, 31.9mm and 31.65mm in the following frames. The endocardial radius in the reference TMRI frame is 21.78mm, and is 19.75mm,
16.65mm, 14.25mm and 13.95mm in the following frames. The phantom is rotated with 1, 2, 3, 4 degrees on the following frames. The radiuses of the phantom are obtained from a healthy heart in-vivo TMRI. We show the two phantoms at the end of diastole and the middle of the systole.

We deform the phantom with meshless deformable models formed of 1368 points and calculate the strain with moving least squares (MLS). The size of the meshless kernel is 8 points. The size of the MLS kernel is 4 points. Table 5.3 shows the mean displacement between consecutive MRI frames and the displacement variance. The outer radius contraction and inner radius contraction is calculated with the reference frame. The other displacements are calculated with the previous frame as reference. The displacements are compared with the ground truth. The median and the variance of errors are also shown in the following table. The 2D strain field is computed based on the displacement field.

Figure 5.2: The ground truth of the phantom strain in Figure 5.1 is shown in the left image. The average radial strain is 0.13. The average shear strain is $-2.5 \times 10^{-4}$. The variance of the radial strain and shear strain are both close to zero. The circumferential strain is decreasing from -0.1 to -0.24. The result of meshless deformable model is shown in the right image. The average radial strain is 0.124, variance is 0.005. The average shear strain is -0.0015, variance is 0.002. The circumferential strain is decreasing from -0.1 to -0.2.

The strain ground truth and the phantom strain results are displayed in Figure 5.2. The average radial strain is 0.13. The average shear strain is $-2.5 \times 10^{-4}$. The variance of the radial strain and shear strain are both close to zero. The circumferential strain is decreasing from -0.1 to -0.24. The result of meshless deformable model is shown in the right image. The
<table>
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<th>3</th>
<th>4</th>
<th>5</th>
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<td>-3.13</td>
<td>-4.23</td>
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<tr>
<td>inner radius contraction</td>
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<td>-5.13</td>
<td>-7.53</td>
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<td>0.1472</td>
<td>0.0814</td>
<td>0.0043</td>
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<tr>
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<td>0.0160</td>
<td>0.0355</td>
<td>0.0373</td>
</tr>
</tbody>
</table>

Figure 5.3: Displacement results in millimeter and errors of a sequence of contracting TMRI phantom. The outer radius contraction and inner radius contraction is calculated with the reference frame. The other displacements are calculated with the previous frame as reference.

average radial strain is 0.124, variance is 0.005. The average shear strain is -0.0015, variance is 0.002. The circumferential strain is decreasing from -0.1 to -0.2. The shear strains have very small magnitudes and hard to get accurate measurements. The errors of shear strains are large compared to their magnitudes.

Figure 5.4: Linear regression plot (left) and Bland-altman plot(right) of circumferential strain between the numerical results and the meshless volume models results. The error between results of meshless models and the numerical phantom has the average value 0.0199. Both strains have the similar patterns that strains in the center have larger magnitudes, shown in Figure 5.4. The error is larger near the center of the phantom. The $R^2$ is 0.695.

We evaluate the estimation of circumferential and radial strains with regression plots and Bland-Altman plots. In Figure 5.2, the circumferential strains have larger magnitudes near endocardium. The regression line fits the data very well. $R^2$ is 0.695. The error is larger near the center of the phantom too. From the Bland-Altman plot we can see the error pattern. The errors increase from epicardium toward the endocardium. The errors between meshless model results and the ground truth have the average value −0.02. The radial strains are around 0.15. The error between meshless deformable model result and ground truth is 0.0011. Some of the
radial strain magnitudes are underestimated because of the neighboring points in the kernel are not selected evenly around the points. Because we use small kernels for less stiff deformable models, the uneven distribution of neighbors causes the inaccuracy. In the real patient MRI data, we use a kernel with more than 20 neighbors in it, the uneven distribution would cause less problem.

### 5.2 Comparison to FEM

We compare the results of FEM [98] and meshless methods. Both phantoms used for the FEM based model and the meshless deformable model have the same parameters. The meshless phantom has denser points. There are points at the same locations where the vertices of the finite element mesh are located. Errors on these FEM points are compared. Results of meshless method have the average error 0.0146, nearly two less order of magnitude of the FEM error 0.9288. Compared to FEM, meshless volume models can model the motion of more material points in a piece of volume by avoiding the flat element problem in FEM and achieve better results on the same places.
Figure 5.6: Comparison of FEM and meshless method. The left column is the initialization and the right column is deformed results.

## 5.3 3D Phantoms

We build a 3D cardiac deformable phantom with methods in Chapter 3 and validate the strain results. The models can be interpreted with parameterized functions with contraction, twisting, bending and tapering parameters. The deformation can be controlled by changing parameters. The reconstruction of the motion can be done by projecting the movement to the parameter space and integrate over the volume. The deformable model phantom is displayed in Figure 5.7. It is generated with two nested half ellipsoids. The outer half ellipsoid spans from -90 degree to 25 degree in latitude, and the inner half ellipsoid spans from -90 degree to 30 degree in latitude. The outer short axis radius is set to 42mm and the inner short axis radius is 28mm. The outer long axis is 64.8mm and the inner long axis is 50mm. The model is synthesized with slight bending and tapping. At the end of systole, in the short axis view it contracts to the outer radius 31.65mm and the inner radius 14mm. In the long axis view it contracts to the outer radius 47mm.
and inner radius 30mm. Rotation, twisting, bending and tapering during the systole have also been simulated in the model contraction, shown in Figure 5.7. The rotation is represented with quaternion to avoid the singularity problem. The twisting angle is proportional to the distance to the center along long axis. The base and the apex rotate along different directions. The left ventricle is bend toward the septum. We tracked the tagging line, extract external forces from tagging line information, deformed the shape with meshless deformable models, and calculate strains with MLS method. The experimental results of the phantom in Figure 5.7 demonstrates that the meshless deformable models can model the cardiac deformation such as contraction, rotation, tapping, bending, twisting and the combination of these motions in high accuracy.

A experiment is run with the same model deforming with different portion of points as control points. The model converges to the target with partial control points to reach the same level of accuracy. Figure 5.8 displays the number of iterations versus the proportion of control points we use for the reconstruction. The blue line shows the average number of iterations taken to achieve the same accuracy threshold in motion reconstruction. It takes about 40 iterations when all tagging line points are used as control points. When we only use 10% of all control points, the model can still converge to the same accuracy level within 160 iterations. This feature enables the model to track deformation when control points are relatively sparse, which is common for tMRI data.

In Figure 5.9, the 3D strain field is computed and projected to three orthogonal directions, circumferential, radial and tangential longitudinal. Circumferential strain and longitudinal strain are negative. Radial strain is positive due to the wall thickening. The magnitudes of circumferential strains are increasing through the myocardium toward the inside wall. Longitudinal strains are more uniform. The phantom shows less strain at the area of the apex, which we observe later in the strain results from the clinical medical images. The thickening of the apex wall shown in MRI is probably caused by the collapse of circumferential wall near apex.
Figure 5.7: Deformation on part of a deformable phantom (from left to right): initial model, contraction, rotation, twisting, combination of three deformation. Twisting in different directions is showed in different colors.

Figure 5.8: The number of iterations versus the proportion of control points.
Figure 5.9: The strain field of the meshless deformable model in Figure 5.7. 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. Circumferential strain and longitudinal strain are negative. Radial strain is positive due to the wall thickening. Circumferential strain is increasing through the myocardium toward the inside wall. Longitudinal strains are more uniform and with less magnitude.
Chapter 6

Experimental Results on TMRI

6.1 Reconstruction of Cardiac Motion

To register the model with image data, two sets of landmarks, 50 per slice and 300 in total, on the myocardial contours are detected based on local curvature. The matched point pairs provided long range external forces for the convergence of the meshless deformable model and the image data. The LA and SA were previously registered using rigid registration based on the spatial information in the DICOM header file. In the 3D motion reconstruction procedure, first we segment the heart in SA and LA images using a machine learning based method (Zhen et al. [35]), then the meshless deformable model is simultaneously registered onto SA and LA images.

The automatic tracking of tag intersections was critical in preprocessing since it provided external forces on control points in the meshless deformable model. As introduced in Chen et al. [42, 43], a Gabor filter bank was implemented to generate corresponding phase maps for TMRI images. A Robust Point Matching (RPM) module has been integrated into the approach to avoid false tracking results caused by through-plane motion and irregular tag spacing. Tracked tag intersections are shown in Figure 6.1.

6.2 Displacement Field Analysis

We reconstructed the motion of a normal heart and the overall motion is show in Figure 6.5. The heart motion in a cardiac cycle is complicated. For visualization purpose, 3D motion is
Figure 6.1: RPM tracking results for SA (first row) and LA (second row) tagged MRI. In the left column are original images with the initial locations of tag intersections highlighted using red dots. In the right column are deformed images. Notice that the deformation between two images is large enough that it is impossible to reliably match two tag intersections by their locations alone. RPM maps intersections in consecutive frames based on their distribution patterns.

Figure 6.2: (a)Registered LV on SA images. (b) The intersections of grid tagging lines tracked by gabor filters.
decomposed into three components corresponding to longitudinal, radial and circumferential directions.

To further analyze the motion based on LV anatomy, we divide each LV into 17 parts. In 2D SA and LA TMRI, only the in-plane displacements can be measured. Due to the through-plane motion, the myocardium shown in the same image plane is not formed of the same material points of the left ventricle. In our model, the trajectories of the same material points are tracked and the deformation of the volumetric myocardium is reconstructed. The displacements are projected to three directions, and the average value in each direction is analyzed. We cut off a small part off apex. The rest of the LV are divided as: 6 parts at base, 6 parts at middle ventricle and 4 parts near apex. Inferior junction between LV and RV is identified. Viewed from base, the 6 sectors starts from inferior junction and goes counter-clockwise are inferior septum, anterior septum, anterior, anterior lateral, inferior lateral, inferior. 4 parts near apex are septum, anterior, lateral, inferior. This division makes it convenient to compare displacements and strain along LA, between anterior and inferior, between septum and free wall.

The experiments were carried on 5 normal LVs about 10cm long and with 3cm SA radius. The largest movement of the LV we observed is the shortening along the LA direction. The centroid of the LV moves toward the apex during the systole. In Figure 6.3, we compare the longitudinal displacements of base, middle ventricle and apex. From the displacement magnitudes of different parts we can see that the apex is almost holding still during a heart cycle and the base is dragged to the apex by muscle. At the end of systole, the average longitudinal displacements of base part is 13.85mm and the average longitudinal displacements of the part near apex is 3.12mm. Viewed from LV base, the upper half of the LV rotates clockwise for 1.81 degree and the lower half of the LV rotates counter clockwise for 3.69 degree at the end of systole (Figure 6.4).

The hypertrophic heart has thicker wall. The motion magnitude of the hypertrophic heart is smaller than that of a normal heart. Compared to the healthy LV, hypotrophic LV contracts less
in radial and longitudinal directions, while keeping similar degree of twisting angles (Figure 6.5). The contraction and relaxation of the hypertrophic heart takes longer time in a cardiac cycle as shown in Figure 6.10.

![Figure 6.3: Comparison of average longitudinal displacements between base, middle ventricle and apex. The apex almost keep still. The base moves toward apex.](image)

### 6.3 Strain Analysis

After the displacements are computed, strain tensors are calculated at each point. The deformation gradient is approximated with MLS [97]. Strains are calculated with formula 4.17 and 4.18.

The strain results at the end of systole are shown in Figure 6.9, overlayed with the TMRI slices. Circumferential strain has larger magnitude near the endocardium in a heart beating cycle. We can see the smooth increase of the strain in the first column of Figure 6.9. In Figure 6.8, the middle ventricle circumferential strain is -0.150 at the endocardium compared to -0.115 at the epicardium at the end of systole. Both circumferential strain and longitudinal strain are negative. Longitudinal strain is more uniform in the radial direction. The free wall has larger
Figure 6.4: Viewed from LV base, the upper half of the LV rotates clockwise for 1.81 degree and the lower half of the LV rotates counter clockwise for 3.69 degree at the end of systole. In the beginning of diastole, the LV bounces back quickly from the twisted state to the relaxed state in about 10% cardiac cycle. The untwisting starts and ends earlier than the relaxation in longitudinal and radial direction.

In Figure 6.6 and 6.7, average circumferential strain and longitudinal strain are nearly double at the free wall compared to those at the septum in a heart beating cycle. At the end of systole, the circumferential strain is -0.275 at the free wall and -0.139 at the septum, and the longitudinal strain is -0.257 at the free wall and -0.123 at the septum. This fits the current understanding of myocardium anatomy. Radial strain is positive. Artifacts near the boundary are due to the lack of tagging line intersections in this area. The strains of the in-vivo LV in three directions fit the pattern predicted by the numerical phantom. The meshless model provides enough flexibility for strain local variation.

From the strain time series in the middle anterior calculated from 5 subjects in each group shown in Figure 6.10. The magnitude of the strain in hypertrophic hearts is smaller than that in normal hearts. The average strain magnitude of hypertrophic hearts is about half of the value of healthy hearts at the end of systole. Healthy hearts contract early in a cardiac cycle. The
Figure 6.5: The first row is a healthy heart and the second row is a hypertrophic heart. The first column shows the LV shape at the end of diastole. The rest columns show the LV at the end of systole. The 2-4 columns show radial displacements, circumferential displacements and longitudinal displacements respectively in model centered prolate spheroidal coordinates. The LV contracts in radial and longitudinal directions. The circumferential displacements show that the base half and the apex half rotates in different directions. Myocardium has a torsion along LA axis. Compared to the healthy LV, hypotrophic LV contracts less in radial and longitudinal directions, while keeping similar degree of twisting angles.

end of systole of a hypertrophic heart lags about 0.2 heart beating cycle compared to a normal heart. The motion of a hypertrophic heart is much slower, hence the contraction and relaxation procedure almost last for a whole cardiac cycle.

Tagged MR images were obtained from a Siemens Trio 3T MR scanner with 2D grid tagging. The LA and SA tag MR images were aligned with the spatial information in the dicom header file. The heart wall around the LV is segmented semi-automatically using a machine-learning based approach as in [35]. We detected hundreds of landmarks on the myocardial contours based on local curvature. The landmarks were then matched between image contours and the corresponding slices of the model. The matched point pairs provided long range external forces for the convergence of the meshless deformable model and the image data. The boundary of the registered heart is displayed in Figure 6.2(a).

The automatic tracking of tag intersections provided the external forces for the meshless deformable model. As introduced in Chen et al. [42][43], a Gabor filter bank was implemented to generate corresponding phase maps for TMRI images. A Robust Point Matching (RPM)
module has been integrated into the approach to avoid false tracking results caused by through-plane motion and irregular tag spacing. Tracked tag intersections are shown in Figure 6.2(b).

After getting the deformation of the LV with meshless methods, we compute strain based on the deformation. Some videos on the strain field and deformations are submitted as supplemental materials.

The global deformation of the LV can be described as radial contraction, longitudinal shortening and torsion along the LA. The longitudinal strain in the middle ventricle is negative. Circumferential strains reveal larger contraction near the endocardium than near the epicardium. In the circumferential and longitudinal strain fields, we can observe that a high strain area starts from the apical endocardium and passes quickly toward the base, which can be explained by the activation of myocardium. The radial strain in the middle ventricle is mostly positive. Due to the fact that there is less tag information along the radial direction, the strain obtained along the radial direction is less reliable than the other two directions.
6.4 Pathological Analysis

We divide each LV into 17 parts and compute the average strain of each part. From the strain time series in the middle anterior calculated from 5 subjects in each group shown in Figure 6.10, we observe that a healthy heart contracts early in a cardiac cycle, and holds for a short period of time at the end of systolic before it relaxes. The magnitude of the strain in a hypertrophic heart is smaller than a normal heart. The motion of a hypertrophic heart is much slower, hence the contraction and relaxation procedure almost last for a whole cardiac cycle. The tense stage at the end of systolic is not as clear as a normal heart either.

6.5 Evaluation

In meshless deformable models, we can track the deformation of an arbitrary point inside the myocardium. We tracked the deformation of a tagging plane with our model for a whole cardiac cycle and projected the tagging plane onto the TMRI at the end of systolic. The projections of the deformed tagging plane align very well with the tagging lines in images. We evaluate
Figure 6.8: Comparison of average circumferential displacements between the middle ventricle endocardium and the middle ventricle epicardium.

the difference between the projections and the tagging lines on 156 tag planes, the MAE is 1.383mm (The pixel spacing in TMRI is 1.0938mm). The projections lie in the 95% confidence interval of the semi-automatically tracked tagging line ground truth. This experiment demonstrated that our model can reconstruct the 3D deformation field accurately.
Figure 6.9: Strains at the end of systole are projected to 3 orthogonal directions: tangential circumferential, tangential longitudinal, and tangential radial. Strains on Mid-ventricle SA slice, three-chamber view, and four-chamber view are calculated and overlaid with the TMRI. The global pattern of the strain matches the numerical phantom results in Figure 5.9. Local variation is well caught by meshless model. With our method, not only strains within the TMRI plane can be calculated, strains on an arbitrary oblique plane can be calculated.
Figure 6.10: The strain of the middle anterior of a healthy heart and hypertrophic heart. (a) Circumferential strain (b) Longitudinal strain

Figure 6.11: (a) is a tag plane in the initial state when the LV is at the end of diastolic. (b) is a tag plane at the end of systolic.
Chapter 7

Extension on Cardiac Motion Reconstruction from CT

7.1 Motivation

Early diagnosis of cardiovascular diseases with the aid of medical imaging technologies and early treatment of these diseases can greatly reduce the risk of death. Medical image technology such as Computed Tomography (CT) and tagged Magnetic Resonance Image (TMRI) provide non-invasive ways to view anatomic structure and motion of the atria and ventricles. The multi-detector CT with high rotation speed provides a high resolution view of the ventricle endocardial surface, especially the anatomic structures such as papillary muscles and trabeculae carneae on ventricle endocardial surface. The papillary muscles are attached to the mitral valves (MV) with some tissue and help to keep the mitral valve from being inverted when the blood pressure rises inside the ventricles. The dysfunction of the papillary muscles due to ischemia or infarction can adversely affect cardiac function through the insufficient strain on mitral valves. The deformation of the papillary muscles causes great interest in cardiovascular disease research (Axel 2004 [99]). The time resolution of CT is comparably lower than MRI. The CT data we have has 10 frames in a heart beating cycle, while MRI data has 30 frames. Besides better time resolution, with tagging techniques, MRI can show not only the surface deformation, but also the myocardium motion such as the twisting along the LV long axis. The clinical MRI are a set of slices sparsely located at different parts of the heart and viewed from different angles. With meshless deformable models, the motion of myocardium can be reconstructed from tagged MRI. The deformation of detailed anatomic structure such as papillary
muscles and trabeculae carneae cannot be achieved solely based on MRI. The LV endocardium increases the blood pressure directly and pump the blood to the whole body. Their motion is highly related to the cardiac function. Our goal is to build a dynamic deformable model, which can reconstruct the motion of the LV, especially the endocardial surface, during a heart beating cycle.

A lot of research has been dedicated to heart reconstruction from CT data. Chen et al. 2004([100]) reconstructed the whole heart from high resolution CT data, with the emphasis on the ventricle endocardial surfaces. His experimental results further proved that the papillary muscles are attached on the trabeculae carneae lining of the ventricle wall instead of directly on the solid wall (Axel 2004 [99]). Ionasec et al. 2008 ([101]) built a 4D physiological model, which combines learning-based technologies into a coarse-to-fine approach, to reconstruct the mitral valve motion based on the CT data. Zheng et al. 2008 ([102]) built a four-chamber heart model from the automatic segmentation results of cardiac CT volumes. In their work, 3D CT volumes are segmented with marginal space learning and a mesh is fitted onto the data with corresponding landmarks. Though they reconstructed the whole heart in a full heart beating cycle, their mesh is smooth and does not keep the detailed structure on endocardial surfaces.

We propose a novel dynamic deformable model for LV endocardial motion reconstruction. A CT frame at the end of diastole is chosen as the reference frame since the heart is most static at this moment. The 3D volume is smoothed with median filter. The LV endocardial surface was segmented with isosurface. This mesh is registered onto a meshless deformable model driven by tMRI data with corresponding landmarks. The endocardial surface was deformed with the model in a heart beating cycle and was confined with the rest frames of the CT data.
7.2 Application and Results

The physical location of the heart can be obtained from the Dicom files. Anatomical landmarks such as aorta, ventricular septum cusps, papillary muscles are semi-automatic detected by curvature and manual marking. 300 corresponding points are sampled on those landmarks. These point pairs provide long range external forces for meshless deformable models. The mesh generated from CT data is aligned with the MRI data with these corresponding points as shown in Figure 7.2.

We applied our method to a healthy cardiac dataset. The CT images were acquired on a 320-MSCT scanner (Toshiba Aquilion ONE, Toshiba Medical Systems Corporation). This advanced diagnostic imaging system is the world’s first dynamic volume CT scanner that captures
Figure 7.3: LV deformation results. We cut the septum off the LV. The trabeculae carneae and two papillary muscles, one is larger than the other, can be seen clearly in the image. The 15 frames are in the half heart beating cycle when the systole happens. The sequence starts at the end of diastole. The eight or nine frame shows the LV at the end of diastole. In the other half heart beating cycle the LV deforms less, and we do not show them due to the limited space of the paper.

a whole-heart scan in a single rotation, and achieves an isotropic 0.5mm volumetric resolution with much less motion artifact than the conventional 64-MSCT scanners. The created data had 512 by 512 by 330 pixels, with an effective atrio-ventricular region measuring about $300^3$ pixels. In Figure 7.3, we show the 3D motion of LV surfaces generated from meshless deformable models. From the segmentation results, we can observe that most of trabeculae carneae are distributed on the free wall. Two papillary muscles of the LV are connected to the trabeculae carneae instead of the solid wall. The reconstructed motion of the LV endocardial surfaces are more readily appreciated with such rendering than from the 3D volume. Two papillary muscles contract with the LV myocardium during the systole. At the end of systole, some of the trabeculae carneae clasp on the heart wall. More feature points on the papillary muscles and trabeculae would make the cardiac model contraction more close to the ground truth.
Chapter 8
Discussion and Future Work

We have presented a new meshless deformable model for tracking of the complex 3D motion of myocardium. Our model can track the translation, rotation, scaling, twisting, and local deformation simultaneously. The model avoids time consuming remeshing procedure by simulating the volume with particles.

The model is aligned on the tagged MRI with translation, rotation calculated with polar decomposition, and uniform scaling. The initial model is locally deformed to fit the heart boundary at the end of diastole. Meshless deformable models deform the object by iterating two steps. One step is to calculate the similarity deformation parameters by assuming its neighboring points are doing the same transformation. The other step is to calculate the location of each point with the similarity transformation. The model will deform until the landmarks fitting their locations in the next frame.

The comparison between our results and the ground truth of the numerical phantom demonstrated the robust motion reconstruction performance of the model, even with sparse external forces. The experiments on in vivo TMRI data prove the strength of the model against motion complexity, image artifacts, and noises. The strain analysis based on this model can help for the early diagnosis of cardiac deceases such as hypertrophic cardiomyopathy.
Appendices
.1 Exponential of a $3 \times 3$ skew-symmetric matrix

Let $h \in \mathbb{R}^3$ be a vector and $H \in \mathbb{R}^{3 \times 3}$ be a skew-symmetric matrix, so that $Hx = h \times x$, $x \in \mathbb{R}^3$. We are interested in expressing the exponential of $H$ in terms of the coefficients of $H$, i.e. the elements of $h$. The matrix exponential is computed using the series expression

$$exp(H) = I + \frac{1}{1!}H + \frac{1}{2!}H^2 + \frac{1}{3!}H^3 + ...$$  \hspace{1cm} (1)

The powers of skew-symmetric matrices in three dimensions have particularly simple forms. For the square we find

$$H^2 = \begin{pmatrix}
-h_2^2 - h_3^2 & h_1 h_2 & h_1 h_3 \\
h_1 h_2 & -h_1^2 - h_3^2 & h_2 h_3 \\
h_1 h_3 & h_2 h_3 & -h_1^2 - h_2^2
\end{pmatrix} = hh^T - h^T h I$$  \hspace{1cm} (2)

and using this expression (together with the simple fact that $Hh = 0$) it follows by induction that

$$H^{2n} = (-h^T h)^{n-1} hh^T + (-h^T h)^n I$$  \hspace{1cm} (3)

and

$$H^{2n-1} = (-h^T h)^{n-1} H$$  \hspace{1cm} (4)

for $n \in \mathbb{N}$. Thus, all powers of $H$ can be expressed as linear combination of $I$, $H$, and $hh^T$, and therefore,

$$exp(H) = \alpha I + \beta H + \gamma hh^T$$  \hspace{1cm} (5)

for appropriate factors $\alpha, \beta, \gamma$. 
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