

Abstract

Image Analysis of 3D Cardiac Motion

Using Physical and Geometrical Models

Pengcheng Shi

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A novel approach has been developed to analyze the three-dimensional non-rigid motion and deformation of the left ventricle of the heart from medical images. The hypothesis is that a continuum biomechanical model based, integrated approach which allows information integration of multiple complementary imaging data can more accurately and objectively quantify the motion and deformation of the left ventricle. This approach also provides a natural framework to incorporate physical constraints related to known cardiac parameters.

The left ventricle model is built upon continuum mechanics and is embedded in a finite element framework, represented by a three-dimensional volumetric mesh. The motion field on the myocardial boundaries is determined based on locating and matching differential geometric features of the endocardial and epicardial surfaces. A mathematical optimization strategy is used to combine a locally coherent smoothness model with data-derived information. In addition, magnetic resonance phase contrast images provide robust instantaneous velocity information within the myocardial wall. A finite element framework and the governing equations of the system have been constructed, and the mid-wall velocity and the boundary displacement vectors are used as data-based constraints within the integration process. Displacement and strain measures are derived from the solution of the system.

The algorithms have been implemented and applied to three-dimensional images of normal and infarcted hearts. These algorithm-derived results are statistically compared to implanted marker-derived measures for validation purposes.

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Using Physical and Geometrical Models

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Pengcheng Shi

Dissertation Director: James Scott Duncan

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Chapter 1

Introduction

A computer vision system analyzes an image or sequence of images and produces descriptions of objects that are imaged. Recovery of motion and deformation information from pictorial data is an important part of many vision systems. The goal is to extract quantitatively the temporal changes, rigid or non-rigid, of the objects depicted in the image sequence. Motion recovery in general is a correspondence problem, which involves finding the positions of the object points at successive image frames (the motion of each point), as well as measuring the motion difference among different object points (the deformation of the object) if non-rigid motion is presented in the image sequence. For cardiac motion, which is the focus of this thesis, the heart moves and deforms in three-dimensional space. Hence, the goal of our image analysis system is to depict the non-rigid motion characteristics of the heart from three-dimensional image sequences.

The intensity and texture variations of the image sequence provide initial visual cues of the changes of the object. However, as Horn suggested, a motion field, the displacement vector field of each point of the object in the image, is usually not exactly the same as the optical flow, the apparent motion of the brightness pattern[52]. Furthermore,

it has been demonstrated that the actual correspondence process takes place beyond the level of the raw gray level intensity values[70]. It has been suggested in Ullman's report that, at least in the human visual system, the edges or the boundaries of the objects are the tokens used in the correspondence process[130].

In the analysis of cardiac motion, characteristics of the boundary shape of the left ventricle have been used as the tracking tokens over the temporal sequence. One important recent study that attempts to track cardiac point trajectories using visually extracted shape landmarks is that of Slager[120]. The results of this two-dimensional effort have been carefully validated using implanted markers, with the correlation between the movement of shape landmarks and implanted markers found to be 0.86. At least for cardiac motion, provided that the temporal sampling of the image sequence is not too long in relation to the velocities of the motion, it is not hard to see that the closer and more similar two boundary features are in the successive frames, the more likely they are to correspond to each other. The challenge then becomes how to define this similarity which is both visually and physically meaningful for the matching process. Local shape properties of the boundary provide powerful matching cues, especially for differential geometric landmarks, such as corners. However, the correspondence process involves more than finding purely local minima of the similarity function. A mathematical optimization strategy is needed to combine the similarity information with the effects of various kinds of other local competition to determine the final mapping[3, 114, 116].

With the new progress in magnetic resonance imaging, dense instantaneous velocity maps of the moving heart become available, in addition to traditional anatomical images. In principle, the integration of the velocity map yields the estimated positions of the object points at the next time frame. In practice, however, serious numerical difficul-

ties can arise because of the temporal sampling rate and the noise in the imaging process. Nonetheless, the instantaneous velocity map can help solve the correspondence problem, if not alone, in conjunction with other matching cues.

The integration of multiple image-derived information should only take place in frameworks which account for the strength and weakness of each data source. This could be done either through a statistical model using a maximum a posteriori framework, or through a physical model using the minimum potential energy approach upon which this thesis is based. For the physics-based framework, the constraints should be based on the geometric and physical models of the object and the statistical models of the temporal changes. Continuum mechanical models and finite element analysis provide a reasonable framework to accomplish this task.

1.1 Introduction to the Problem

Motion and deformation analysis is of great interest in many image understanding and computer vision applications including biomedical image analysis, robot vision, and pattern recognition. It plays an especially essential role in computer vision research areas which analyze natural objects, such as facial identification and recognition, articulated motion analysis, satellite weather map analysis, and cardiac function analysis, which is the focus of this thesis.

The measurement of regional myocardial injury due to ischemic heart disease is an important clinical problem. Accurate estimates of heart motion and deformation are essential to evaluate normal and abnormal cardiac physiology and mechanics. It is the goal of many forms of cardiac imaging and image analysis methods to measure the regional function of the left ventricle (LV) in an effort to isolate the location, severity, and

extent of ischemic or infarcted myocardium. The complexity of the LV non-rigid motion and the lack of reference landmarks within the myocardium imply that the true motion trajectories of tissue elements are, at best, difficult to infer from sequential images.

This thesis presents a novel approach of estimating left ventricular motion and deformation by integrating instantaneous velocity information obtained within the mid-wall region with shape-based displacement information found on the boundaries of the left ventricle. The framework is based on continuum mechanical constraints of the myocardium, and is numerically solved using finite element method.

1.2 Overview of the Framework

A complete system using geometric and physical models for recovering motion and deformation of the left ventricle from image sequences has been developed. The approach is composed of three main elements: the geometric representation of the left ventricle, the modeling and motion tracking of the boundary surfaces, and the integration of complementary information using continuum mechanical models and finite element analysis. In Chapter 3, the geometrical representation of the left ventricle is constructed by surface and volumetric Delaunay tessellation. In Chapter 4, the myocardial surface points are characterized by their local differential geometrical properties, computed in a multi-scale fashion based on the multi-order natural neighbor relationship. The boundary matching measure is based on an ideal thin plate model of a local surface patch and a minimum bending energy criterion. Combined with local smoothness constraints, the boundary matching process yields a set of optimal matched displacement vectors, $\mathbf{U}_{boundary}(t_i, t_{i+1})$, between pairs of image frames. In Chapter 5, the need for, and examples of the biomechanical models to help solve the inverse recovery problem are discussed, and a finite element

integration framework is developed. The governing equations of the system are derived, based on the minimum potential energy principle. The boundary displacement information and the mid-wall velocity constraints $\dot{\mathbf{U}}_{midwall}(t_i)$ from phase contrast images are used as the boundary and initial conditions of the framework. Numerical solution to the governing equations gives the motion and deformation descriptions of the left ventricle.

A diagram outlining the system is shown in Figure 1.1.

1.3 Contributions

A novel approach has been developed to analyze three dimensional non-rigid motion and deformation of the left ventricle of the heart from medical images. It is a new physically modeled dynamic system which combines physical information of the left ventricle with multiple, complementary sources of imaging data to depict the temporal motion and deformation information. The algorithms are implemented and applied to real medical images of normal and infarcted canine hearts.

We developed a new, shape-based strategy to track myocardial boundary motion in three dimensions based on matching multi-scale geometric features and a local smoothness model. We have proposed the first volumetric continuum mechanical model-based approach to analyze the temporal dynamics of moving objects from imaging data. And we have constructed the first finite element framework to integrate complementary boundary displacement and mid-wall instantaneous velocity information to recover motion and deformation of the left ventricle.

We have exploited the attractive new research direction of using continuum mechanical models as a means to guide dynamic information analysis from complementary imaging data. The approach provides a natural framework to integrate physical informa-

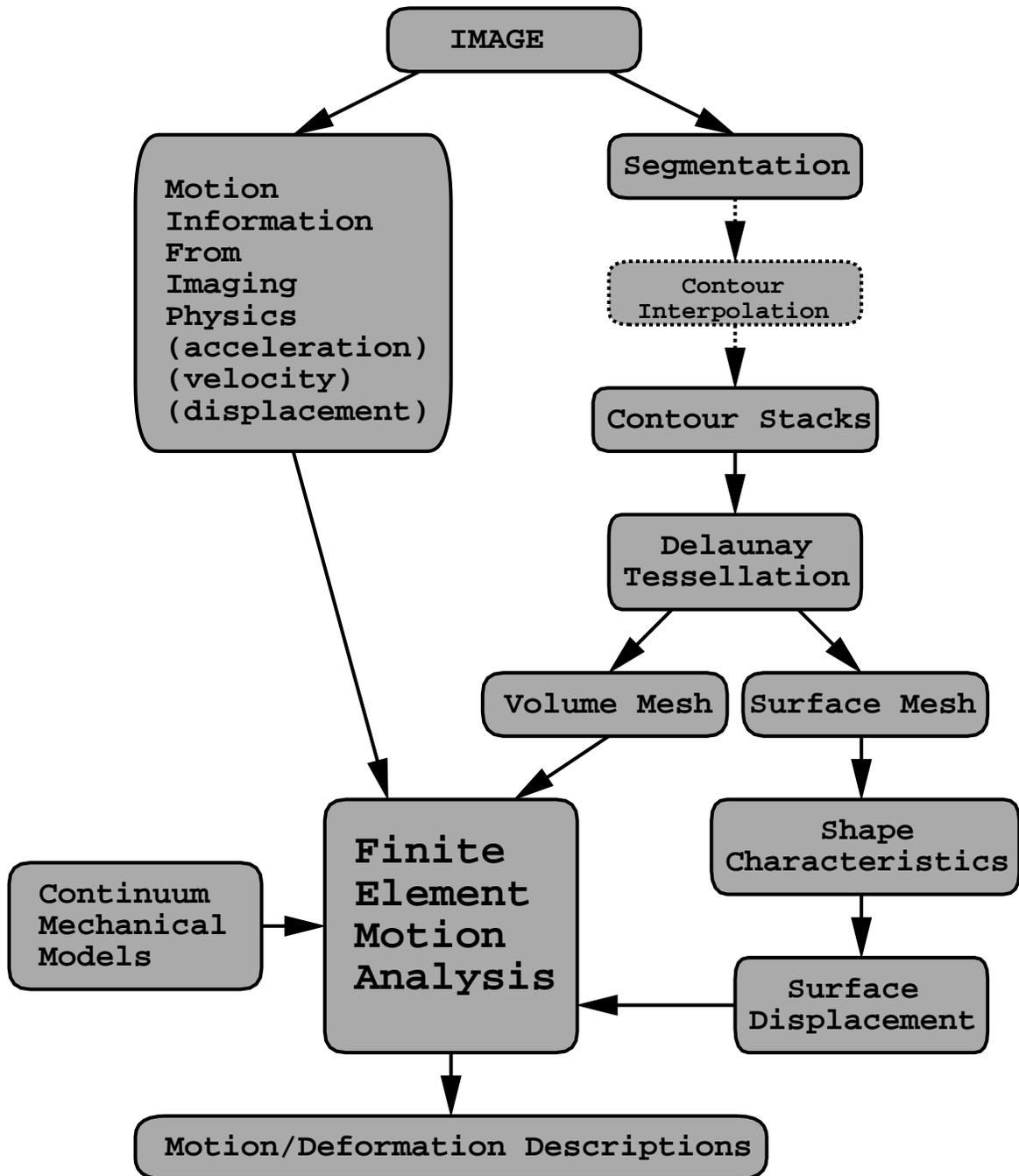


Figure 1.1: Overview of the system.

tion of an object with visual image constraints. This model-based, integrated strategy should allow us to obtain more robust descriptions of motion and deformation of the myocardial wall.

Chapter 2

Background and Related Work

Ischemic heart disease is a major clinical problem. Accurate estimation of heart motion and deformation is essential to evaluate normal and abnormal cardiac physiology and mechanics. It is the fundamental goal of many efforts of cardiac imaging and image analysis to measure the regional function of the left ventricle (LV), through LV wall motion, thickening, and strain measurements, in an effort to isolate the location, severity, and extent of ischemic or infarcted myocardium. It is also felt that image-based serial analysis of regional function is helpful in assessing myocardial salvage to determine the efficacy of therapeutic agents and/or angioplasty (e.g. [22, 43]), and has important implications for understanding the pathophysiology of the remodeling process, especially issues related to the extent of injury.

Motion and deformation analysis is also of great interest in general computer vision research and application. Motion recovery plays an essential role in analyzing the dynamic behavior of natural objects. The goal is to depict the temporal changes of objects from sequential images, and the results are usually represented by dense trajectory fields or correspondence maps. The non-medical applications include robot navigation[34],

facial recognition[15, 32], articulated motion[42, 83], satellite weather map analysis[93], etc.

There have been considerable efforts within the medical image analysis and computer vision communities aimed at trying to find sparse correspondences and then map one object into another at the next time instant, which is an important underlying aspect of many motion measurement approaches. In addition, a significant level of activity has been performed within the magnetic resonance imaging (MRI) community regarding the measurement of LV motion and strain using MR tagging, and to a lesser extent, MR phase velocity measurements. Some very active research in the biomechanics community aimed at deriving local LV deformation information and constitutive relationships experimentally is also invaluable to be incorporated into image analysis based efforts.

2.1 Medical Imaging Based LV Analysis

In the cardiac imaging and image analysis community, there have been a number of approaches aimed at addressing the problem of quantifying LV function using image data, most often related to quantifying parameters related to either myocardial boundary motion or LV thickening from 2D image sequence data, and rarely focused on trying to fully characterize transmural function. Out of plane motion, and twisting or torsional motion are typically ignored. Recently, new progress in imaging physics, such as MR tagging and phase contrast MR, has provided new directions in analyzing the true 3D motion of the LV.

2.1.1 Image Analysis Approaches

In the medical image analysis community, earlier approaches to measuring cardiac motion fall into two different groups. The first group attempts to measure LV function and motion by detecting grey level changes over time for each pixel. Included in this school are techniques which compute phase changes across the temporal dimension[68], find regional ejection fractions between end-systole (ES) and end-diastole (ED) in a set of radial sections extending from the centroid of the ventricle[6], etc. Many efforts have tried to compute the optical flow under different assumptions and conditions, including work by Mailloux[69], Song[122], and Tistarelli[128]. For these work, assumptions about the object and its motion fields are needed to obtain a unique solution. In addition to the fact that optical flow is usually not the same as the motion field of the physical material points[52], it is quite difficult to post-process the optical flow to separate the LV wall from any other motion in the image for diagnostic purposes.

The second type of approach tracks the motion of the pre-extracted boundaries, contours in 2D and surfaces in 3D, of the cardiac wall. The task is to estimate the motion of boundary points between frames and is performed using geometric measures. The algorithms include the chord shortening method by Gelberg[39], which depends on accurately locating a reference point or line, and the centerline method by Bolson[17], which measures the thickness of the region between the ED and ES contours. This latter method essentially treats the measurement of the ED-ES contour difference as a thickness that must be quantified, ignoring the more fundamental goal of motion analysis of tracking the trajectory of each point of the LV wall through the cardiac cycle. One important study by Slager[120] attempts to use contour shape landmarks to track point motion over time from two-dimensional image sequence, and validates the results using

implanted markers. The correlation between the motion of visually extracted shape landmarks and the implanted marker movement is 0.86, which seems to support the concept of tracking identifiable shape cues over time. More recently, several researchers have been pursuing boundary shape matching ideas. Goldgof used Gaussian curvature under a conformal stretching model[63], Amini and Duncan developed a hybrid bending and stretching model[3], McEachen and Duncan used an elastic rod bending model[61, 92], to track LV motion. Another effort of interest is that of Bookstein's[18]. It used morphometrics for measuring shape change to effectively interpolate motion in regions between the landmarks for cases where these corresponding landmarks are already clearly distinguished.

The issue of tracking object points over a multi-frame temporal sequence has often been avoided in cardiac image analysis. Many of the LV motion quantification approaches(e.g.[17, 39, 144]) use only the ED and ES image frames. However, the heart actually goes through a temporal wave of contraction, twisting and expansion, and the asynchrony of LV motion and deformation from time to time, as well as from region to region, may be indicative of the state of health. This asynchrony has been shown to be very important in studying coronary artery disease[40]. Unfortunately, even several attempts that do aim at motion measurement over the entire cardiac cycle, including some early work on characteristics of LV contraction[23, 47] and work using nuclear medicine images[6], are limited by the need to set up a reference system that measures motion as if it were emanating radially from a single point[112].

Many methods[6, 17, 23, 39, 61, 92, 120, 144] have been hampered in making accurate and reliable quantitative regional LV function measurements due to the fact that the heart is a non-rigid moving object that rotates, translates, and deforms in 3D space,

whereas these approaches rely on 2D image sequence data (either projections of a 3D object onto fixed 2D planes, or 2D sections). Motion and thickening measurements from 2D image sequences most likely are not made from the same points on the LV boundaries at different time instants, and hence do not track the true movement of the heart. Work in the general area of 3D quantitative analysis of cardiac motion has been relatively minimal[33, 105, 104]. In addition to the few 3D optical flow based[122] and surface based[3, 63] methods mentioned above, Baker's weaving-wall-surface-building approach uses Laplacian zero crossings as the features upon which motion tracking is based[10]. One difficulty with this method is that a reference path for motion finding must be known beforehand.

The study of volumetric LV motion and deformation has been almost nonexistent, although the progress in imaging physics has made it a more attackable problem[24, 28, 142]. However, volumetric analysis for classification of myocardial infarction into transmural or non-transmural injury is valuable and has interested many investigators for more than 30 years. The transmural extent of myocardial injury has important implications regarding infarct expansion[31], aneurysm formation[45], LV remodeling[101], myocardial denervation[27] and most importantly, patient survival[31]. The *in vivo* characterization of 3D transmural strain from non-invasive image data should be helpful for determining the transmural extent of injury. Measures of strain have been shown to be useful clinically (e.g. [14]) as well as for basic understanding of biomechanical properties of the heart[58].

2.1.2 Imaging Physics Based Approach

2.1.2.1 Magnetic Resonance Tagging

In magnetic resonance tagging, a spatially varying pattern of magnetization is encoded into the myocardium prior to each phase-encoded data acquisition cycle of a spin-echo imaging sequence, forming a grid pattern of image voids generated at each time instant in the cardiac cycle[8, 143]. Motion occurring between the tag pulse sequence and the image pulse sequence results in a distortion of the tag pattern, and their deformation can be tracked over a portion of the cycle, primarily using gated acquisition techniques. Much of the current efforts (such as those of Axel[8] and Zerhouni[143]) on using the grid tagging approach to the measurement of myocardial motion and deformation are focused on how to create dense fields of measurements in 3D by putting together several orthogonal tagging grid acquisitions. The motion and deformation descriptions are then derived from the sparse set of tag-tag or tag-boundary crossings.

The MR tagging based approaches certainly show promise but still have some major limitations. It remains a fundamental issue to track the tags over the complete LV cycle due to decay of the tags with time, which is often remedied by performing a second acquisition (a re-tagging) somewhere later in the cardiac cycle. In general, the same tissue elements are not tagged in each of the two tagging processes, hence the motion trajectory of the tag crossing point in each tagging sequence is not for the same tissue or point. This issue, plus the fact that the grid spacings are often quite far apart (on the order of 7mm spacings and 2-5mm thick tags for the SPAMM tagging[139] and even further apart at the epicardium for the radial Star-burst tagging[143]), means that the interpolated dense displacement fields from two tagging processes may well be incoherent between each other. In addition to the common practice of hand picking tag crossing points, algorithms to

segment the tag lines and detect the tag crossings over time have been mainly based on deformable snake and tag profile models[2, 46, 113, 141] with modest success.

It is still quite difficult to obtain acquisitions and assemble the detected tags for a robust 3D analysis. One can only obtain sparse in-plane motion, the approximated 2D projection of the 3D motion of the material points being imaged, from tagging image sequence[94]. In order to obtain data pertaining to deformation in three dimensions, 2D tag data must be acquired in two orthogonal views, typically short axis and long axis[9]. Once again, the same tissue elements are not tagged in each of the two views, and thus the deformation in each view must be seen as partial 2D data at different points that contributes to an overall scheme aimed at estimating the complete 3D motion and deformation. A variety of approaches have been designed to attack this interpolation/estimation problem, with each approach making certain assumptions. Several of the most interesting ideas are the use of finite element models using spring-like interconnections and nonlinear basis functions by Young and Axel[139], the use of locally deformable superquadrics by Metaxas and Park[95, 94], the use of stochastic models and statistical estimation techniques by Denney and Prince[28], and the use of B-snake grid by Amini[2].

In [139], a finite element grid is fitted to the corresponded SPAMM tag crossing displacements in order to interpolate between the sparse actual data points. The grid itself has a fairly small number of nodes however, and results in a fairly gross interpolation, although the errors computed in the simulations are reasonable. The goal of the work was to compute the mid-ventricular strain present in the LV, and the paper includes a smooth surface visualization of the interpolated strains. This effort is related to our approach in using finite element based framework, although key differences are in the density and formation of the 3D grid (a uniformly dense transmural grid versus sparse endocardial

and epicardial meshes with linear interpolation to fill in transmurally), and the physical models used (a continuum mechanics model versus a spring-like connected mesh). More recently, there has been new work moving toward the use of locally deformable superquadrics[95, 94] as a parameterized model that can be used as the framework for assembling MR tag data. This provides an interesting and possibly robust basis upon which to assemble tag information, and the global motion parameters of interest can be extracted. All of these efforts have typically proceeded using MR tag data in the mid-wall, and extrapolating constraints to the endocardial and epicardial surfaces through the constructed finite element grid, although simple boundary constraints (closest point correspondence) are used in the latter approach[94]. However, due to the sparse $x - y$ grid nature of the SPAMM tags, the only truly reliable, corresponded tag-crossing displacement information will come from the mid-wall tag sites. This means that at any one time instant, point-based LV function measures such as strain will be quite accurate in the mid-LV wall region, but will tend to be noisy and inaccurate near the endocardial and epicardial boundaries, as the grids cross over into the LV blood pool or the pericardial space. We note that the authors claim that useful information is also available from the tag lines, not just the crossings. However, MR tagging itself *does not* provides the correspondences of the non-crossing tag line points, they needed to be computed from image analysis algorithms.

Several other efforts aimed at assembling 3D maps of myocardial deformation use the Star-burst radial MR tagging scheme, which provides accurate displacement information at the vary sparse tag-boundary crossing points, typically sixteen points per slice. In [85], a special MR acquisition sequence is used to obtain 3D tag information one component at a time, again generating a sparse set of corresponded tag points. Then, a high

order polynomial is fitted to the displacement field in order to interpolate between the sparse data points. Alternatively, an estimation theory based idea has been proposed to use a stochastic vector field to assist in the interpolation[28]. This approach uses fairly weak assumptions on the specifics of heart wall motion as compared to some of the other techniques mentioned above, and the Fisher estimate that is used in the approach can help relating estimation accuracy to the number of tag lines needed. On the down side, however, this approach actually increases the errors at the boundaries of the myocardium, according to the phantom studies.

While some of the approaches described above are related to and can be used by our continuum model-based approach, these ideas are geared toward dealing exclusively with different types of MR tagging data, and provide trustworthy results only at mid-wall (SPAMM) or boundary (Star-burst). Also, while there is no doubt that MR tagging potentially provides unique and interesting data regarding LV myocardial movement, there are quite a few processing steps required to assemble the data into meaningful measures of 3D deformation even after the acquisition. Just having the MR tag data available does not alone mean that physiologically and clinically accurate analyses are forthcoming. The proper choice of image analysis and processing algorithms for assembling these data remains a significant open question.

2.1.2.2 Magnetic Resonance Phase Contrast

Another new approach for motion tracking is the use of phase contrast MR imaging. Changes in magnetic resonance phase signal due to motion of tissue within a fixed voxel or volume of interest are used to assist in estimating instantaneous, localized velocities, and ultimately cardiac motion and deformation throughout the cardiac cycle[24, 81, 99, 96, 98, 97].

The magnetic resonance phase contrast velocity technique relies on the fact that a uniform motion of tissue in the presence of a magnetic field gradient produces a change in the MR signal phase that is proportional to its velocity. The velocity in a particular spatial direction can be estimated by measuring the difference in phase shift between two acquisitions with different first gradient moments. Velocity maps encoded for motion in three spatial dimensions may easily be obtained at multiple time instances throughout the cardiac cycle using a phase contrast cine-MR imaging sequence. The acquired velocity maps may then be used to provide information on tissue displacement, strain, strain rate, and other quantitative measures of deformation. In principle, these instantaneous velocities can be derived for each pixel in an image acquisition. However, currently phase contrast velocity estimates near the endocardium and epicardium are extremely noisy because some spatial averaging must occur, and thus pixels outside the myocardial wall (the blood pool for the endocardium and the air or other tissues for the epicardium) are sometimes included for the velocity estimates of the myocardial points. Thus, as with SPAMM MR tagging, the most accurate LV function information is obtainable from the middle of the myocardial wall, and is least accurate near the endocardial and epicardial wall boundaries.

The important first step in using phase velocity maps to estimate quantitative parameters of motion and deformation is to devise methods that can accurately track each segment of myocardium as it deforms through the heart cycle. However, the velocity maps themselves only provide instantaneous motion information. They do not establish the point correspondences between image frames. Assembling the dense field phase velocity information into a complete and accurate 3D myocardial motion and deformation map is a limiting problem to date for this technology. Methods that use direct forward,

backward, or the combination of the two, integration of the velocity to estimate the displacement vector have been proposed[24, 48, 97, 137]. Clusters of pixels within region of interests (ROI) are typically analyzed when predicting pointwise motion, primarily due to signal-to-noise issues. These methods assume various kinds of constant velocity conditions between time frames. These assumptions suffer from the fact that myocardial motion is the result of complex interaction between electrical activation, myocardium active contraction, blood flow pressure, etc, and it is not constant between even small time intervals. Errors resulting from the constant velocity assumptions can be significant if the velocity change rate is big. In addition, small error accumulates as velocity is integrated through the cardiac cycle. More recently, a framework combining a spatially regularizing velocity field with temporal Kalman filtering has been proposed by Meyer to characterize the deforming LV in 2D[75]. The tracking is modeled as an estimation problem which makes it possible to take into account the uncertainties in the velocity measurement.

2.2 Computer Vision Based Motion Analysis

The measurement of motion from image sequences has long been studied by many computer vision researchers. The primary emphasis has been on the determination of optical flow which includes work by Anandan[5], Hildreth[50], Horn[53] and Nagel[79], and the determination of point correspondences between successive frames of rigid objects by Barnard[11] and Glazer[41]. These work cannot, in general, be extended to the measurement of non-rigid motion. Deformable objects, along with their corresponding non-rigid motion, are more general than rigid objects and motion in that more parameters are needed for their description. Non-linear mapping functions are needed to express the

point correspondence between image frames.

Although many of the optical flow based methods are based upon solid theoretical foundations[69, 122], including physical and geometrical models of the object and various coherent constraints on its motion, they are generally not very successful in estimating the true motion field of deformable objects. The primary reason seems to arise from the fact that for discrete image sequences, inter-frame displacements are often larger than one pixel or voxel, which makes the local operation difficult to depict the true motion. Also, non-rigid motion makes it more difficult to enforce the smoothness constraints on the optical flow field which is necessary to deal with the aperture problem.

Quantifying the motion and deformation of non-rigid objects, both with 2D contours and 3D surfaces, has often been seen as a two step process: establishing correspondence between certain sub-sampled points of the boundary at time t and time $t + 1$, then using these correspondences as a guide to solve for a complete mapping (embedding) of the object points between two time frames. There has been considerable effort in general on these two topics, although rarely have they been addressed together. While early approaches used simple global distance measure to find correspondence, more recent matching methods have been mainly based on tracking salient image features over time, from simple tokens such as points or line segments to complex structures. Curvatures of contour or surface are used for non-rigid bending motion[61, 92, 116]. Gaussian curvature is used to estimate point correspondence when the surface is undergoing conformal motion with constant, linear, and polynomial stretching[63, 77], and the two principal curvatures are used under a bending and stretching motion model[3]. An interesting approach by Sclaroff and Pentland establishes correspondence by matching eigenmodes of a finite element representation of the objects[110].

The task of establishing a complete non-linear mapping between object frames has received more attention. In all of these approaches, estimates of correspondence between sparse individual points on objects are either specifically assumed to be known or established based on some global distance measure. Physically-based, finite element models are used by Pentland[54] and Ayache[80] to provide a framework for the mappings, and modal analysis is adopted to reduce computational cost. Other finite element mesh-based approaches have introduced flexible adaptive-size models of Terzopoulos[127] and Goldgof[55]. The work of Bookstein[18] uses deformable thin-plate splines to interpolate dense correspondence from very sparse initial matches. Some other approaches by Metaxas and Terzopoulos have been based on general global parameterized deformable superquadrics that can be locally deformed or modified to fit the non-rigid problem[74, 126], including several using the SPAMM MR tagging data to establish initial correspondence[95, 94].

While the above mentioned various approaches have attacked some aspects (point matching or dense field mapping) of the non-rigid motion problem from different angles, they have mostly concentrated on boundary analysis alone, which is inherently incomplete. Also, there has been no work attempting to merge computer vision based matching strategies with imaging physics based concepts such as MR phase velocity within a unified framework.

2.3 Biomechanical Models and Myocardial Deformation Analysis

There has been very active research in the biomechanics community aimed at deriving quantitative descriptions of regional myocardial function, including the distributions of

stress and strain, the local tissue mechanical properties represented by constitutive relationships, etc. These regional quantities are particularly important in understanding the mechanics of pathological conditions such as myocardial ischemia and hypertrophy, and they are also invaluable for mathematical and computational modeling of the beating heart. For our purposes, we are interested in computationally accessible ideas that focus on the solid mechanics modeling of the myocardium which are suitable to be integrated with our image-derived data. It is our assertion that the use of continuum mechanics models as a means to guide dense field deformation analysis using image information is an attractive new direction for LV motion research.

Myocardial *in vivo* strain has been measured in the beating heart in one, two[7, 131], and three dimensions[132, 72] from biplane cine-radiography of implanted markers and sonomicrometry. Finite strain is obtained at isolated regions of LV wall based on continuum mechanics theory, the finite element method (FEM), and both homogeneous[132] (Waldman) and non-homogeneous[30, 72] (McCulloch) assumptions about the strain. However, the usefulness of these efforts in assessing myocardial strain distributions has been limited, due to the limited displacement information provided by the invasive implanted markers. More recently, tagged MR images have been used to track myocardial motion and deformation by Axel[139], Azhari[9], and Zerhouni[78]. Although the MR tagging based approaches are able to analyze a dense strain field, the sparseness of tag crossing makes it impossible to observe the non-homogeneous nature of the strain distribution, especially transmurally.

Regional stresses still cannot be measured reliably with the currently available techniques[84]. Rather, they must be calculated using the methods of continuum mechanics, which in turn require knowledge of regional mechanical properties. Experi-

ments have conducted to measure myocardial elasticity (Honda[51], McCulloch[90], and Yamada[138]), to develop constitutive relationships between strain and stress (McCulloch[44] and Humphrey[84]), and to evaluate different constitutive models (Creswell[26] and Young[140]). It has been experimentally found that mechanical properties of the heart are qualitatively similar from region to region, but quantitatively different. It has also been proven that nonlinear and anisotropic constitutive relations are required to describe the myocardial mechanical behavior.

There are also several more global approaches which are interesting for cardiac modeling. These include extremely computationally intense efforts of Peskin[100] which aim at complete forward modeling of flow in the left ventricle by simulating the interaction of fluid and the moving boundaries of cardiovascular tissue by solving Navier-Stokes equations, and also the anatomical heart model by Hunter[59] which tries to model the left ventricular geometry and myocardial fiber distribution to study the mechanical and electrical behavior of the heart. While these models provide more detailed descriptions of the heart, the associated computational cost makes them quite impractical for use in LV motion and deformation analysis.

Chapter 3

Geometrical Representation

3.1 Introduction

The purpose of this chapter is to build a geometrical representation of the primary object under study in this dissertation, the left ventricle of the heart, from a set of sampled spatial data points. This representation must be suitable for achieving a number of tasks such as boundary shape characterization, motion correspondence field generation, deformation descriptions, etc. For computational reasons, we would like to have the representation as simple as possible in order to accomplish the tasks at hand. Yet, we also would like the representation to be as rich as future relevant tasks may need, and as accurate as the image data can provide.

Dense field motion and deformation descriptions require that volume be a basic element of the representation. On the other hand, boundary characterization requires surface models to be included in the representation. To be able to deal with image data of different resolutions, e.g. high resolution magnetic resonance images and low resolution echocardiographic images, the representation should be suitable for sparse as well as dense

data. In addition, the representations should be easily upgradeable when new data or new constraints become available. And finally, for a continuum mechanics based framework, the representations must allow the incorporation of physical constraints into the system, and should facilitate efficient computation.

Here, we propose to use a bounded and constrained Delaunay triangulation of the data points as the geometrical representation of the left ventricle. Delaunay tessellation defines a symmetrical and isotropic neighborhood relationship between the data points, and is globally optimal in the sense that the tetrahedra are as *regular* as possible. With the exception of the degenerate case, the Delaunay triangulation is a unique minimal shape representation for a given set of 3D points. The tetrahedra become the natural candidates for the volumetric elements of the finite element analysis framework to incorporate the physical constraints. The neighboring relationship between the boundary surface data points provides the foundation for the recovery of complex shape characteristics of the underlying object. Since the tessellation produces a meaningful mesh with no a priori connectivity information, it can be used for both dense and sparse data sets. In addition, other available information, including acceleration, velocity, displacement and external load, can be plugged into the framework after the governing physical system has been set up.

3.2 Object Segmentation

Since our geometrical representation of the left ventricle is formed from the sampled spatial data points of the object, these sample points (including endocardial boundary, epicardial boundary, and myocardial mid-wall points) need to be detected from the 4D image dataset as a pre-processing step. Due to the fact that it remains difficult to extract

the LV accurately and reproducibly by automated means from most three dimensional image datasets directly, we take the more conservative approach of segmenting the two dimensional LV wall slice by slice, isolating the endocardium and the epicardium, and then reconstruct the volume from the 2D segment stack.

Since segmentation is not the main emphasis of this dissertation, we will only briefly describe the procedures we use to detect the object sample points. Readers are referred to [21, 124] for details.

3.2.1 Boundary Segmentation

The boundary finding problem is solved twice for each 2D image slice of a 3D image frame, once for the endocardial border and another for the epicardial one. Over the years a large number approaches have been developed for image segmentation, including region based methods, boundary based methods, and integrated approaches. Even though many of these methods can often achieve plausible segmentations of myocardial boundaries, including those using energy minimizing deformable snake[64], few are robust to the variations encountered over large datasets. To specifically address robustness, we are currently using an integrated approach which combines gradient based parametrically deformable boundary finding with region based segmentation[21]. This approach uses Green's theorem to derive the boundary of a homogeneous region-classified area in the image, and integrates this with a grey level gradient based boundary finder. It combines the perceptual notion of edge information with grey level homogeneity, and is more robust to noise and poor initialization. Figure 3.1 shows the results using this integrated approach on one of the 2D MR image slices in our test data (courtesy of Dr. Amit Chakraborty).

For either endocardial or epicardial boundary segmentation, a contour is manually

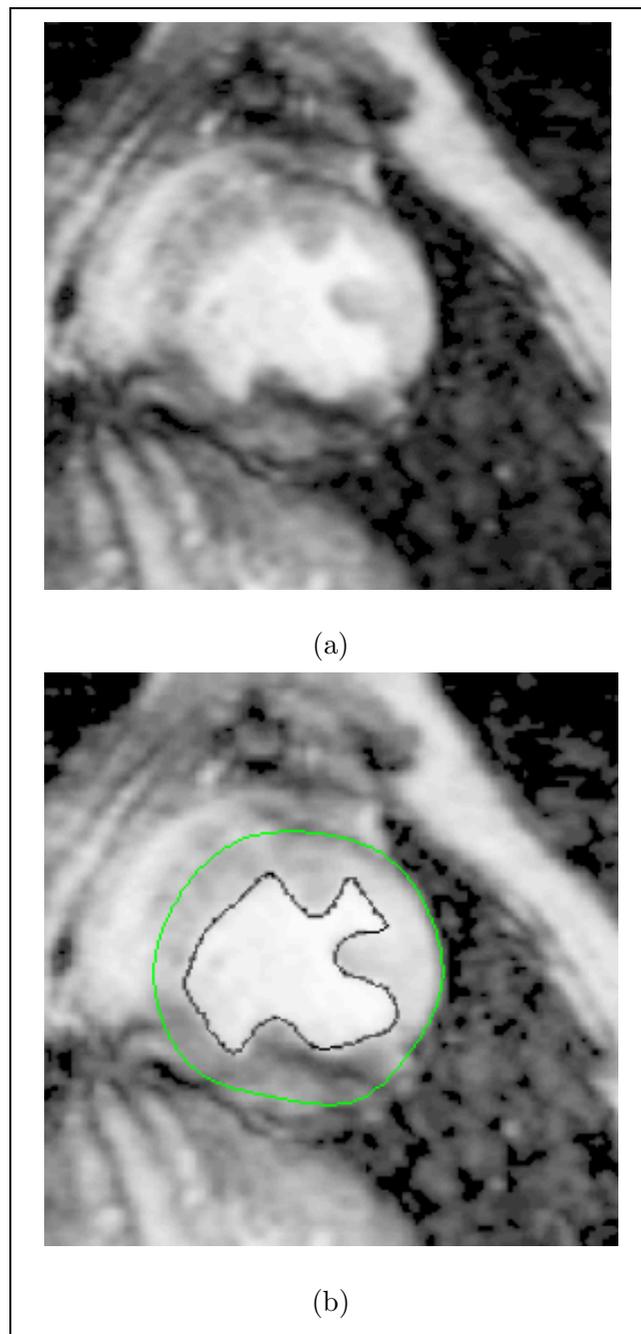


Figure 3.1: LV boundary segmentation of a 2D MR image acquired from a baseline canine study: (a): original MR image; (b): endocardial and epicardial boundaries superimposed on the image.

initialized within a 2D image frame representing the middle-left-ventricle slice of the 3D image, halfway between end-diastole (ED) and end-systole (ES). The above described boundary finding algorithm is run, and the result is used to initialize similar 2D boundary finding problems in image frames spatially and temporally adjacent to the starting frame. The results are propagated and the process is repeated until all of the contours that make up the LV surfaces in all 3D frames of the dataset are detected. During the process, human users re-initialize the algorithm if needed. The segmentation program is written by Dr. Amit Chakraborty of Yale Image Processing and Analysis Group.

3.2.2 Shape-Based Interpolation of Contours

Some of the 3D cardiac image sequence data of interest have higher in-plane resolution than inter-plane resolution because of the imaging protocol. However, it is more desirable to have roughly equally sampled object representations in all three dimensions to achieve more accurate quantitative analysis and display[129]. For this purpose, we need to interpolate between slices. The classical way of doing this is to do some type of interpolation of the gray values of the known slices to estimate the gray values in the *missing* slices, and then further process (i.e. boundary segment for our problem) the extended dataset. This approach, however, could be very expensive as now we need to run the boundary finding algorithm over a far larger dataset. Since we are initially only interested in the boundary points of the object, interpolation methods based on only the LV contour locations would be more computationally efficient. A shape-based contour interpolation method[49], using the chamfer distance transformation[19, 20], has been implemented.

The segmented image contour is converted into a gray-value image, where pixel values represent the shortest distance (within the slice) of points from the contour, with positive values for inside the contour and negative values for outside. After the initial-

14	10	14
10	0	

(a)

	0	10
14	10	14

(b)

Figure 3.2: The two templates used by the dual chamfering processes to calculating the distance maps: template (a) for the top-to-bottom, left-to-right chamfering, and template (b) for the bottom-to-top, right-to-left chamfering.

ization (assign positive numbers to points inside the contour and negative numbers to points outside the contour), the distance map is calculated from two consecutive *chamfering* processes. The first chamfering updates the pixels row by row from top to bottom with a left-to-right ordering within the rows, using the template in Figure 3.2(a). The second chamfering updates the pixels row by row from bottom to top with a right-to-left ordering within the rows, using the template in Figure 3.2(b). The choices of the two 3x3 templates have been justified to be near-optimal[49]. The resulting image represents the chamfer distance map of the given contour. The algorithm was implemented by Lei Zhang of Yale Image Processing and Analysis Group.

After calculating chamfer distance maps for all the endocardial or epicardial con-

tours segmented from the known image data, the estimated distance maps for unknown intermediate slices are computed from the linear or high order combination of the distance maps of the adjacent data contours. The number of these intermediate slices depends on the disparity between in-plane and inter-plane resolutions. The boundary contours of these interpolated slices are found by a border following scheme suggested in [107]. Points with positive distance values are considered inside the contour, and points with negative distance values are considered outside the contour. Figure 3.3 shows one example for MR images where two intermediate contours are estimated from the linear interpolation of the distance maps of two adjacent data contours.

Endocardial and epicardial boundary contour stacks are formed for all the time frames of the cardiac cycle, using both data and interpolated contours. In Figure 3.4, the top two stacks are data endocardial and epicardial contours, while the bottom two include both data and interpolated contours.

3.2.3 Mid-Wall Sample Points

Since we want a volumetric representation of the left ventricle, we need not only boundary sample points, detected from segmentation or interpolated from the shape-based contour interpolation, but also the sample points of the mid-wall region. The mid-wall region of each 2D slice is defined as the region bounded by the endocardial and epicardial contours, and mid-wall sample points are found by using simple region filling algorithms[36]. Then, 2D myocardial sample points (boundary and mid-wall) are stacked to form the 3D sample point set for each time frame.

A pair of example 2D endocardial and epicardial contours is shown in Figure 3.5(a), the 2D myocardial sample points bounded by the contour pair are shown in Figure 3.5(b), and an example of the entire 3D myocardial sample point set, including

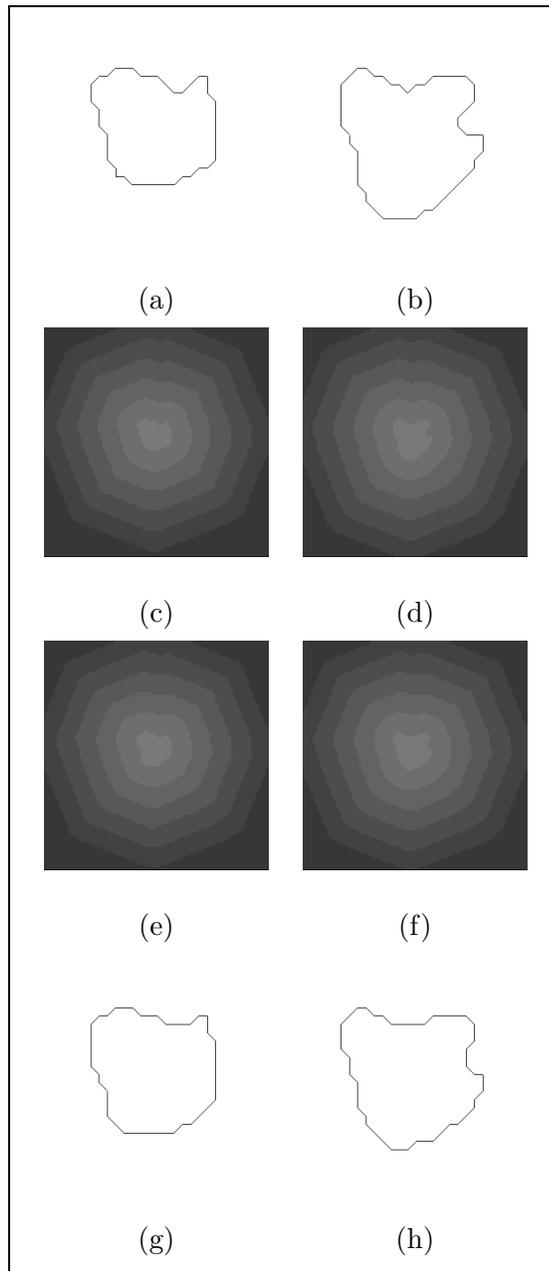


Figure 3.3: Shape based contour interpolation: (a) and (b) are the two original data contours; (c) and (d) are the chamfer distance maps of the data contours; (e) and (f) are the chamfer distance maps linearly interpolated from (c) and (d); (g) and (h) are the two interpolated intermediate contours.

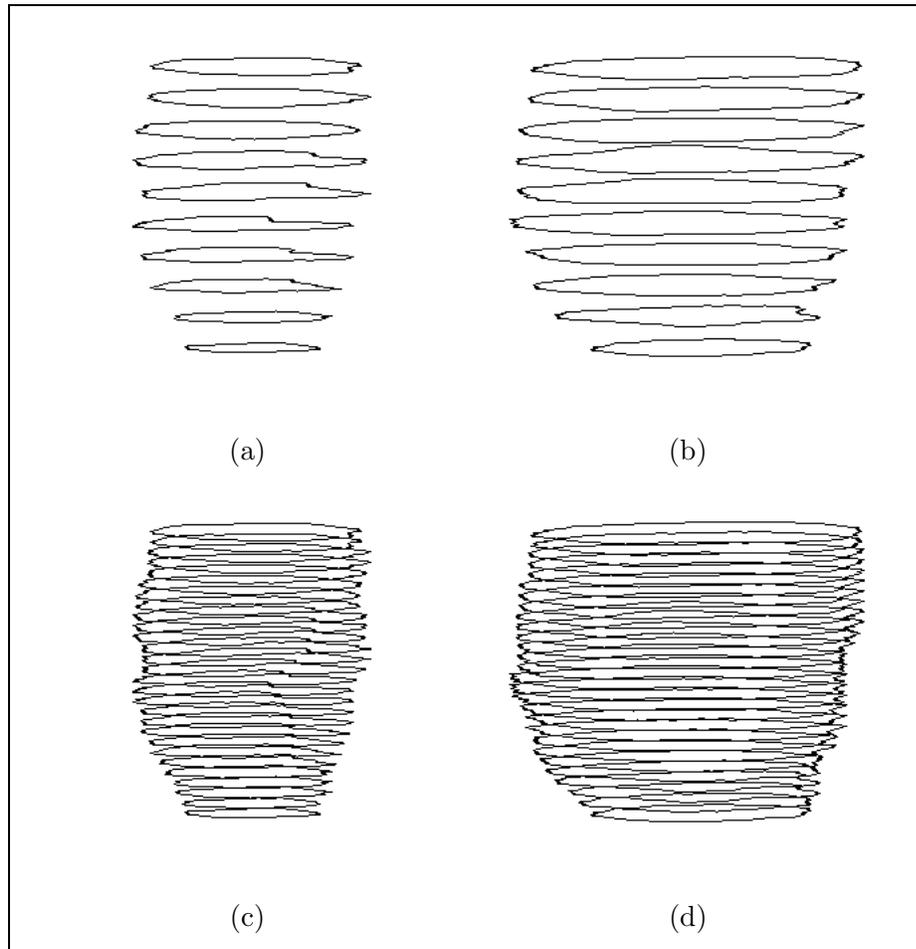


Figure 3.4: Endocardial and epicardial contour stacks: (a) and (b) are the data contours; (c) and (d) are the complete contour sets (include both data and shape-interpolated contours).

endocardial, epicardial, and mid-wall points, is shown in Figure 3.5(c).

3.3 Delaunay Tessellation

Delaunay tessellation is most suitable for volumetric representation of a set of three dimensional sample points without *a priori* connectivity information. The tessellation provides an essential step for spatial analysis of discrete data, and becomes the optimal finite element mesh for our planned continuum mechanical model based analysis of LV dynamics since the tessellation defines a symmetrical and isotropic neighborhood relationship between the data points, and is globally optimal in the sense that the triangles (2D) or tetrahedra (3D) are as regularly shaped as possible. It is generic, that is, it is not limited to any specific classes of objects. And its discrete topology can be used to construct other less detailed representations.

3.3.1 Assumptions and Definitions

Even though we will only deal with two- and three-dimensional datasets, we begin with some general assumptions and definitions associated with Delaunay tessellation and its geometric dual, the Voronoi diagram, that we will use in our later discussion. Further discussion can be found in computational geometry and spatial data analysis literature, including [88, 91, 111].

Definition 1. A **triangle** in \mathbb{R}^d is a d -dimensional simplex (d -simplex), which is defined by its $(d + 1)$ vertices.

Hence, a triangle is a *plane triangle* in \mathbb{R}^2 , and is a tetrahedron in \mathbb{R}^3 .

Definition 2. A **circumsphere** of a triangle in \mathbb{R}^d is a d -dimensional hypersphere such that the $(d + 1)$ vertices of the d -simplex lie on its $(d - 1)$ -dimensional surface. The center

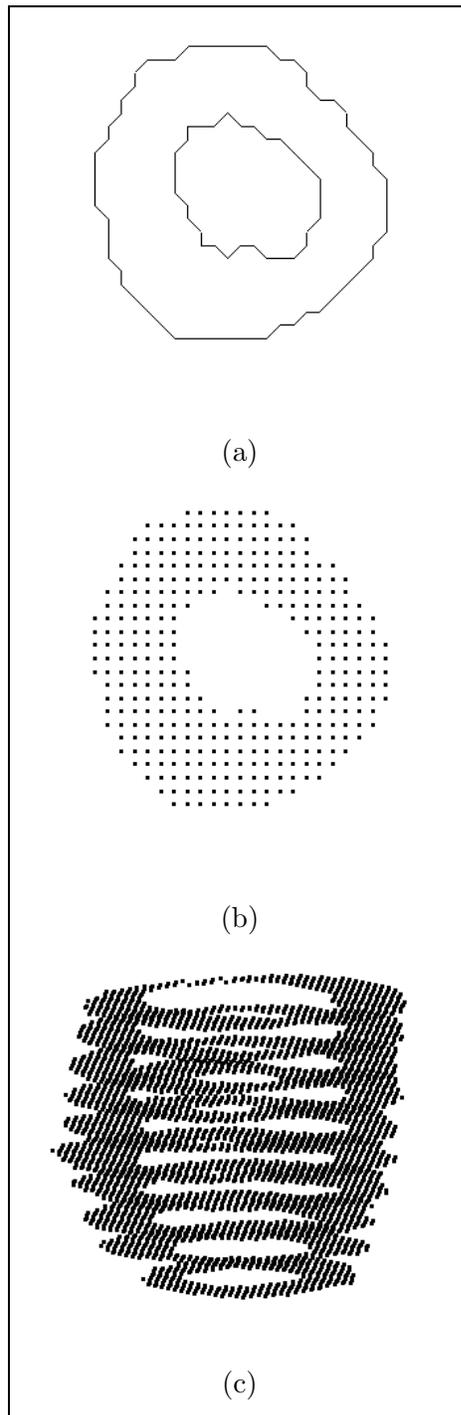


Figure 3.5: Myocardial sample point set. (a): 2D endocardial/epicardial contour pair; (b): 2D filled myocardial region bounded by the contour pair; (c): 3D myocardial sample point set.

of the circumsphere is called the circumcenter, the radius is called the circumradius. The circumsphere and its interior constitute the circumball.

Definition 3. A triangle is a **self-centered triangle** if the circumcenter of the triangle lies inside or on its boundary.

In \mathbb{R}^2 , all nonobtuse triangles are self-centered and vice versa, thus a self-centered triangle is a generalization to \mathbb{R}^d of nonobtuse triangles.

Definition 4. The **min-containment sphere** of a triangle is the smallest sphere containing the triangle.

For a self-centered triangle, the min-containment sphere is the same as the circumsphere. However, for a non-self-centered triangle, it is the circumsphere of one of the facets of the triangle, its center lies on the boundary, and its radius is less than the circumradius.

Definition 5. A **triangulation** of a set of points $\{P_i, i = 0, \dots, N - 1, N > d\}$ in \mathbb{R}^d is a simplicial decomposition of the convex hull of the point set where the vertices of the triangles are contained in the point set.

In \mathbb{R}^2 , a triangulation is an array of plane triangles. While in \mathbb{R}^3 , it becomes an aggregate of space-filling, disjoint, and usually irregular tetrahedra.

Assumption 1. (*non-collinearity assumption*) For a given set of points $\{P_i, i = 0, \dots, N - 1, N > d\}$ in \mathbb{R}^d , P_0, \dots, P_{N-1} are not on the same line.

A simple example to show the necessity of having the non-collinearity assumption is that for three collinear points in \mathbb{R}^2 , one cannot obtain a triangulation of these points.

Assumption 2. (*non-cosphericity assumption*) For a given set of points $\{P_i, i = 0, \dots, N - 1, N > d\}$ in \mathbb{R}^d , there does not exist a (hyper)sphere, C , such that $P_{i_0}, \dots, P_{i_{k-1}} \in \{P_i\}, k \geq (d + 2)$, are on C , and all other points in $\{P_i\}$ are outside C .

Cospherical points will yield a degenerate Voronoi diagram (defined later). In some derivations, a degenerate Voronoi diagram requires special lengthy treatments which are not always essential[88].

If a set of points $\{P_i\}$ satisfies both the non-collinearity assumption and the non-cosphericity assumption, it is in general position in the Delaunay-Voronoi sense. This means that the Delaunay triangulation and Voronoi diagram of the point set will not have degeneracies. From here on in this thesis, we will only deal with point sets which are in general positions in the Delaunay-Voronoi sense.

Definition D. (*empty circumsphere definition*) The **Delaunay triangulation** $\mathcal{D}(P)$ of a set of points $\{P_i, i = 0, \dots, N - 1, N > d\}$ in \mathbb{R}^d is defined to be the triangulation such that the circumsphere of every triangle in the triangulation contains no other point from the set in its circumball. The circumspheres are called the natural neighbor spheres, and the circumcenter of each circumsphere is a vertex in the dual d -dimensional Voronoi diagram.

Formally, the boundary of a d -dimensional Delaunay triangle is made up of $(d-1)$ -dimensional Delaunay faces; the boundary of a $(d-1)$ -dimensional Delaunay face is made up of $(d-2)$ -dimensional Delaunay faces; ...; the boundary of a three-dimensional Delaunay face is made up of *two-dimensional Delaunay faces* or simply *Delaunay faces*; the boundary of a two-dimensional Delaunay face is made up of *one-dimensional Delaunay faces* or *Delaunay edges*; and the boundary of a one-dimensional Delaunay face is made up of *zero-dimensional Delaunay faces* or *Delaunay vertices*, which are the points of $\{P_i\}$.

Obviously, a Delaunay triangulation is always bounded by the convex hull of $\{P_i\}$. A Delaunay edge is always a finite line segment. Figure 3.6(a) shows the 2-dimensional Delaunay triangulation of a set of plane points (filled dots). The Delaunay edges are the

broken lines, and the associated natural neighbor circles are the solid lines. Note that all the Delaunay vertices are on the circumcircles.

A Delaunay triangulation has a geometrical dual – the set of Voronoi polytopes $\{V(P_i)\}$ associated with the point set $\{P_i\}$.

Definition V. For a set of points $\{P_i, i = 0, \dots, N-1, N > d\}$ in \mathbb{R}^d , we called the region given by the intersection of halfspaces defined by perpendicular bi-secting hyperplanes between pairs of P_i

$$V(P_i) = \{x \in \mathbb{R}^d : \|x - P_i\| \leq \|x - P_j\|, i, j = 0, \dots, N-1, j \neq i\}. \quad (3.1)$$

the d -dimensional Voronoi polyhedron associated with P_i , and the set for all the points $\mathcal{V}(P) = \{V(P_0), \dots, V(P_{N-1})\}$ the d -dimensional **Voronoi diagram** of $\{P_i\}$. $\{P_i\}$ is called the generator set of the $\mathcal{V}(P)$.

Similar to notions in Delaunay triangulation, the boundary of a d -dimensional Voronoi polyhedron is made up of $(d-1)$ -dimensional *Voronoi faces*; the boundary of a $(d-1)$ -dimensional Voronoi face is made up of $(d-2)$ -dimensional *Voronoi faces*; ...; the boundary of a three-dimensional Voronoi face is made up of *two-dimensional Voronoi faces* or simply *Voronoi faces*; the boundary of a two-dimensional Voronoi face is made up of *one-dimensional Voronoi faces* or *Voronoi edges*; and the boundary of a one-dimensional Voronoi face is made up of *zero-dimensional Voronoi faces* or *Voronoi vertices*.

However, a Voronoi diagram is always unbounded because the $\mathcal{V}(P)$ on the perimeter are unbounded. Hence, the Voronoi edges could be line segments, half lines or infinite lines. Figure 3.6(b) shows the dual 2-dimensional Voronoi diagram of the Delaunay triangulation in Figure 3.6(a). Here, the Voronoi edges are the broken lines, the Voronoi

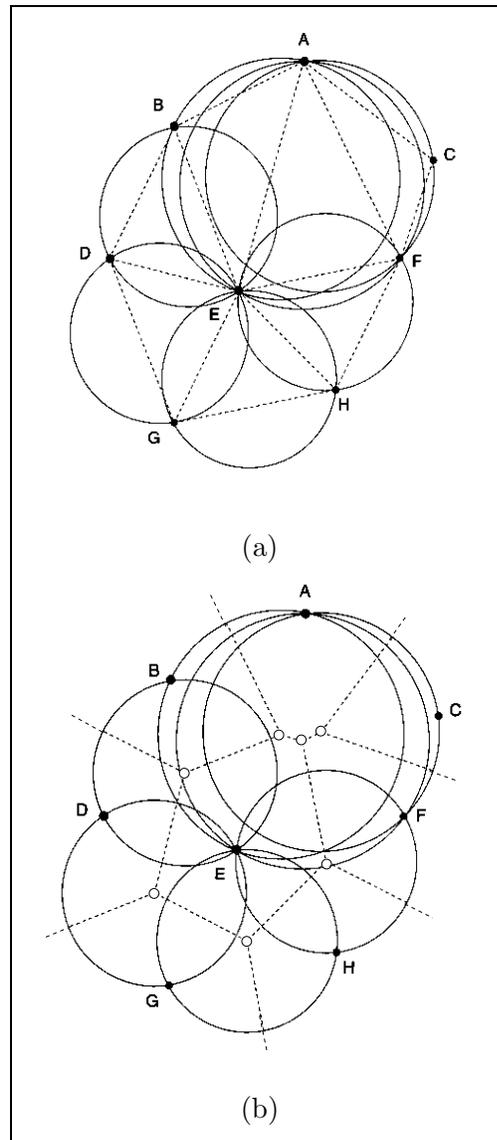


Figure 3.6: Delaunay Tessellation and Voronoi diagram. (a): the 2-dimensional Delaunay triangulation of a set of plane points: the data points/Delaunay vertices (filled dots), the Delaunay edges (broken lines), and the associated natural neighbor circles (solid lines); (b): the dual Voronoi diagram: the Voronoi vertices (unfilled dots), the Voronoi edges (broken lines), and the associated natural neighbor circles (solid lines).

vertices are the unfilled dots, and the associated natural neighbor circles are again the solid lines. Note that the Voronoi vertices are the centers of their corresponding circum-circles.

3.3.2 Properties

One of the reasons to use Delaunay triangulation as the geometrical representation of the object is obtaining a *good* finite element mesh, which for given sample points is often loosely defined as the one whose elements are of, or as close as possible to, uniform size and shape. An element constructed from the Delaunay triangulation, a plane triangle in \mathbb{R}^2 and a tetrahedron in \mathbb{R}^3 , comes with many optimal properties to be generally considered as a good mesh element [88, 91, 103, 111].

Property 1. If a point set $\{P_i\}$ is in *general* position (satisfying both non-collinearity and non-cosphericity assumptions), then its Delaunay triangulation and Voronoi diagram are unique.

This means that a mesh generated from the Delaunay triangulation of a point set is not only a good mesh, but also a unique one.

Property 2. Among all triangulations of a set of points in \mathbb{R}^2 , the Delaunay triangulation lexicographically maximizes the minimal angles, and also lexicographically minimizes the maximal angles.

Property 3. The maximum min-containment radius of the Delaunay triangulation of a point set in \mathbb{R}^d is less than or equal to the maximum min-containment radius of any other triangulation of the point set.

Property 4. The weighted sum of squares of the edge lengths, where the weight is proportional to the sum of volumes of the triangles incident on the edge, is the smallest for Delaunay triangulation.

Property 5. The union of circumballs of triangles incident on an interior point in the Delaunay triangulation of a point set lies inside the union of circumballs of triangles incident on the same point in any other triangulation of the point set. For a point on the convex hull of the point set, this result is true provided only the portion of the union which lies in the interior cone of the convex hull at the point is considered.

Property 2, 3, 4, 5 ensure that the triangles in the Delaunay triangulation are as uniform in size and as regular in shape as possible. In the finite element analysis of a dynamic system discussed later, it is often desired (for accuracy reason) to have regular-shaped elements (or as close to regularly shaped as possible) in order to obtain well behaving field variable functions which are interpolated from the nodal values of the elements. Thus, the Delaunay triangles are good finite element mesh elements.

Property 6. The external boundary Delaunay edges in $\mathcal{D}(P)$ constitute the boundary of the convex hull of $\{P_i\}$.

We will see that for bounded Delaunay triangulation which we will discuss later in the chapter, the external boundary Delaunay edges may or may not constitute the boundary of the convex hull. Hence, strictly speaking, bounded Delaunay triangulation is *not* a Delaunay triangulation.

Property 7. Each Voronoi polyhedron $V(P_i)$ is convex.

Property 8. $V(P_i)$ is unbounded if and only if P_i is on the convex hull of the point set (P_i is a boundary point).

Property 9. In \mathbb{R}^d , if the point set is in general position, and point Q belongs to the point set, then each $(d-2)$ -dimensional Voronoi face of $V(Q)$ is the intersection of exactly $d+1$ $(d-1)$ -dimensional Voronoi faces, among which exactly d $(d-1)$ -dimensional Voronoi faces are on the boundary of $V(Q)$.

In the two-dimensional example, each of the six Voronoi vertices ((2-2)-dimensional Voronoi face) of $V(E)$ in Figure 3.6(b) has three (2+1) Voronoi edges ((2-1)-dimensional Voronoi face), among which two (2) are Voronoi edges ((2-1)-dimensional Voronoi face) of $V(E)$.

3.3.3 Construction

Given an array of data points, $\{P_i\}$, in general positions in \mathbb{R}^d , there exists a unique Delaunay triangulation of these points such that the d -dimensional circumsphere coincident to the vertices of any d -simplex (triangle) in the tessellation has no data point in its interior. A simple yet powerful method of constructing the Delaunay triangulation $\mathcal{D}(P)$, or equivalently its geometrical dual the Voronoi diagram $\mathcal{V}(P)$, is an incremental method first proposed by Watson[88, 134]. We start with a simple existing Delaunay triangulation for $d + 1$ or more points, and modify the triangulation by adding data points one by one. In the worst case, each addition of a point requires time proportional to the number of points in the triangulation so far, and consequently the total time complexity is of $O(n^2)$. However, the average time complexity can be decreased to $O(n)$ by the use of special data structures such as buckets and a quaternary tree[34, 62, 87].

Given an initial aggregate of one or more triangles whose circumspheres are empty, (thus it is a Delaunay triangulation), we may introduce additional data points by observing which circumspheres are intersected by this new point. Each of the old triangles whose circumsphere contains the new data point form a simplicial d -polytope, with all the old data points of this triangle lying on its $(d - 1)$ -dimensional boundary. The new point is interior to the simplicial d -polytope, and forms new d -simplices (triangles) with each of the boundary $(d - 1)$ -simplices. The circumspheres of these new triangles are checked against all the current data points to make sure that only those new triangles

whose circumspheres do not intersect any of the current data points are kept to be parts of the new Delaunay triangulation.

If a new point fails to intersect any of the existing circumspheres of a Delaunay triangulation, then the existing tessellation is not altered. However, new Delaunay d -simplices (triangles) now must be constructed between the new point and the $(d - 1)$ -simplices on the boundary of the old tessellation. And again, the circumspheres of these new triangles are checked against all the current data points to make sure that only those new triangles whose circumspheres do not intersect any of the current data points are kept to be part of the new Delaunay triangulation.

When each new point is introduced in this manner, the aggregate must remain a Delaunay triangulation since all circumspheres remain empty[134]. And the order in which the points are introduced does not affect the final configuration, because this procedure depends only on the number and position of the data points in the data set. Figure 3.7 shows the computational flow of this approach.

A two-dimensional example of the incremental construction of a Delaunay triangulation is shown in Figure 3.8. Initially, a Delaunay triangulation of eight points (A , B , C , D , E , F , G , and H) is given in Figure 3.8(a), where the data points are the filled dots, the Delaunay edges are the broken lines, and the circumcircles are the solid lines. The new data point (point X) is added to the data set, and it is within the circumcircles of ABE , AEF , and ACF . Next, the new circumcircles of XAB , XBE , XAE , XAF , XEF , XAC , and XCF are constructed. The new triangles with empty circumcircles (without data points inside) are kept as the new Delaunay triangles (XAB , XBE , XEF , XCF , and XAC). The updated Delaunay triangulation is shown in Figure 3.8(b).

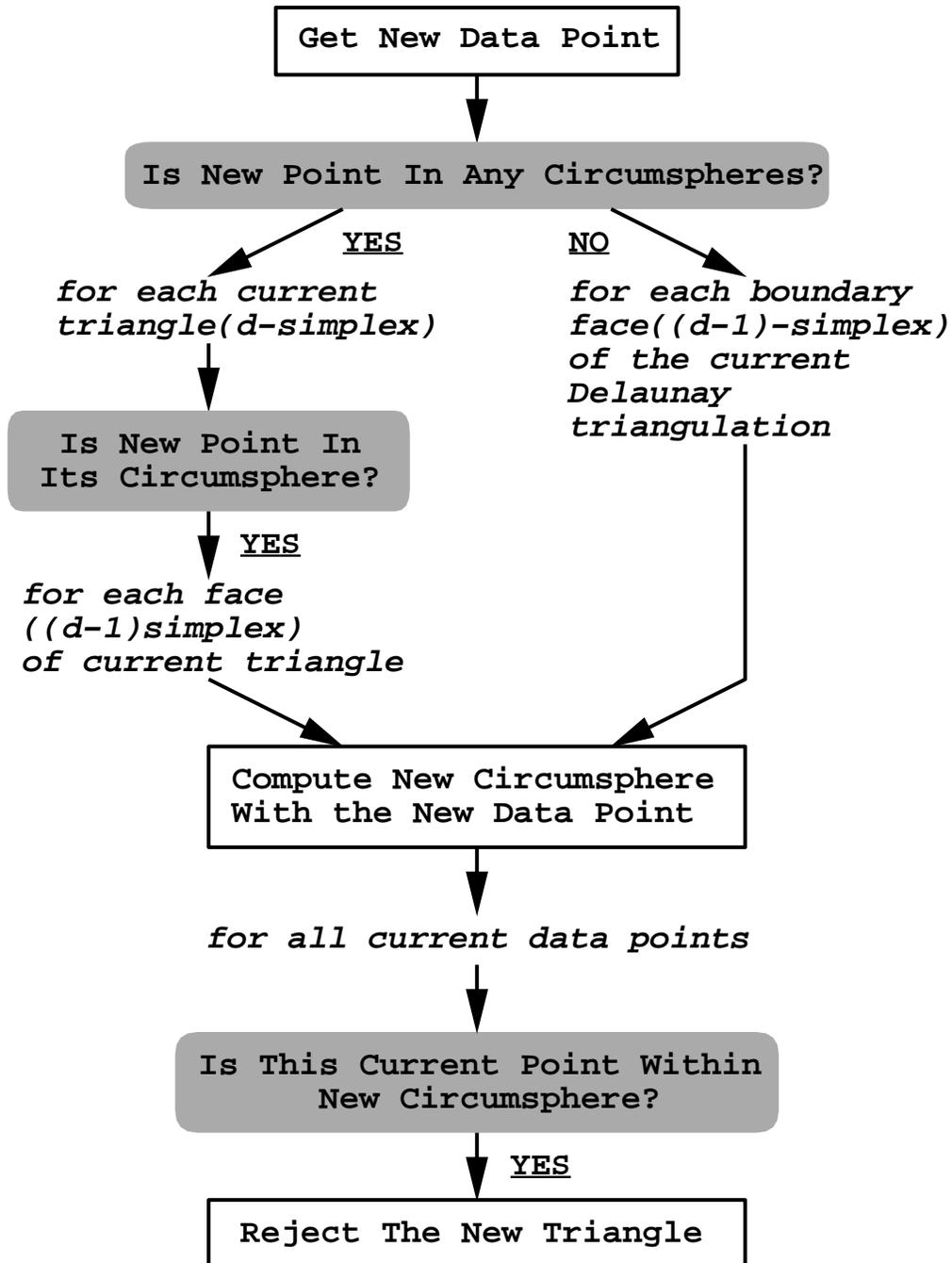


Figure 3.7: Computational flow of incremental insertion of new point into a Delaunay triangulation.

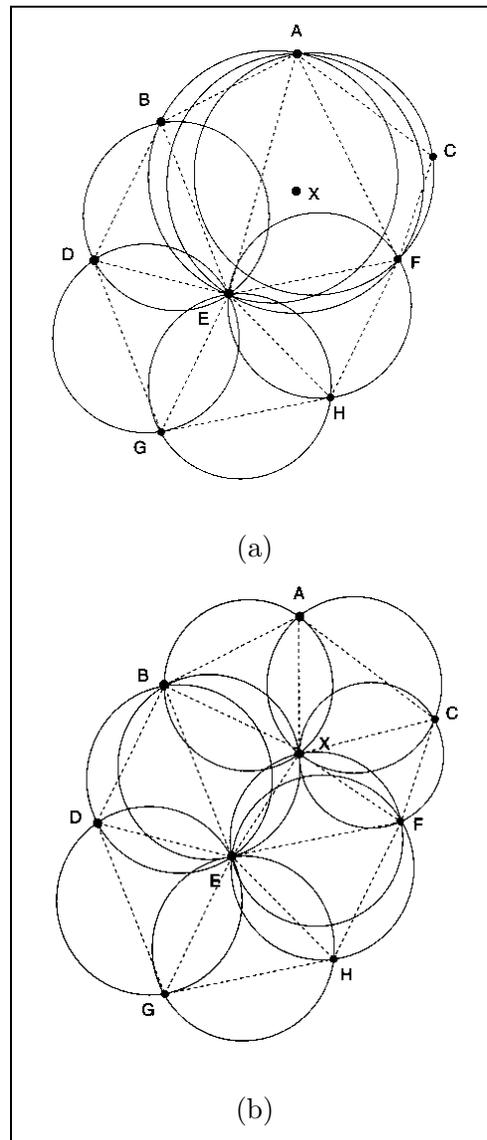


Figure 3.8: Two-dimensional example of Delaunay tessellation using incremental insertion methods. (a): the existing Delaunay triangulation of eight points; (b): the resulting Delaunay triangulation after inserting point X into the point set.

3.3.4 Natural Neighbor Relationship

3.3.4.1 k -order Natural Neighbor Relationship

The natural neighbor circumferences of the Delaunay triangles express a special adjacency relationship among a set of spatial points[136]. For any point Q in point set $\{P_i\}$ in \mathbb{R}^d , the natural neighbor points of Q are those points of $\{P_i\}$ whose Voronoi regions are contiguous to $V(Q)$. Or equivalently, natural neighbor points of Q are those points of $\{P_i\}$ which share the same Delaunay edges with Q . For example, points A, B, E, F, C in Figure 3.8(b) are the natural neighbor points of point X .

Extended from the natural neighbor concept, we define multiple *orders* of natural neighbor relationships of spatial points from the Delaunay triangulation or Voronoi diagram of the point set as following:

Definition MONN (*multi-order natural neighbor*). For point Q of point set $\{P_i, i = 0, \dots, N - 1, N > d\}$ in \mathbb{R}^d , its 0-order natural neighbor point set $\{NN(Q, 0)\}$ only contains point Q itself, its 1-order natural neighbor point set $\{NN(Q, 1)\}$ contains points which share the same Delaunay edges with Q , its 2-order natural neighbor point set $\{NN(Q, 2)\}$ contains points which share the same Delaunay edges with points in $\{NN(Q, 1)\}$ but are not included in $\{NN(Q, 0)\}$, ..., and its **k-order natural neighbor point set** $\{NN(Q, k)\}$ contains points which share the same Delaunay edges with points in $\{NN(Q, k - 1)\}$ but are not included in $\{NN(Q, k - 2)\}$.

For two arbitrary points, the multi-order natural neighbor relationship describes their natural *closeness*. Even though the distance measure performs similar function, the natural neighbor relationship takes into account the geometrical structure between these two points. Along with the natural neighbor coordinate measure, it provides a more accurate description of the relationship between points.

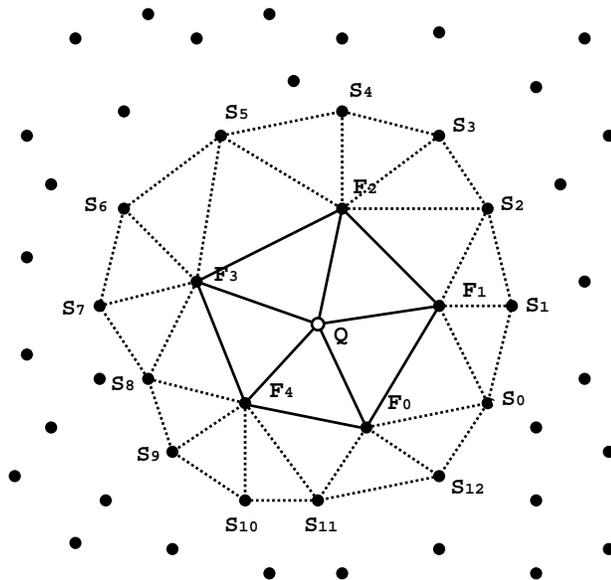


Figure 3.9: Natural neighbor relationships. For point Q , points $F_i, i = 0, \dots, 4$ are its 1-order natural neighbor points, points $S_i, i = 0, \dots, 12$ are its 2-order natural neighbor points.

A two-dimensional example of natural neighbor relationships is shown in Figure 3.9. Here, for data points on the plane (filled and unfilled dots), part of the Delaunay edges are the solid and broken lines. For point Q in the center, points $F_i, i = 0, \dots, 4$ are its 1-order natural neighbor points, and points $S_i, i = 0, \dots, 12$ are its 2-order natural neighbor points.

Property 10. In \mathbb{R}^d , point Q has the same number of 1-order natural neighbor points as the number of $(d - 1)$ -dimensional Voronoi faces of $V(Q)$.

3.3.4.2 Multi-Order Natural Neighbor Smoothing and Interpolation

Many computer vision and image analysis methods rely on smoothing and interpolation algorithms in two and three dimensions. Spatial interpolation and smoothing problems are often posed as estimating the value of a variable at a given location from the known values of the variable at its influence locations, usually nearby points, and it is often in the discrete form of

$$f(x_{new}) = \lambda f(x_{data}) + (1 - \lambda) \left(\sum_{i=0}^{N-1} \omega_i f(x_i) \right), \quad (3.2)$$

$$\sum_{i=0}^{N-1} \omega_i = 1. \quad (3.3)$$

where $f(x_{new})$ is the estimated value at position x , $f(x_{data})$ is its data value, $f(x_i)$ are the values at the influence points $\{x_i\}$, λ is the smoothing factor, and $\{\omega_i\}$ are the weighting coefficients of the influence points. For interpolation problem, λ is always zero so that $f(x_{new})$ is purely interpolated from the $f(x_i)$. For smoothing problem, λ is determined by the confidence towards the data value at x , $f(x_{data})$, with $\lambda = 1$ if it is completely trustworthy and $\lambda = 0$ if it cannot be trusted at all (it is degraded to interpolation problem).

Points in $\{x_i\}$ are traditionally used in the smoothing and interpolation process without considering their geometric connectivity relationship with point x , even though some arbitrary distance thresholds or distance weights are often used to determine the weighting coefficients $\{\omega_i\}$. The natural neighbor relationship between point x and points in $\{x_i\}$ provides a new possibility of choosing proper influence point set for the smoothing and interpolation problems[108, 136]. Furthermore, we make a new definition of multi-order natural neighbor relationship between x and points in $\{x_i\}$ which enables us to

treat the problem in a *multi-order* manner.

Definition MONNSI (*multi-order natural neighbor smoothing/interpolation*). For the **k-order smoothing/interpolation** ($k > 0$) of function f at point x , the influence point set only includes points which belong to the m -order ($m = 1, \dots, k$.) natural neighbor point sets of point x ($\{NN(x, 1)\}, \dots, \{NN(x, k)\}$).

Hence, the influence point set for 1-order smoothing/interpolation of point Q in Figure 3.9 involves points $F_i, i = 0, \dots, 4$, and the influence point set for 2-order smoothing/interpolation of point Q involves $F_i, i = 0, \dots, 4$ and $S_i, i = 0, \dots, 12$. The choice of different orders of smoothing/interpolation could depend on the prior knowledge about functional affinity and desired level of smoothness between the different orders of natural neighbor points, and a multi-order procedure may help to gain more insight into this functional affinity for region classifications.

3.3.4.3 Natural Weighted Smoothing and Interpolation

The choice of weighting coefficients, $\{\omega_i\}$, is a complicated issue, especially for non-uniformly or irregularly distributed spatial points. The traditional approaches include equally weighted coefficients among influence points:

$$\omega_i = \frac{1}{N}, \quad (3.4)$$

and coefficients inversely weighted by distances between influence points and point x :

$$\omega_i = \frac{\frac{1}{\|x-x_i\|}}{\sum_{i=0}^{N-1} \frac{1}{\|x-x_i\|}}. \quad (3.5)$$

Using Equation 3.5, the weights for the 1-order smoothing/interpolation of point Q in the two-dimensional example shown in Figure 3.9 are given by:

$$\omega_i = \frac{\frac{1}{\|Q-F_i\|}}{\sum_{i=0}^4 \frac{1}{\|Q-F_i\|}}. \quad (3.6)$$

Even with influence points chosen by natural neighbor relationship, weights chosen by these traditional methods may not always be proper. Natural neighbor local coordinates (NNLC), similar to barycentric local coordinates, quantitatively express the geometrical position of point x relative to each of its natural neighbor points[117]. For natural neighbor-based smoothing/interpolation, these quantitative coordinates become the natural choices as the weighting coefficient set $\{\omega_i\}$. Below, we will only discuss NNLC with respect to 1-order natural neighbor points, since NNLC involving higher order natural neighbor points requires concepts of higher order Voronoi diagrams (see [88, 117] for further information and proof). Because the natural neighbor local coordinates can properly describe the influence of highly irregularly distributed influence points, they are ideally suited as the weighting for smoothing/interpolation irregularly spaced point set. Since much of the research on natural neighbor coordinates has been on two dimensions[117, 108, 136], we will extend the concepts to d dimensions.

From Properties 7 and 8 of the Delaunay triangulation and Voronoi diagram, we know that for a point set in general position in \mathbb{R}^d , the Voronoi region associated with a non-boundary point Q , $V(Q)$, is a convex and bounded polyhedron. Hence, $V(Q)$ has the same number of $(d-1)$ -dimensional Voronoi faces and $(d-2)$ -dimensional Voronoi faces. While from Property 10, we know that the number of 1-order natural neighbor points of point Q equals the number of $(d-1)$ -dimensional Voronoi faces of $V(Q)$. It is

clear from Property 9 that each $(d - 2)$ -dimensional Voronoi face of $V(Q)$ has only one $(d - 1)$ -dimensional Voronoi face which is not part of the boundary of $V(Q)$.

Suppose point Q has n 1-order natural neighbor points, then the Voronoi polytope $V(Q)$ has n $(d - 1)$ -dimensional Voronoi faces and n $(d - 2)$ -dimensional Voronoi faces. In addition, each of the n $(d - 2)$ -dimensional Voronoi faces has one $(d - 1)$ -dimensional Voronoi face which is not part of the boundary of $V(Q)$. Furthermore, the Voronoi polytope $V(Q)$ can be subdivided into n sub-regions which are constructed by extending each of the non- $V(Q)$ -boundary $(d - 1)$ -dimensional Voronoi face of each $(d - 2)$ -dimensional Voronoi face into $V(Q)$. The results of the intersection of these n $(d - 1)$ -dimensional Voronoi face are n d -dimensional polyhedra, with each polyhedron having one of the n $(d - 1)$ -dimensional Voronoi faces of $V(Q)$ as its $(d - 1)$ -dimensional face. Since each $(d - 1)$ -dimensional Voronoi face of $V(Q)$ is associated with one point $(P_{NN(Q,1)_i})$ of $\{NN(Q, 1)\}$, each of the new generated polyhedron is associated with one of these points. Denote these polyhedra as $Poly(Q, P_{NN(Q,1)_i}), i = 0, \dots, n - 1$, the volume of each polyhedron can be calculated as $Vol(Q, P_{NN(Q,1)_i}), i = 0, \dots, n - 1$. The natural neighbor local coordinates of point Q , $Q(nnlc_0, \dots, nnlc_{n-1})$, with respect to its n 1-order natural neighbor points are now given by

$$nnlc_i = \frac{Vol(Q, P_{NN(Q,1)_i})}{Vol(V(Q))}, i = 0, \dots, n - 1. \quad (3.7)$$

where $Vol(V(Q))$ is the volume of the Voronoi polytope $V(Q)$. $nnlc_i$ is non-negative everywhere, and the sum of all the natural neighbor local coordinates of any point with respect to its 1-order natural neighbor points will always be unity.

A two-dimensional example of the natural neighbor local coordinates is given in Figure 3.10. Here, point X has five 1-order natural neighbor points, A , B , E , F and C , and Voronoi polygon $V(X)$ has five edges and five vertices. Extending each of the non- $V(X)$ -edge of each vertex into $V(X)$, we now have five sub-regions inside $V(X)$, with each associated with one of the five 1-order natural neighbor points. The natural neighbor local coordinate of X with respect to A is the shaded area as a fraction of the area of $V(X)$.

Natural weighted smoothing/interpolation uses the natural neighbor local coordinates as the weights in estimating the weighted average of the functional values at given points from the influence points[108]. The generated function has a continuous derivative everywhere except at the data points[135]. In the cases represented by Equation 3.2, the weighting coefficients $\{\omega_i\}$ of the corresponding influence points are the values of the natural neighbor local coordinates of the given point. For the two-dimensional example in Figure 3.9, we have

$$\omega_i = nnlc_i = \frac{Vol(Q, F_i)}{Vol(V(Q))}, i = 0, \dots, 4. \quad (3.8)$$

3.4 Modified Delaunay Tessellation

From the earlier discussion in the chapter, we know that for a given point set $\{P_i\}$ in \mathbb{R}^d , the Delaunay tessellation defines a symmetrical and isotropic neighborhood relationship between the data points, and produces a unique minimal shape representation of the point set without a prior connectivity information. In practical application such as our LV representation, however, the distribution of the points is often limited to a certain subspace of \mathbb{R}^d , and a subset of the points may have *a priori* connectivity relationships which need

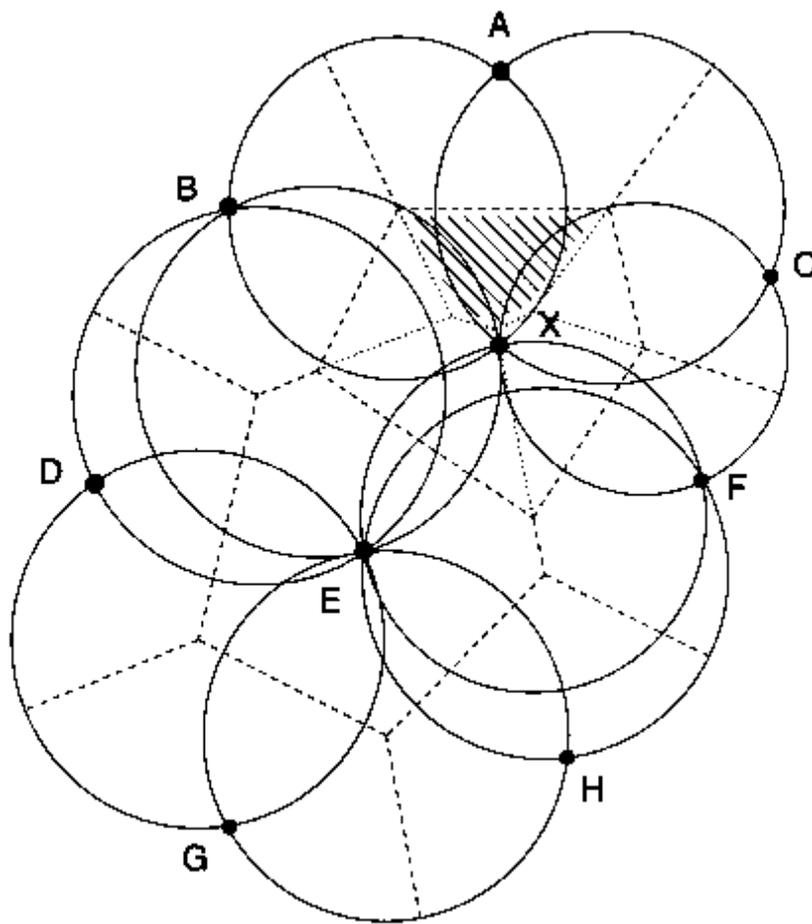


Figure 3.10: Natural neighbor local coordinates. For point X , points A , B , E , F , and C are its 1-order natural neighbor points, and the natural neighbor local coordinate of X with respect to A is the shaded area as a fraction of area of $V(X)$.

to be included in the final tessellation. Thus, triangulations based on modifications of the Delaunay tessellation become more useful under these practical conditions.

3.4.1 Bounded Delaunay Tessellation

We often need to tessellate a set of points $\{P_i\}$ which are placed inside a bounded region S . For the representation of the left ventricle, the point set is bounded by the endocardial and epicardial boundaries. Similar to the bounded Voronoi diagram defined by Okabe[88], we consider the tessellation set given by

$$\mathcal{D}_B(P) = \mathcal{D}(P) \cap S \quad (3.9)$$

$$= \{T_0 \cap S, \dots, T_i \cap S, \dots, T_{(N-1)_v} \cap S\} \quad (3.10)$$

where $T_i \cap S = \emptyset$ if any part of triangle T_i is outside of S . Hence, this set only includes Delaunay triangles which are *completely* inside region S . We call this set the **bounded Delaunay triangulation** of point set $\{P_i\}$ by region S , and the region covered by the bounded Delaunay triangulation the **bounded Delaunay region**. Obviously, depending on the characteristics of the bounding region, a bounded Delaunay region may be disconnected, and it may not be a convex hull.

A two-dimensional example is given in Figure 3.11. An unbounded point set is shown in Figure 3.11(a), and a similarly distributed yet bounded point set is in Figure 3.11(c). The Delaunay triangulation of the unbounded point set is in Figure 3.11(b), while the bounded Delaunay triangulation of the bounded point set is shown in Figure 3.11(d). Note that the bounded Delaunay region is not convex in this example.

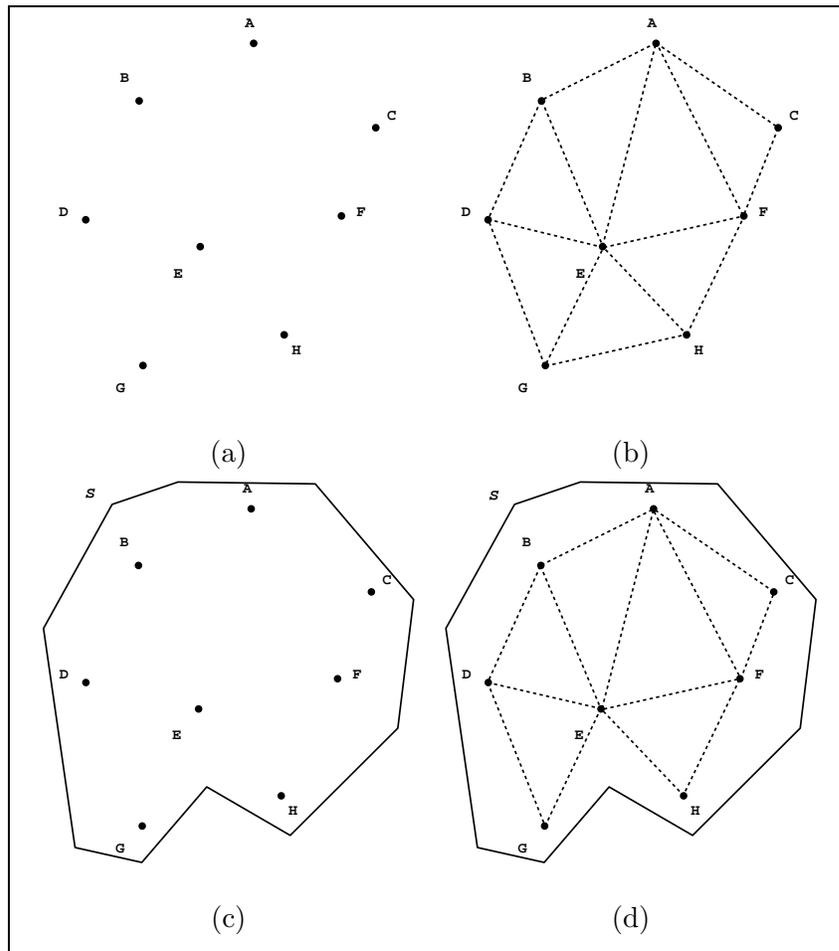


Figure 3.11: Bounded Delaunay triangulation. (a) and (b): an unbounded point set and its Delaunay triangulation; (c) and (d): a bounded point set and its bounded Delaunay triangulation. The data points are the filled dots, the bound of the region is the thick line, and the Delaunay edges are the broken lines.

3.4.2 Constrained Delaunay Tessellation

There may also be cases where we deal not only with point set $\{P_i\}$ in \mathbb{R}^d , but also with k -dimensional ($k < d$) simplicial structures $\{L_i\}$ of special topographical significance, such as line segments and two-dimensional facets in \mathbb{R}^3 , whose endpoints belong to $\{P_i\}$. We want the triangulation of these points to include those k -dimensional structures as k -dimensional faces or aggregates of several k -dimensional faces of the final triangulation. The triangulation of $\{P_i\}$ in this nature is called the **constrained Delaunay tessellation**, $\mathcal{D}_C(P)$, of point set $\{P_i\}$ by constraints $\{L_i\}$, even though strictly speaking some of triangles are no longer Delaunay triangles in the sense that the circumspheres of these triangles are not empty[88].

If we simply compute the Delaunay triangulation of the point set, including the endpoints of the constraint structures, these simplicial structures may not always be k -dimensional Delaunay faces or aggregates of several k -dimensional faces of the Delaunay structure $\mathcal{D}(P)$. The modification of $\mathcal{D}(P)$ which must be undertaken to create $\mathcal{D}_C(P)$ arises when the presence of $\{L_i\}$ in \mathbb{R}^d affects the mutual visibility of members of $\{P_i\}$.

In \mathbb{R}^2 , two points P_r and P_s are said to be mutually visible if the line segment $\overline{P_r P_s}$ does not intersect any member of $\{L_i\}$ [88]. For example, in Figure 3.12 points P_1 and P_2 are mutually visible while points P_2 and P_4 are not. Let E be the set of edges joining data points which are mutually visible. The $\mathcal{D}_C(P)$ consists of $\{L_i\}$ along with a subset of E in which the circumball of each triangle with vertices P_r , P_s and P_t does not contain in its interior any other point which is visible from P_r , P_s and P_t . Thus, points P_1 , P_2 and P_3 in Figure 3.12 form a triangle of $\mathcal{D}_C(P)$ even though their circumcircle contains P_4 because P_2 and P_4 are not mutually visible. Obviously triangle $\overline{P_1 P_2 P_3}$ is not a Delaunay triangle in strict sense. Figure 3.13 shows the two-dimensional examples

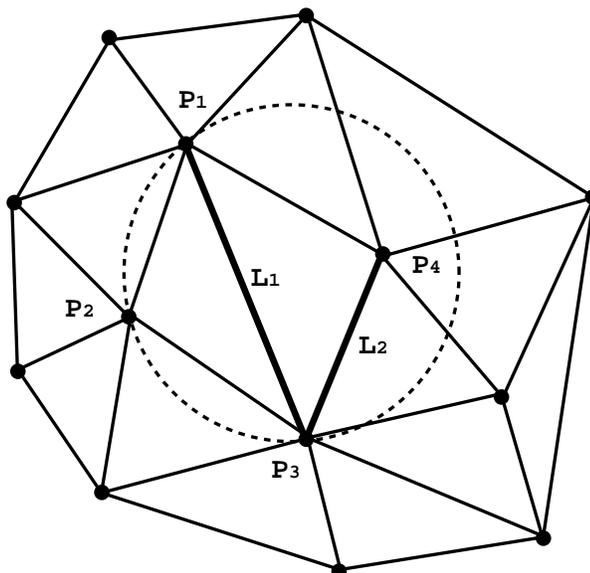


Figure 3.12: Mutual visibility criterion for defining triangles in a two-dimensional constrained Delaunay triangulation. L_1 and L_2 are line segment constraints, $\overline{P_1P_2P_3}$ is a valid triangle in the $\mathcal{D}_C(P)$ even though their circumcircle (broken line) contains P_4 , because P_2 and P_4 are not mutually visible

of constrained Delaunay tessellation $\mathcal{D}_C(P)$ along with their unconstrained counterparts $\mathcal{D}(P)$.

We extend the definition of mutual visibility into higher dimensions. For higher dimensional cases, the definition of the mutual visibility criterion for defining valid triangles is similar to the two dimensional case. Here, mutual visibility of k -dimensional ($k = 1, \dots, d - 1$) faces of the triangle in \mathbb{R}^d needs to be checked against the constraint set $\{L_i\}$. A triangle with $d + 1$ vertices P_{i_0}, \dots, P_{i_d} is a valid triangle of the constrained Delaunay triangulation of the point set if its circumball does not contain in its interior any other points which are visible from points P_{i_0}, \dots, P_{i_d} .

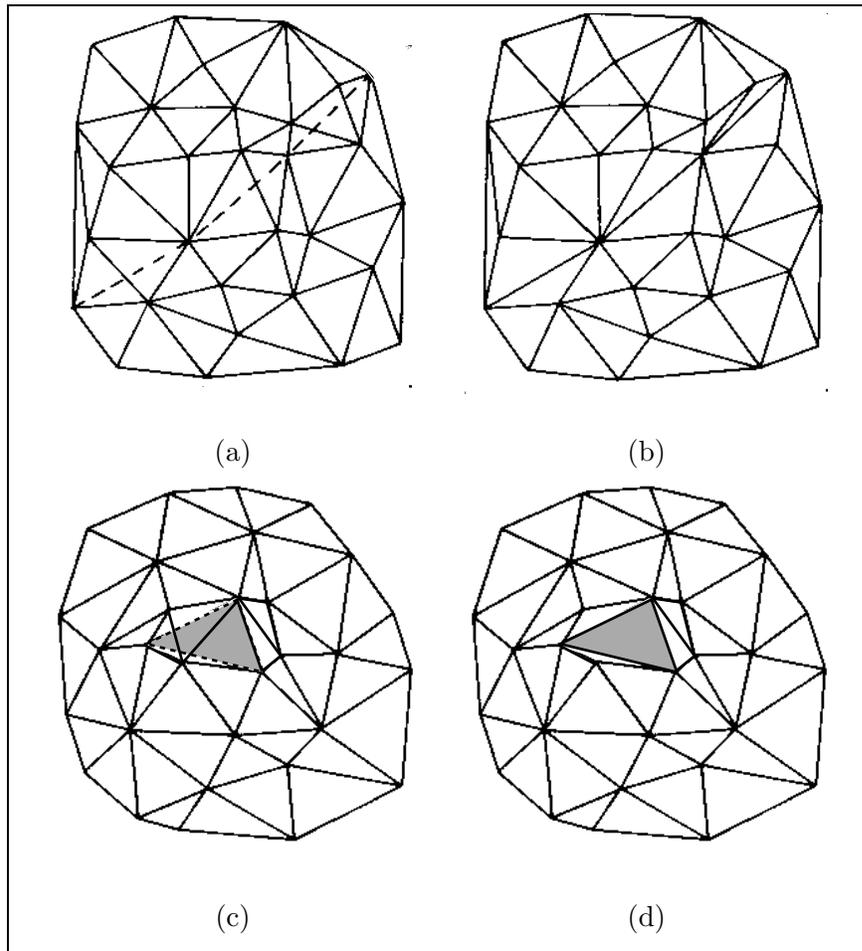


Figure 3.13: Examples of the constrained Delaunay tessellation. (a): the unconstrained Delaunay triangulation of the points; (b): the corresponding $\mathcal{D}_C(P)$ constrained by line segments (broken lines in (a)); (c): the unconstrained Delaunay triangulation of the points; (d): the corresponding $\mathcal{D}_C(P)$ constrained by a triangle (shaded area).

It should be pointed out that the constrained Delaunay tessellation described above is *different* from the same named definition given by Faugeras[34]. In our definition, the pre-determined constraint structures are preserved while the triangulation is not in strict Delaunay sense. On the other hand, in [34] which only deals with 2D point set, the constraint structures such as line segments are modified by adding as many as needed new points to these segments in such a way that the resulting Delaunay triangulation contains each of these line segments as a Delaunay edge (no point added to this segment) or aggregate of Delaunay edges (points have been added to this segment). Hence, this definition will yield true Delaunay triangulation. However, the pre-determined constraint structures no longer exist in their original forms. We believe for our problem of LV representation, it is more important to preserve the pre-determined structures. The first reason is that the pre-determined structures can be often of physiological or topological significance which are worthwhile preserving. The second reason is that the finite element mesh need to be as uniform in size as possible, which could be difficult to achieve using Faugeras's definition where the points are added until the triangulation is Delaunay.

3.5 Delaunay Tessellation of Left Ventricle

As described in Section 3.2, the myocardium of the left ventricle is first defined by the bounding endocardial and epicardial contour stacks detected from the image data. Then, the mid-wall points are founded by using a region filling procedure of the bounded area. Finally, these myocardial sample points, including endocardial boundary, epicardial boundary, and mid-wall points, are tessellated to form the discrete geometrical representation of the left ventricle.

The bounded Delaunay tessellation is particularly useful in the representation

of the left ventricle since the myocardial volume is bounded by the endocardial and epicardial boundaries, which are often complex geometrical shapes. The constrained Delaunay tessellation is also useful if certain prior connectivity information is available and needed to be preserved in the final representation.

We have concluded that if the myocardial sample point set satisfies the non-collinearity and non-cosphericity assumptions, it is in general position and its Delaunay tessellation is unique. However, members of the myocardial point set, especially the mid-wall points from the region filling, are usually collinear and/or cospherical. To obtain a unique triangulation, *small* Gaussian-distributed random noise is added to the x -, y - and z -coordinates of the myocardial points to put the point set in a general position. However, this noise-added point set is only used to determine the connectivity relationship between the points from its Delaunay tessellation, while the coordinates of the original points still represent the spatial locations of the sample points, and are used in the motion and deformation algorithms described in the future chapters.

3.5.1 Two Dimensional LV Tessellation

For two-dimensional myocardial slices, the myocardium is bounded by the endocardial and epicardial contours. Since the boundaries are in contour form, the connectivity of the boundary points are pre-determined. The endocardial and epicardial points are connected in an order such that the traces of the connections form the boundary contours. A *bounded and constrained* Delaunay triangulation is needed for the representation of a myocardial slice. Triangles with edges outside of the bounding region, along with triangles whose vertices are boundary points but whose boundary-vertices-defined edges fail to comply with the prior connectivity constraints, are rejected from the tessellation.

In the example in Figure 3.14, (a) shows the boundary contours of a myocardial

slice and (b) shows the whole point set along with the bounding contours. The regular Delaunay triangulation of the point set is shown in Figure 3.14(c) with the bounding contours in bold lines, and the bounded and constrained Delaunay triangulation is shown in Figure 3.14(d).

3.5.2 Three Dimensional LV Tessellation

For three-dimensional myocardial point sets, the myocardium is bounded by the endocardial and epicardial *contour stacks*, and we need to construct a volumetric tessellation. The myocardial points at each imaging plane are bounded by the endocardial and epicardial contours at that plane, and the connectivity of the boundary points at that plane are pre-determined such that the traces of the connections form the boundary contours at that plane. The mid-wall points are again found by using a region filling procedure within the bounded area. However, the volumetric representation of the myocardium requires not only in-plane connections of the sample points, but also the connections between points which belong to different planes. Unlike the two-dimensional case, the contours at different planes, which are unrelated to each other, *cannot* trivially define the bounded region for the myocardium. We need to define the bounded myocardial region either by explicitly forming endocardial and epicardial surfaces or implicitly by keeping/rejecting new triangles using some inside/outside criterion, both from the contour stacks.

To explicitly form the endocardial and epicardial surfaces from the contour stacks, a surface-from-contour-stack pre-process is needed. There are various algorithms available to triangulate the contour stack into a polygonal representation of the surface[37, 65, 76]. Finding connections between points in successive contours is often reduced to a search problem on a toroidal graph, and a *correct* surface is chosen by optimizing some objective function. Choices of metrics for the graph cost function include maximum volume[65],

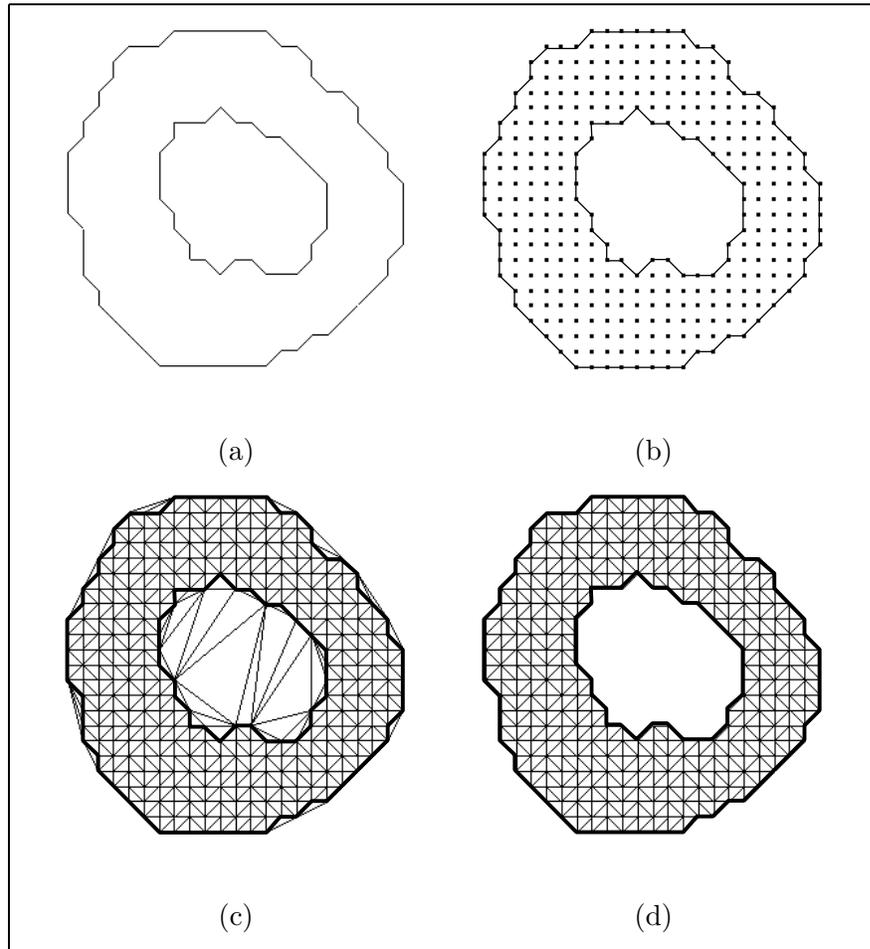


Figure 3.14: Two-dimensional Delaunay tessellation of myocardial slice. (a): the endocardial and epicardial contours; (b): the myocardial sample point set; (c): the regular Delaunay triangulation of the point set with the bounding contours in bold lines; (d): the bounded and constrained Delaunay triangulation of the myocardium.

minimum area[37], minimum spanning tree[76]. These surface forming methods could be computationally expensive if the contours are finely sampled. After the boundary surfaces are formed, a *bounded and constrained* Delaunay triangulation is constructed for the myocardial point set.

The implicit method we propose here adds additional constraints into the *bounded and constrained* Delaunay triangulation process, and is in spirit close to the Delaunay based surface-from-contour method in [16] which is only for surface triangulation.

The first criterion is that only tetrahedra which have their four vertices on two consecutive planes, denoted as “higher-plane” and “lower-plane”, could possibly be valid. In practice, this is achieved by Delaunay triangulation sample points two consecutive slices at a time, then assembling them into one single aggregate. Since each tetrahedron satisfies the empty circumsphere criterion, the aggregate of all the tetrahedra is a Delaunay structure.

The second criterion determines which of the Delaunay tetrahedra are the valid ones, judged from the endocardial and epicardial contour stacks. Tetrahedron with no more than one vertex on the boundary contours (at least three vertices in the mid-wall) is *always* considered inside the myocardium, hence is always valid. Tetrahedron with multiple vertices on the contours is judged by the six mid-points of its edges: the mid-points are projected upward to the higher-plane and downward to the lower-plane. If either all upward projections are inside the bounding region of the higher-plane, or all downward projections are inside the bounding region of the lower-plane, or both, this tetrahedra is a valid Delaunay triangle. Otherwise, it is invalid and rejected. Since this criterion involves only two-dimensional operation on a subset of the tetrahedron, the computational cost of this implicit method is not very high.

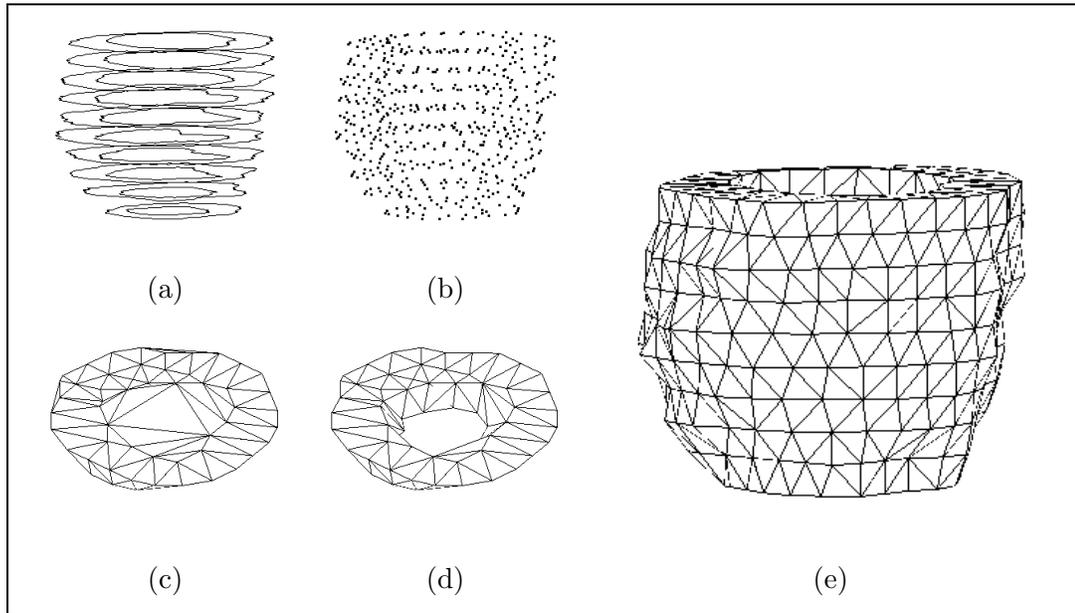


Figure 3.15: Three-dimensional Delaunay tessellation of myocardium. (a): the endocardial and epicardial contour stacks; (b): the myocardial sample point set; (c): a two-slice Delaunay triangulation; (d): the bounded and constrained Delaunay triangulation of these two slices; (e): the bounded and constrained Delaunay triangulation of the myocardium. (only visible Delaunay edges are shown in the figures)

In the example in Figure 3.15, (a) shows the boundary contour stacks of the myocardium and (b) shows the whole point set. The Delaunay triangulation of points on two consecutive slices (the first criterion) is shown in Figure 3.15(c), and the bounded and constrained Delaunay triangulation (the second criterion) of these two slices is shown in Figure 3.15(d). The bounded and constrained Delaunay triangulation of the entire point set is shown in Figure 3.15(e). (only visible Delaunay edges are shown in the figures)

The by-products of the three-dimensional volumetric Delaunay triangulation of the myocardium are the Delaunay triangulations of myocardial surfaces. The two-dimensional

Delaunay facets which are on the *outside boundary* of the triangulation constitute the epicardial surface, while the facets which are on the *inside boundary* of the triangulation constitute the epicardial surface. These surfaces are Delaunay structures because each circumsphere contains no vertex other than the ones which belong to the facet. Examples of triangulated myocardial surfaces are shown in Figure 3.16.

3.6 Conclusion

A geometrical representation, based on bounded and constrained Delaunay triangulation, of the left ventricle has been developed in this chapter. This approach allows three levels of representation of the myocardium: the sample points level, the triangulated boundary surfaces level, and the volumetric level based upon natural neighbor relationships.

The point level representation enables the system to deal with data of different resolutions, e.g. Dynamic Spatial Reconstructor images, magnetic resonance images, echocardiographic images. The surfaces level representation makes it possible to analyze boundary shape characterization and motion. The volumetric level representation facilitates the incorporation of continuum mechanical models and other physical constraints, as well as the adoption of a finite element framework as the unified approach to integrate complementary information. The multi-order natural neighbor relationship between the sample points also provides natural multi-order interpolation, smoothing, and function fitting schemes weighted by natural neighbor coordinates, to further study the characteristics of a set of spatial points.

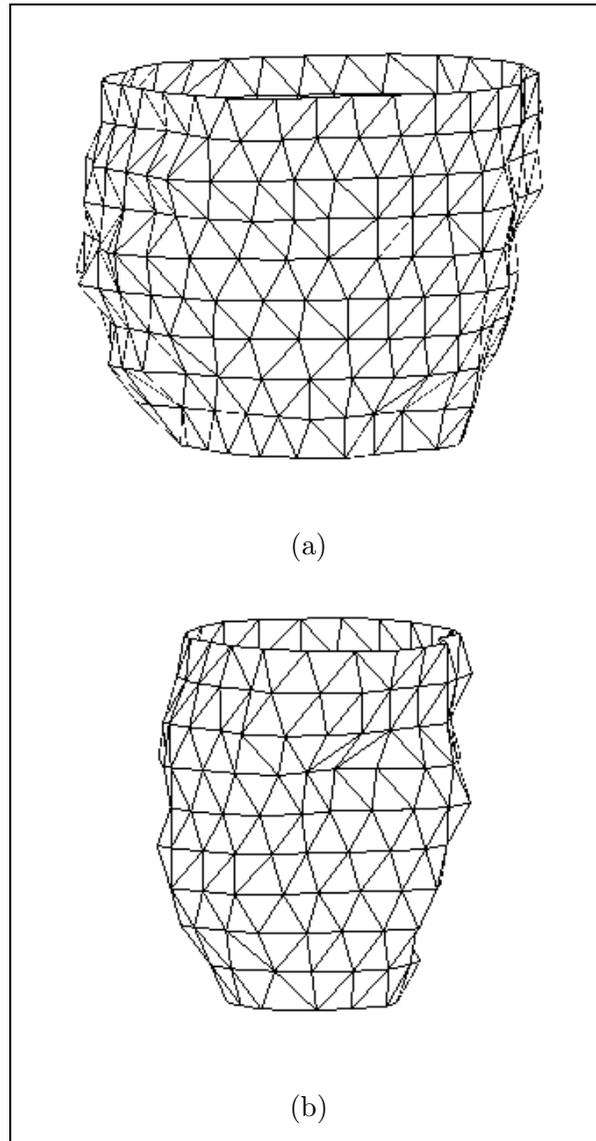


Figure 3.16: Delaunay triangulation of myocardial surfaces. (a): epicardial surface; (b): endocardial surface.

Chapter 4

Boundary Motion Analysis

4.1 Introduction

In this chapter, we will build a system which establishes dense field point correspondences between successive myocardial surfaces over the entire cardiac cycle. Further analysis of the motion parameters of normal and infarcted hearts also inspire new ways to predict the location and extent of myocardial injury from *in vivo* measurement.

Without prior motion knowledge, one can hypothesize that point matching and tracking between successive surfaces should follow a minimum energy principle, which means that a point should move and deform as little as possible. Since the myocardial surface undergoes global motion as well as local motion and deformation, purely minimum distance based approaches[95, 54] often fail to produce consistently good matches, especially for the endocardial surface where motion and deformation are often relatively larger. However, if the temporal sampling is fine enough, sixteen frames per cardiac cycle for our data, it has been tested and validated that shape landmarks are good tracking cues over time[120]. The hypothesis is that for short time intervals, the differential

shape characteristics at surface points, especially the geometrically significant points such as highly curved ones, should not change dramatically between successive frames. The shape features may be more reliable matching cues than the distance measures. However, pure local matching methods often produce incoherent, even conflicting, motion vectors between neighboring surface points. To alleviate this problem, local smoothness constraints, which assume that neighboring surface points should have similar motion characteristics and vary only gradually, are often built into the matching process.

We propose a shape-based motion tracking approach to track the motion trajectories of a dense field of points over the entire cardiac cycle, based on locating and matching differential geometric features and an ideal-thin-plate bending model of local surface patches. The surface characterization is performed by multi-scale fittings of multi-order natural neighbor points. The local smoothness constraint is enforced to achieve a smooth dense motion field.

For validation purposes, canine experiments have been performed using two different imaging modalities. Point tracking accuracy is validated using the gold-standard motion of implanted imaging-opaque markers. The differences of two motion-derived parameters, path length and wall thickening measures, between baseline and post-infarct data are quantified to assess regional myocardial viability, and are validated using gold-standard *post mortem* TTC staining of cardiac perfusion activity.

4.2 Triangulated Surface Smoothing

As described in the previous chapter, the myocardial boundary surfaces can be represented by the aggregate of all the two-dimensional Delaunay facets which are on the boundary of the volumetric Delaunay triangulation of the myocardium. These polyhedral surfaces,

however, often appear faceted. One reason for this non-smooth appearance is that each plane boundary contour from the segmentation is digitized, often at the resolution of the image sampling lattice which may not be fine enough for smooth visualization and/or reconstruction of the continuous contour. The more fundamental reason arises from the fact that contours of different planes are segmented independently, which means that there is no smoothness, relational, or other spatial constraints between contour points of different planes. Even though the Delaunay triangulation establishes the connectivity relationship between points, the triangulated surfaces usually are not *smooth* surfaces, not even locally.

For visualization and shape characterization purposes, the jagged boundary surfaces need to be smoothed to achieve locally coherent surface representations. Most of the existing smoothing methods suffer from the *shrinkage* problem, which means that when the smoothing process is applied iteratively a large number of times, a surface will collapse into a point[125]. One notable example is the popular Gaussian smoothing method, in which the new position of each point is iteratively computed as the weighted average of the current positions of this points and its neighbor points. It can be expressed in a regularization form in the continuous domain as:

$$\mathbf{x}^*(\mathbf{u}) = \arg \min_{\mathbf{x}} \int \int_S \left\{ \lambda(\mathbf{u}) [\mathbf{x}(\mathbf{u}) - \mathbf{x}_{init}(\mathbf{u})]^2 + \left(\frac{\partial \mathbf{x}(\mathbf{u})}{\partial \mathbf{u}} \right)^2 \right\} d\mathbf{u} \quad (4.1)$$

Here, S is the surface space and \mathbf{u} is the parameter vector representing a point in S , \mathbf{x}_{init} and \mathbf{x}^* are the initial and final position vectors, respectively, and λ is the smoothing factor.

For polyhedral surfaces, the neighborhood relationship can be derived from the

connectivity between the points. Hence, we approximate the derivative by the weighted average finite differences performed on the neighboring points:

$$\frac{\partial \mathbf{x}(\mathbf{u})}{\partial \mathbf{u}} = \sum_{i=0}^{N-1} \omega_i \{\mathbf{x}(\mathbf{u}) - \mathbf{x}(\mathbf{u}_i)\}, \quad i = 0, \dots, N-1 \quad (4.2)$$

$$\sum_{i=0}^{N-1} \omega_i = 1 \quad (4.3)$$

where $\{\mathbf{u}_i\}$ is the neighbor point set, and $\{\omega_i\}$ is the weighting coefficient set associated with the neighbor points. Furthermore, the discrete version of Equation 4.1 can be conveniently posed as a series of linear equations with the local surface patch defined by the triangulation. The linear equations can be solved iteratively for each point $\mathbf{x}(\mathbf{u})$ by:

$$\mathbf{x}_{new} = (1 - \lambda') \mathbf{x}_{current} + \lambda' \sum_{i=0}^{N-1} \omega_i \mathbf{x}_i \quad (4.4)$$

$$\lambda' = \frac{1}{\lambda + 1} \quad (4.5)$$

Since the method is very local, Gaussian smoothing often has to be applied iteratively a large number of times in order to obtain the desired smoothing effect. However, this also produces significant shrinkage as a by-product. A two-stage Gaussian smoothing algorithm has been proposed by Taubin[125] to reduce the shrinkage effect, and can be expressed as:

$$\mathbf{x}_{new1} = (1 - \lambda'_1) \mathbf{x}_{current} + \lambda'_1 \sum_{i=0}^{N-1} \omega_i \mathbf{x}_i \quad (4.6)$$

$$\mathbf{x}_{new2} = (1 - \lambda'_2) \mathbf{x}_{new1} + \lambda'_2 \sum_{i=0}^{N-1} \omega_i \mathbf{x}_i \quad (4.7)$$

For each iterative smoothing step, after a first Gaussian smoothing stage with a positive smoothing factor λ'_1 which produces a slightly shrunk surface, a second Gaussian smoothing stage is applied with a negative smoothing factor λ'_2 which produces a slightly expanded surface. λ'_2 has slightly greater magnitude than λ'_1 ($0 < \lambda'_1 < -\lambda'_2$), with the difference determined by a bounded band which makes sure that the surface does not shrink or expand after each two-stage smoothing. This new method is in fact a linear low-pass filter that removes high curvature variations, with the two smoothing factors determining the passing band.

Figure 4.1 shows the different effects of traditional Gaussian smoothing and two-stage non-shrinkage smoothing. The original triangulated endocardial surface is shown in Figure 4.1(a) (rendered) and Figure 4.1(b) (wireframe). The next three figures on the right side are the smoothing results for the traditional Gaussian smoothing process ($\lambda' = 0.33$, iteration number $n = 10$ (Figure 4.1(d)), 50 (Figure 4.1(f)), and 100 (Figure 4.1(h))). The three figures on the left side are the smoothing results for the two-stage non-shrinkage Gaussian smoothing process ($\lambda'_1 = 0.33$, $\lambda'_2 = -0.34$, iteration number $n = 10$ (Figure 4.1(c)), 50 (Figure 4.1(e)), and 100 (Figure 4.1(g))). In both smoothing procedures, the z-coordinates of the points in top and bottom contours are fixed. It is quite obvious, at least visually, that the non-shrinkage process keeps the overall size and shape-feature of the surface while the traditional Gaussian smoothing produces severe shrinkage when the iteration number becomes large. Because the relative positions of neighbor points are better preserved in the non-shrinkage process, the geometrical structure of the surface is also better preserved.

The weighting coefficients of the neighbor points are often set to be the normalized values (the sum of the weighting coefficients equals to unity) which are inversely

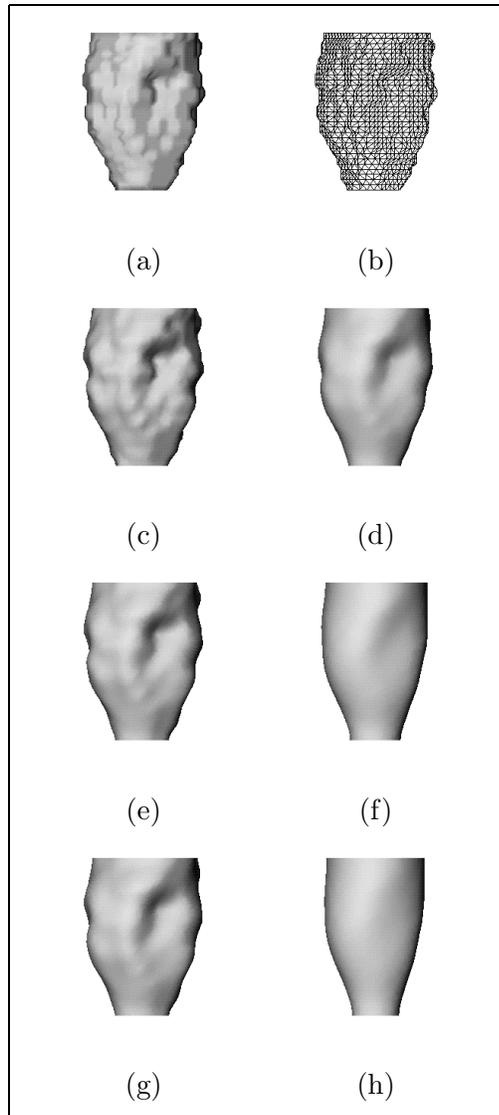


Figure 4.1: Regular and non-shrinkage Gaussian smoothing of triangulated surface. (a): the original triangulated endocardial surface (rendered); (b): the wireframe of the original surface; (c)(e)(g): non-shrinkage Gaussian smoothing results with $\lambda'_1 = 0.33$, $\lambda'_2 = -0.34$ and iteration number $n = 10$ (c), 50 (e), and 100 (g); (d)(f)(h): regular Gaussian smoothing results with $\lambda' = 0.33$, and iteration number $n = 10$ (d), 50 (f), and 100 (h).

proportional to the distances between the fiducial point and its neighbor points[125]. It has been shown experimentally that the weighting coefficients determined this way are usually good enough for visualization purposes, even though it may be troublesome for non-uniformly distributed point sets where distances no longer reflect the true geometrical influence between points. However, if the purpose is to *recover* the true geometry of the noisy surface, we need to choose weighting coefficients which are more closely related to the geometry of the local point distributions. The natural neighbor coordinates discussed in chapter 3, which quantitatively express the geometrical position of any point relative to each of its natural neighbor points, become good candidates:

$$\omega_i = nnlc_i \tag{4.8}$$

An experiment using a synthetic ellipsoidal surface is conducted to demonstrate the advantage of using natural neighbor coordinates as the weighting coefficients. Two ellipsoidal surfaces with axis lengths 10, 10, and 20 are synthetically generated. One surface is spatially uniformly sampled (Figure 4.2(a)), and the other one is non-uniformly sampled (Figure 4.3(a)). Each of the sample points is then rounded off to its nearest lattice point to mimic the quantization effect (Figure 4.2(c) and Figure 4.3(c)), with the average distance error being 0.826 ± 0.500 for the uniformly sampled surface and 0.769 ± 0.465 for the non-uniform one. The distance weighted smoothing and the natural weighted smoothing are applied to the two surfaces over several different number of iterations, and the results are shown in Table 4.1. These results clearly show that the natural weighted smoothing is far superior in the recovery of the true geometry, the ellipsoidal surfaces in this experiment, from noisy surface approximations with both uniform and non-uniform

		Error After Smoothing		
Surface Type	Quantization Error	Iteration Number	Distance Weighted	Natural Weighted
Uniformly Sampled	0.826±0.500	10	0.814±0.469	0.340±0.116
		50	0.774±0.456	0.272±0.103
		100	0.731±0.443	0.215±0.095
Non-uniformly Sampled	0.769±0.465	10	0.791±0.440	0.332±0.093
		50	0.682±0.419	0.274±0.085
		100	0.641±0.387	0.222±0.067

Table 4.1: Comparison of distance and natural weighted smoothing. The error (mean±standard deviation) is the distance between sample points and their true positions before roundoff.

sampling.

The visual results of this experiment are shown in Figure 4.2 for the uniformly sampled surface, and in Figure 4.3 for the non-uniformly sampled surface. The left column figures are the rendered surfaces, and the right column ones are the corresponding wireframes. The top figures are the ideal surfaces, the second row figures are the quantized noisy surfaces, the third rows are the smoothed surfaces using distance weighted coefficients, and the bottom figures are the results from the natural weighted smoothing. Visually, it seems that two smoothed surfaces are quite similar in the uniformly sampled

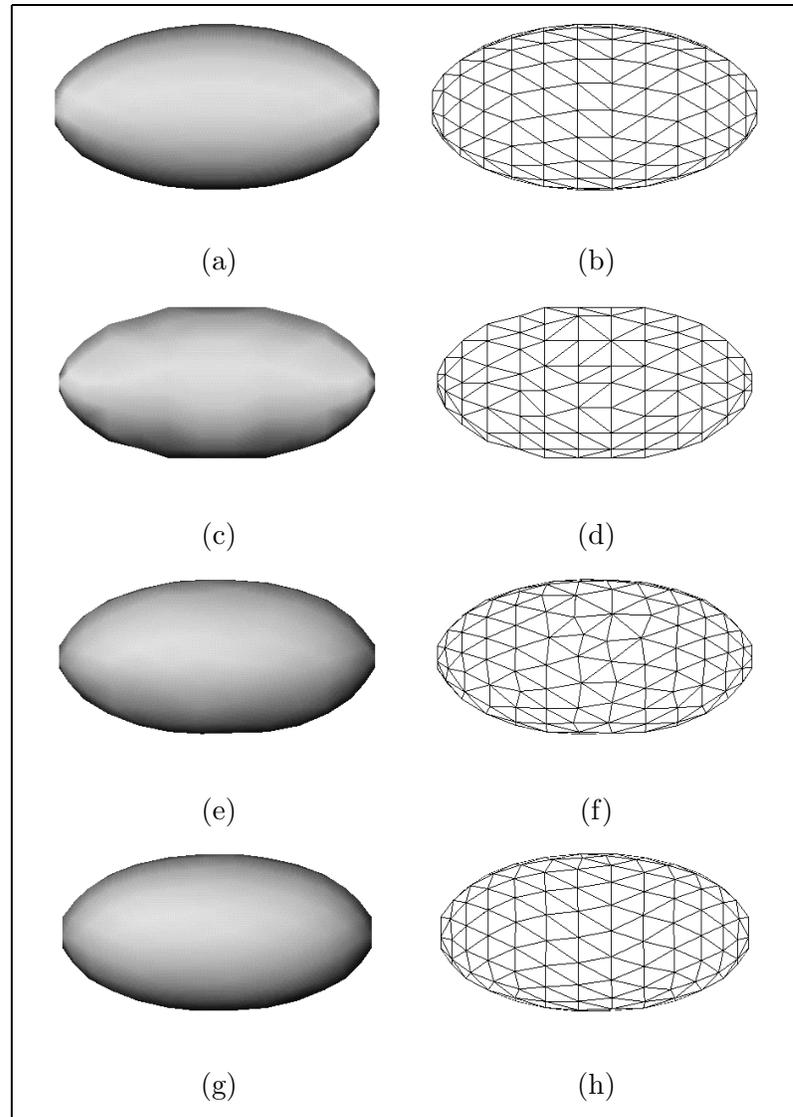


Figure 4.2: Distance and natural weighted smoothing of uniformly sampled ellipsoidal surface. On the right are the rendered surfaces, and the corresponding wireframes are on the left. (a)(b): ideal surface; (c)(d): quantized noisy surface; (e)(f): smoothed surface using distance weighted coefficients; (g)(h): smoothed surface using natural weighted coefficients. (smoothing factors: $\lambda'_1 = 0.33$, $\lambda'_2 = -0.34$; iteration number: $n = 10$)

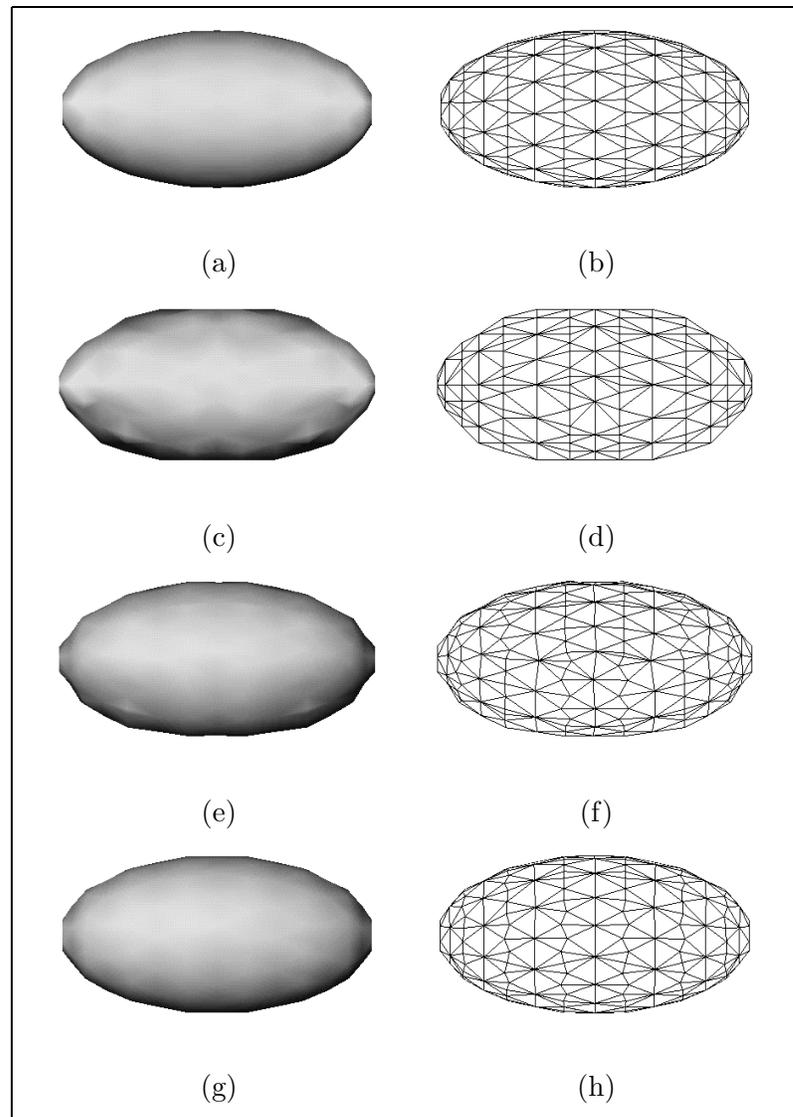


Figure 4.3: Distance and natural weighted smoothing of non-uniformly sampled ellipsoidal surface. On the left are the rendered surfaces, and the corresponding wireframes are on the right. (a)(b): ideal surface; (c)(d): quantized noisy surface; (e)(f): smoothed surface using distance weighted coefficients; (g)(h): smoothed surface using natural weighted coefficients. (smoothing factors: $\lambda'_1 = 0.33$, $\lambda'_2 = -0.34$; iteration number: $n = 10$)

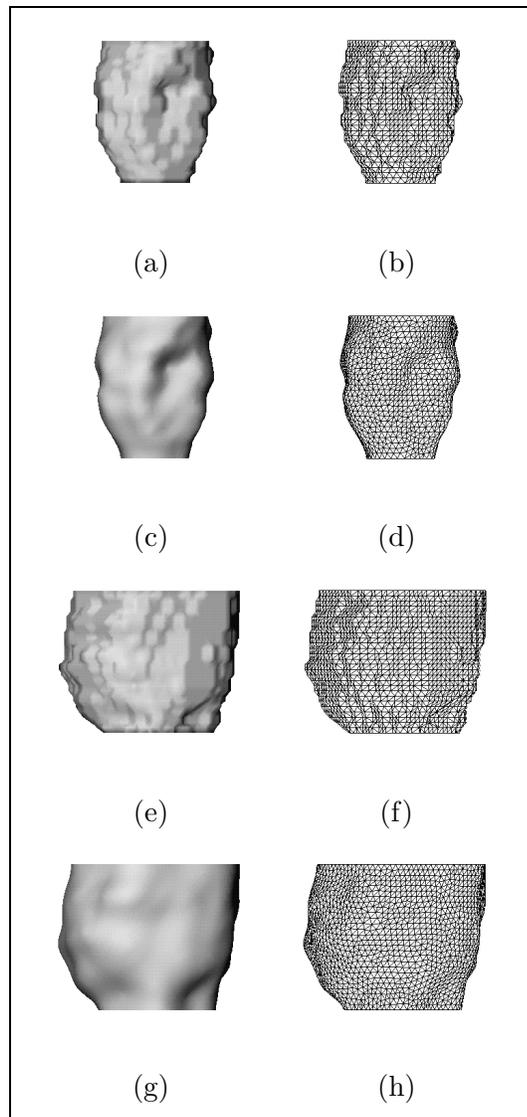


Figure 4.4: Natural weighted non-shrinkage smoothing of myocardial surfaces. On the left are the rendered surfaces, and the corresponding wireframes are on the right. (a)(b): original endocardial surface; (c)(d): smoothed endocardial surface; (e)(f): original epicardial surface; (g)(h): smoothed epicardial surface. (smoothing factors: $\lambda'_1 = 0.33$, $\lambda'_2 = -0.34$; iteration number: $n = 50$)

case, while the natural weighted smoothed surface looks smoother in the non-uniform case.

Finally, examples of the natural weighted smoothed endocardial and epicardial surfaces are shown in Figure 4.4.

4.3 Shape Characterization

In this section, we will discuss the characterization of local surface properties which will be used in the surface matching process.

4.3.1 Differential Geometry of Surface

Classical differential geometry studies the local properties of curves and surfaces. These local properties depend only on the behavior of the curve or surface in the neighborhood of the fiducial point, and can be derived using differential calculus. The following is a brief review of the relevant topics in differential geometry. Formal discussion can be found in do Carmo[29] and Besl[13].

A general regular surface $S \subset \mathbb{R}^3$ is defined as: *for each $p \in S$, there exists a neighborhood V in \mathbb{R}^3 and a map $\mathbf{x} : U \rightarrow V \cap S$ of an open set $U \subset \mathbb{R}^2$ onto $V \cap S \subset \mathbb{R}^3$ such that*

- $\mathbf{x}(u, v) = (x(u, v), y(u, v), z(u, v)), (u, v) \in S$ is differentiable. (This condition ensures that a differential process can be performed on S .)
- \mathbf{x} is a homeomorphism. And since \mathbf{x} is continuous by the previous condition, this means that \mathbf{x} has an inverse $\mathbf{x}^{-1} : V \cap S \rightarrow U$ which is continuous; that is, \mathbf{x}^{-1} is the restriction of a continuous map $F : W \subset \mathbb{R}^3 \rightarrow \mathbb{R}^2$ defined on an open set W containing $V \cap S$. (This condition prevents self-intersections in S , and also

means that objects defined in terms of a parameterization do not depend on this parameterization but rather only on the set S itself.)

- For each $q \in U$, the differential $d\mathbf{x}_q : \mathbb{R}^2 \rightarrow \mathbb{R}^3$ is one-to-one. (This condition guarantees the existence of a tangent plane at all points of S).

The mapping \mathbf{x} is called a *parameterization* or a *system of local coordinates* in a neighborhood of p . The neighborhood $V \cap S$ of p in S is called a *coordinate neighborhood*. From this definition, each point p of a regular surface belongs to a coordinate neighborhood. The points of such a neighborhood are characterized by their coordinates, therefore, we are able to define the local properties in terms of these coordinates.

The plane $d\mathbf{x}_q$, which passes through $\mathbf{x}(q) = p$, does not depend on the parameterization \mathbf{x} . This plane is called the *tangent plane* to S at p , and is denoted by $T_p(S)$. The choice of the parameterization \mathbf{x} determines a basis $\{(\partial\mathbf{x}/\partial u)(q), (\partial\mathbf{x}/\partial v)(q)\}$, or $\{\mathbf{x}_u(q), \mathbf{x}_v(q)\}$, of $T_p(S)$, called the basis associated to \mathbf{x} . Similarly, a unit *normal vector* at point $\mathbf{x}(q) = p$ of S is determined by

$$N_p = \frac{\mathbf{x}_u \wedge \mathbf{x}_v}{|\mathbf{x}_u \wedge \mathbf{x}_v|}(q) \quad (4.9)$$

where \wedge denotes cross product.

First Fundamental Form[29]: *the quadratic form*

$$I_p(w) = \langle w, w \rangle_p = |w|^2 \geq 0 \quad (4.10)$$

is called the *first fundamental form* of the regular surface $S \subset \mathbb{R}^3$ at $p \in S$, where $w \in T_p(S)$, and \langle, \rangle denotes inner product.

In the basis $\{\mathbf{x}_u, \mathbf{x}_v\}$ associated with a parameterization $\mathbf{x}(u, v)$ at p , the tangent vector $w \in T_p(S)$ is the tangent vector to a parameterized curve $\alpha(t) = \mathbf{x}(u(t), v(t))$, $t \in (-\epsilon, \epsilon)$, with $p = \alpha(0) = \mathbf{x}(u_0, v_0)$, we obtain

$$I_p(\alpha'(0)) = \langle \alpha'(0), \alpha'(0) \rangle_p \quad (4.11)$$

$$= \langle \mathbf{x}_u u' + \mathbf{x}_v v', \mathbf{x}_u u' + \mathbf{x}_v v' \rangle_p \quad (4.12)$$

$$= Eu'^2 + 2Fu'v' + Gv'^2 \quad (4.13)$$

where the values of the functions involved are computed for $t = 0$, and

$$E(u_0, v_0) = \langle \mathbf{x}_u, \mathbf{x}_u \rangle_p \quad (4.14)$$

$$F(u_0, v_0) = \langle \mathbf{x}_u, \mathbf{x}_v \rangle_p \quad (4.15)$$

$$G(u_0, v_0) = \langle \mathbf{x}_v, \mathbf{x}_v \rangle_p \quad (4.16)$$

are the coefficients of the first fundamental form in the basis $\{\mathbf{x}_u, \mathbf{x}_v\}$ of $T_p(S)$. By letting p run in the coordinate neighborhood corresponding to $\mathbf{x}(u, v)$, we obtain functions $E(u, v)$, $F(u, v)$, $G(u, v)$ which are differentiable in that neighborhood.

The first fundamental form is the expression of how the surface S inherits the natural inner product of \mathbb{R}^3 . It measures the small amount of movement on the surface for a given small movement in the parameter space. Geometrically, it allows us to make measurements on the surface without referring back to the ambient surface \mathbb{R}^3 where the surface lies. It is invariant to surface parameterization and to translation and rotation of the surface. Therefore, it determines the *intrinsic* properties of the surface.

Second Fundamental Form[29]: *the quadratic form defined in $T_p(S)$ by*

$$II_p(w) = - \langle dN_p(w), w \rangle \quad (4.17)$$

is called the second fundamental form of the regular surface $S \subset \mathbb{R}^3$ at $p \in S$, where $w \in T_p(S)$.

Again, in the basis $\{\mathbf{x}_u, \mathbf{x}_v\}$ associated with a parameterization $\mathbf{x}(u, v)$ at p , the tangent vector $w \in T_p(S)$ is the tangent vector to a parameterized curve $\alpha(t) = \mathbf{x}(u(t), v(t))$, $t \in (-\epsilon, \epsilon)$, with $p = \alpha(0) = \mathbf{x}(u_0, v_0)$. To simplify the notation, we invoke the convention that all functions below denote their values at the point p .

The tangent vector to $\alpha(t)$ at p is

$$\alpha' = \mathbf{x}_u u' + \mathbf{x}_v v' \quad (4.18)$$

and

$$dN_p(\alpha') = N'(u(t), v(t)) = N_u u' + N_v v' \quad (4.19)$$

Therefore, the second fundamental form in the basis $\{\mathbf{x}_u, \mathbf{x}_v\}$ is given by

$$II_p(\alpha') = - \langle dN_p(\alpha'), \alpha' \rangle \quad (4.20)$$

$$= - \langle N_u u' + N_v v', \mathbf{x}_u u' + \mathbf{x}_v v' \rangle \quad (4.21)$$

$$= eu'^2 + 2fu'v' + gv'^2 \quad (4.22)$$

where

$$e = - \langle N_u, \mathbf{x}_u \rangle = \langle N, \mathbf{x}_{uu} \rangle \quad (4.23)$$

$$f = - \langle N_v, \mathbf{x}_u \rangle = \langle N, \mathbf{x}_{uv} \rangle = - \langle N_u, \mathbf{x}_v \rangle \quad (4.24)$$

$$g = - \langle N_v, \mathbf{x}_v \rangle = \langle N, \mathbf{x}_{vv} \rangle \quad (4.25)$$

are the coefficients of the second fundamental form in the basis $\{\mathbf{x}_u, \mathbf{x}_v\}$ of $T_p(S)$.

The second fundamental form measures the correlation between the change in the normal vector and the change in the surface position, as a function of a given small movement in the parameter space. Unlike the first fundamental form, it is dependent on the embedding of the surface in space, and determines the *extrinsic* properties of the surface.

Weingarten Mapping[29]: *the matrix in the form*

$$[\beta] = - \begin{pmatrix} e & f \\ f & g \end{pmatrix} \begin{pmatrix} E & F \\ F & G \end{pmatrix}^{-1} \quad (4.26)$$

is called the Weingarten mapping matrix or the shape operator matrix of the surface. This matrix combines the first and second fundamental forms into one matrix, and determines surface shape by relating the intrinsic geometry of the surface to the Euclidean (extrinsic) geometry of the embedding space.

The *Gaussian curvature* of a surface can be defined from the Weingarten mapping

matrix as its determinant:

$$K = \det[\beta] = \frac{eg - f^2}{EG - F^2} \quad (4.27)$$

Meanwhile, the *mean curvature* of a surface is similarly defined as half of the trace of the Weingarten mapping matrix:

$$H = \frac{\text{tr}[\beta]}{2} = \frac{eG - 2fF + gE}{2(EG - F^2)} \quad (4.28)$$

Since the surface curvatures are the only natural algebraic invariants of the Weingarten mapping matrix, they arise naturally in a detailed analysis of surface shape. Gaussian and mean curvatures are invariant to arbitrary choice of parameterization of a surface, and are also invariant to arbitrary rotations and translations of the surface in space. These invariances are extremely important in uniquely characterizing the view-independent surface shape properties. The analysis of the left ventricular surfaces is based upon these invariances for characterizing their shape properties.

Another way to study surface curvatures is based on the space curves that lie on the surface. At each point $p \in S$, there is a direction of maximum normal curvature and a direction of minimum normal curvature for all curves which

- lie on the surface;
- pass through point p ;
- have normals that align with the surface normal N_p at the point p .

We denote (κ_1, e_1) the maximum principal curvature and its direction (the magnitude and direction of the maximum of the normal curvature function), and (κ_2, e_2) the minimum

principal curvature and its direction (the magnitude and direction of the minimum of the normal curvature function). The principal curvatures are the two eigenvalues of the Weingarten mapping matrix, with their directions the two eigenvectors. They are also related to the Gaussian and mean curvatures in describing the magnitude of the surface shape since:

$$K = \kappa_1 \kappa_2 \quad (4.29)$$

$$H = \frac{\kappa_1 + \kappa_2}{2} \quad (4.30)$$

$$\kappa_1 = H + \sqrt{H^2 - K} \quad (4.31)$$

$$\kappa_2 = H - \sqrt{H^2 - K} \quad (4.32)$$

Moreover, the principal curvatures also provide the directional information of the surface shape, which could be important in finding certain higher order differential features of the surface, such as ridge lines.

The signs of the Gaussian, mean and principal curvatures are often used to determine basic surface types and singular points such as umbilical points[13]. Furthermore, the numerical relationship between the two principal curvatures are used in more detailed classification of surfaces by Koenderink[67]. A shape index function is defined as

$$si = \frac{2}{\pi} \arctan \frac{\kappa_2 + \kappa_1}{\kappa_2 - \kappa_1}, \quad (\kappa_2 \geq \kappa_1) \quad (4.33)$$

All surface patches, except for plane patches where the two principal curvatures equal zero, are mapped onto $si \in [-1, +1]$. This shape index function has many nice properties with regards to the classification of surface types:

Surface Type	Shape Index Range
Spherical Cup	$si \in [-1, -7/8)$
Trough	$si \in [-7/8, -5/8)$
Rut	$si \in [-5/8, -3/8)$
Saddle Rut	$si \in [-3/8, -1/8)$
Saddle	$si \in [-1/8, +1/8)$
Saddle Ridge	$si \in [+1/8, +3/8)$
Ridge	$si \in [+3/8, +5/8)$
Dome	$si \in [+5/8, +7/8)$
Spherical Cap	$si \in [+7/8, +1]$

Table 4.2: Discrete surface classification using shape index function.

- The shape index is scale invariant, i.e. two spherical patches with different radii will have same shape index values.
- Convexities and concavities are on the opposite sides of the shape index scale, separated by saddle-like shapes.
- Two shapes from which the shape index differs only in sign represent complementary pairs will fit to each other as stamp and mold if they are of same scale.

One discrete surface classification scheme using the shape index function is proposed in [67]. Here, surfaces are classified into nine types as in Table 4.2.



Figure 4.5: A color spectrum represents the discrete surface types.

A color spectrum representing these nine discrete surface types is shown in Figure 4.5. We will use this color scale to visualize the shape-classified myocardial surfaces in later sections.

4.3.2 Shape Characterization of Triangulated Surfaces

4.3.2.1 Local Surface in Graph Form

For a regular surface $S \subset \mathbb{R}^3$ and $p \in S$, there always exists a neighborhood V of p in S such that V is the graph of a differentiable function which has one of the following three forms[29]:

$$z = h(x, y) \tag{4.34}$$

$$y = s(x, z) \tag{4.35}$$

$$x = t(y, z) \tag{4.36}$$

Hence, given a point p of a surface S , we can choose the coordinate axis of \mathbb{R}^3 such that the origin O of the coordinates is at p and the z axis is directed along the outward normal of S at p (thus, the xy plane agrees with the tangent plane $T_p(S)$). It follows that a neighborhood of p in S can be represented in the form $z = h(x, y)$, $(x, y) \in U \subset \mathbb{R}^2$, where U is an open set and h is a differentiable function, with $h(0, 0) = 0$, $h_x(0, 0) = 0$, $h_y(0, 0) = 0$.

In this case, the local surface is parameterized by

$$\mathbf{x}(u, v) = (u, v, h(u, v)), (u, v) \in U \quad (4.37)$$

where $u = x$, $v = y$. It can be shown that

$$\mathbf{x}_u = (1, 0, h_u) \quad (4.38)$$

$$\mathbf{x}_v = (0, 1, h_v) \quad (4.39)$$

$$\mathbf{x}_{uu} = (0, 0, h_{uu}) \quad (4.40)$$

$$\mathbf{x}_{uv} = (0, 0, h_{uv}) \quad (4.41)$$

$$\mathbf{x}_{vv} = (0, 0, h_{vv}) \quad (4.42)$$

Thus, the normal vector at (x, y) is

$$N(x, y) = \frac{(-h_x, -h_y, 1)}{(1 + h_x^2 + h_y^2)^{1/2}} \quad (4.43)$$

From the above expressions, it is easy to obtain the coefficients of the first and second

fundamental forms as

$$E(x, y) = 1 + h_x^2 \tag{4.44}$$

$$F(x, y) = h_x h_y \tag{4.45}$$

$$G(x, y) = 1 + h_y^2 \tag{4.46}$$

$$e(x, y) = \frac{h_{xx}}{(1 + h_x^2 + h_y^2)^{1/2}} \tag{4.47}$$

$$f(x, y) = \frac{h_{xy}}{(1 + h_x^2 + h_y^2)^{1/2}} \tag{4.48}$$

$$g(x, y) = \frac{h_{yy}}{(1 + h_x^2 + h_y^2)^{1/2}} \tag{4.49}$$

Hence, the curvatures of the surface can be derived from the Weingarten mapping matrix computed from these coefficients.

4.3.2.2 Multi-Order Local Surface Fitting

For the triangulated discrete surfaces that we are dealing with, regular continuous surfaces are approximated by Delaunay surface triangulations of sets of points in \mathbb{R}^3 . To be able to analyze the local shape properties of point p in a neighborhood of a triangulated surface, polynomials are usually used to approximate this neighborhood, often in the form of the graph of a differentiable function.

We begin the process by defining a local surface patch at point p as a discrete surface triangulation consisting of the point itself, *the fiducial point*, and a set of neighboring 3D points of p . Two questions arise for constructing a smooth local surface for these points:

1. How do we define the neighborhood of the fiducial point?

2. How do we define the parameterization of the surface patch?

The second question has an easier answer, that is we want this local surface to be represented by the graph of a differentiable function. For this reason, we choose a local coordinate system with its origin at the fiducial point p , and the z axis in the normal direction of the surface S in p . The estimated normal at p is determined as the weighted average of the normals of all the Delaunay facets which have p as one of their Delaunay vertices. The weighting coefficient for each facet is its normalized area. To make the normal directions consistent among all the points on the entire surface, we would like to have the *outward* normals. Since the xy plane agrees with the tangent plane $T_p(S)$, we may choose any pair of orthogonal directions as the x and y axes. After this local reference coordinate system is established, the local surface can be represented in the graph form $z = h(x, y)$, which is a one-to-one $\mathbb{R}^2 \rightarrow \mathbb{R}$ mapping if the neighborhood of p is well chosen.

Traditionally, the neighborhood of point p is defined as a sphere centered at p with a radius R in \mathbb{R}^3 , and all the points that fall inside this sphere constitute the local surface point set [4, 109]. However, depending on the value of R and the roughness and folding of the local surface, $z = h(x, y)$ may not be a unique function. Figure 4.6 shows the possible multiple mapping problem in a 2D representation. In this example, the surface patch defined from the neighborhood folds around p , and causes the graph function to have multiple mappings in \mathbb{R}^2 for one value in \mathbb{R} . And since this nearest Euclidean distance based method does not take account of the known connectivity from triangulation, it may also include points which are disconnected from the valid surface points and should not be in the neighborhood of p at all (they are parts of other local surface patches), such as the case shown in Figure 4.7. Of course, these two problems can be avoided by choosing

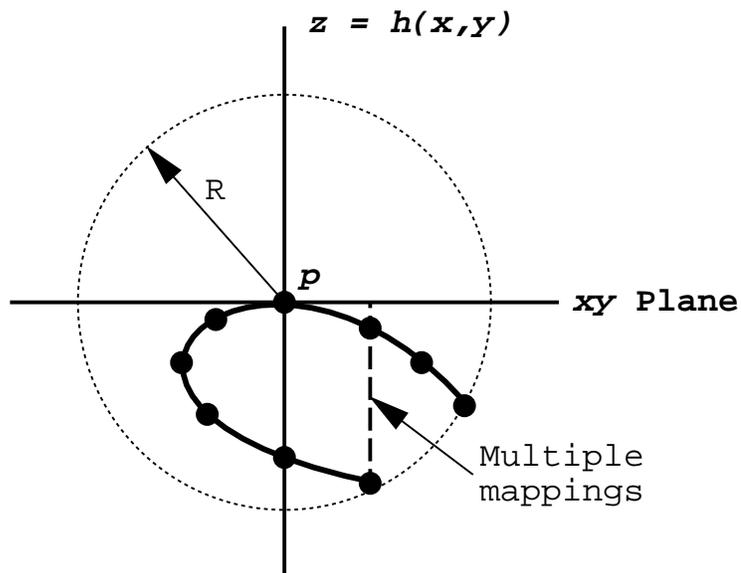


Figure 4.6: Possible multiple mappings in the graph representation of surface patch. The surface is the solid line, with the surface points the filled dots (they are inside the neighborhood sphere). The local reference frame has p as origin, the normal direction at p as z axis, and the tangent plane as xy plane. Obviously, the graph function $z = h(x, y)$ is not a unique mapping.

small radius R . However, the determination of the value for R is a difficult task without the knowledge about the geometry of the underlying surface, which is exactly what we are trying to estimate.

In order to choose a neighborhood of p which is unique (no folding) and local (no non-neighboring points), the natural neighbor relationship between surface points is needed to define a more precise and flexible neighborhood. First of all, if we choose only the 1-order natural neighbors as the neighborhood of p , the graph function will almost always have a unique mapping (only when the point distribution is extremely

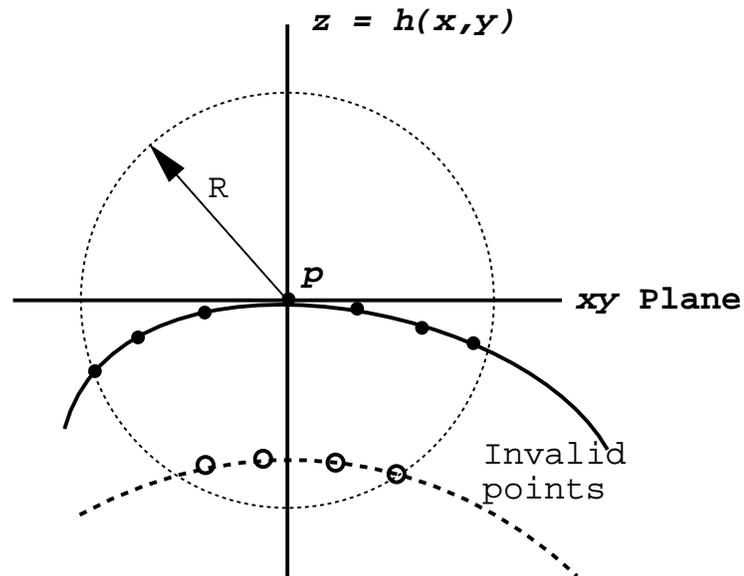


Figure 4.7: Invalid neighborhood points. The valid surface points are the filled dots, while the unfilled dots are invalid points even though they are inside the neighborhood sphere. From the connectivity provided by triangulation, the unfilled dots are disconnected from the valid surface points, and belong to another surface patch.

ill-conditioned will the Delaunay facets fold to each other with respect to the normal direction). If the local surface is well-behaved, which means that the orientation of one facet does not change dramatically from those of its adjacent facets, higher orders of natural neighbor points can also be included in the neighborhood of p . Depending on how many orders of natural neighbor points are included in the neighborhood, the local surface can be considered to have *multi-scale* details. Secondly, the natural connectivity ensures that only valid neighbor points will be chosen, since each of these points is connected to at least one other chosen point. This is true even if higher order natural neighbor points are included in the neighborhood.

Since the Weingarten mapping matrix only depends on the first and second derivatives of the graph function $h(x, y)$, biquadratic functions are all we need to estimate the curvatures of the local surface, assuming that the local surfaces are well behaved such that a biquadratic polynomial can approximate a patch sufficiently closely. The neighborhood points are embedded in the local coordinate system, which has p as the origin, the outward normal as the z axis, and two tangent directions as x and y axes. The estimate of the biquadratic graph function involves finding the five coefficients of the polynomial[4, 109]:

$$z = h(x, y) = a_1x^2 + a_2xy + a_3y^2 + a_4x + a_5y \quad (4.50)$$

If there are at least four neighboring points, say $n - 1$ ($n \geq 5$) points, the least-square estimate of the five coefficients is evident. In matrix form, the coefficient vector \vec{a} which minimizes the fit error is:

$$\vec{a} = (A^T A)^{-1} A^T \vec{Z} \quad (4.51)$$

where A is a $n \times 5$ matrix with row i being $[x_i^2 \ x_i y_i \ y_i^2 \ x_i \ y_i]$, \vec{Z} is a column vector of the z_i values. Once the coefficient vectors are found, computing the actual differential properties on the fiducial point is straightforward.

The graph function estimation and curvature estimation may also follow a multi-scale procedure, depending on how many orders of natural neighbor points are included in the neighborhood. We denote the k -scale graph function as the one estimated from the neighborhood which includes 0-order, ..., k -order natural neighbor points. If certain prior information is available, we could use a lower scale (small k) graph function to

characterize highly curved surfaces to avoid the smoothing effect, and use a higher scale (large k) graph function to characterize flat surfaces to alleviate the noise effect. The consistency of the estimated shape characteristics through different scales, such as from higher to lower, may also indicate the goodness and reliability of predominant shape features (corners, ridge lines, etc) in the surface.

Figure 4.8 shows the Gaussian curvature, mean curvature, the two principal curvatures, and the shape index maps of an endocardial surface derived from 1-scale, 2-scale and 3-scale graph functions. Similar maps of an epicardial surface are shown in Figure 4.9. It is clear that the shape patterns are generally consistent across different scales. The curvature maps from lower scale graph functions (small neighborhood) appear noisier than curvature maps from higher scale graph functions (large neighborhood), while the latter ones may over-smooth the surface shape features.

4.4 Surface Motion Field

The movement over the cardiac cycle of a set of LV surface points is determined by following local surface shape between successive surface frames. In the first step of the tracking algorithm, endocardial and epicardial surfaces at one given time instant are used as reference surfaces and are subsampled, creating a sparser set of points (the later shown experimental results are obtained using ten percent sampling rate). The reason to use this sparse set of points for initial match is to avoid cross-overs between local matches. If the search windows are well chosen (discussed later in the section), the sparse point set usually does not create the cross-over problem. Efforts have been made to choose more points from highly curved regions and fewer points from flat regions by thresholding the curvature values. Under the assumption that the LV surface deforms as little as possible

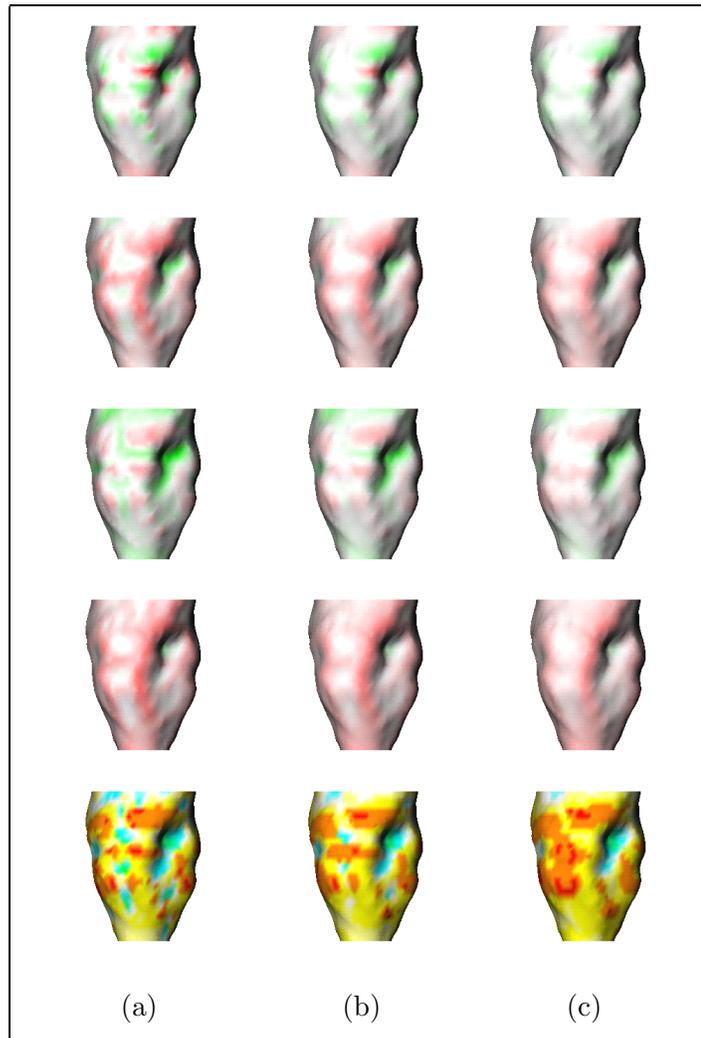


Figure 4.8: Shape maps of an endocardial surface derived from multi-scale graph functions. Column (a) is for the 1-scale, column (b) is for the 2-scale, and column (c) is for the 3-scale graph functions. From top to bottom row: Gaussian curvature, mean curvature, maximum principal curvature, minimum principal curvature, and shape index maps. For the curvature maps, the values from negative to positive are represented by a continuous color spectrum from red to green. The value-to-color scale is the same for all three maps within each row, but it is different between different curvatures. The shape index maps use the color scale shown in Figure 4.5.

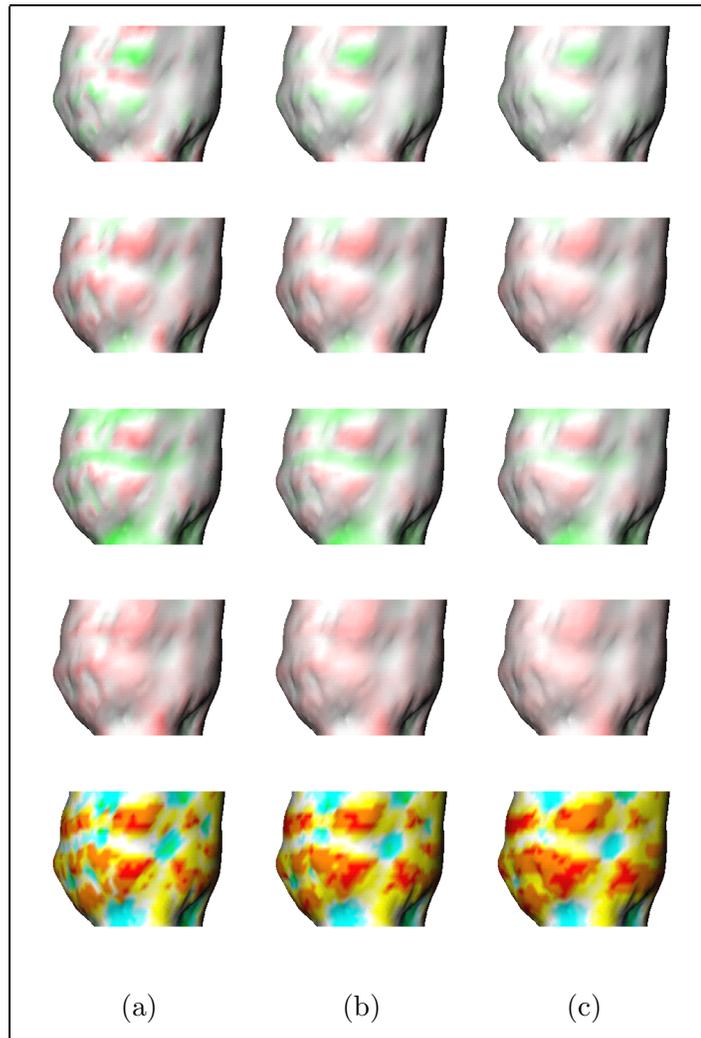


Figure 4.9: Shape maps of an epicardial surface derived from multi-scale graph functions. Column (a) is for the 1-scale, column (b) is for the 2-scale, and column (c) is for the 3-scale graph functions. From top to bottom row: Gaussian curvature, mean curvature, maximum principal curvature, minimum principal curvature, and shape index maps. For the curvature maps, the values from negative to positive are represented by a continuous color spectrum from red to green. The value-to-color scale is the same for all three maps within each row, but it is different between different curvatures. The shape index maps use the color scale shown in Figure 4.5.

between small time intervals, the subsampled surface points are matched and followed over the LV surface sequences under a minimum bending energy model. These initially calculated 3D displacement vectors can be noisy due to inherent data noise and matching uncertainty. Match-confidence-weighted regularization functionals are utilized to help limit these problems and to compute the dense field motion for all the surface points.

4.4.1 Thin Plate Bending Model

Local surface patches on the LV are modeled as thin flexible plates, loosely constrained to deform in a predetermined fashion which will be defined in the next section. The potential energy of an ideal thin flexible plate of elastic material is a measure of the strain energy of the deformation from its equilibrium state, a plane. It is a function of the two principal curvatures of the plate, and is invariant to 3D rotation and translation[25]:

$$\epsilon = A \frac{\kappa_1^2 + \kappa_2^2}{2} \tag{4.52}$$

where A is a material related constant, and κ_1 and κ_2 are the two principal curvatures of the surface patch of interest. Note that even though the principal curvatures have associated directions, only their magnitudes are relevant in the potential energy metric. Also, the potential energy function does not differentiate the different types of surfaces classified by the shape index function.

Figure 4.10 shows the potential energy maps and the shape index maps of two ellipsoidal surfaces estimated from the shape characterization procedure discussed in Section 4.3, one with axis lengths 10, 10, 20, and the other one with 5, 5, 10. Even though the potential energy is not invariant to scale (the smaller ellipsoid has larger potential energy), their shape index maps are virtually the same. The potential energy maps of an

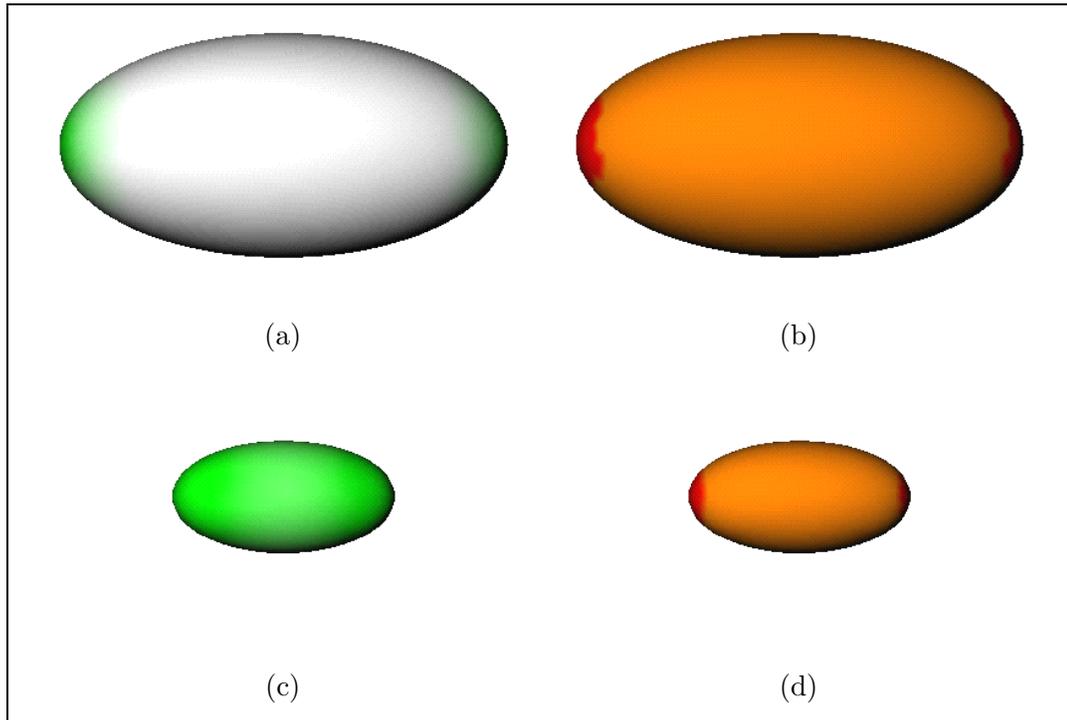


Figure 4.10: Potential energy and shape index maps of ellipsoidal surfaces. (a) and (b): potential energy map (a) and shape index map (b) of an ellipsoidal surface with axis lengths 10, 10, 20; (c) and (d): potential energy map (c) and shape index map (d) of an ellipsoidal surface with axis lengths 5, 5, 10. The potential energy maps have the same color scale: green for larger values, white for smaller values.

endocardial surface over the entire cardiac cycle (sixteen temporal sampling frames) are shown in Figure 4.11, and the maps of an epicardial surface are shown in Figure 4.12. In these maps, most of the high potential energy features run through several temporal frames or even the entire sequence. This consistency of shape feature (the potential energy) over time provides the basis for visually matching surface points based upon shape cues (in this case, the potential energy).

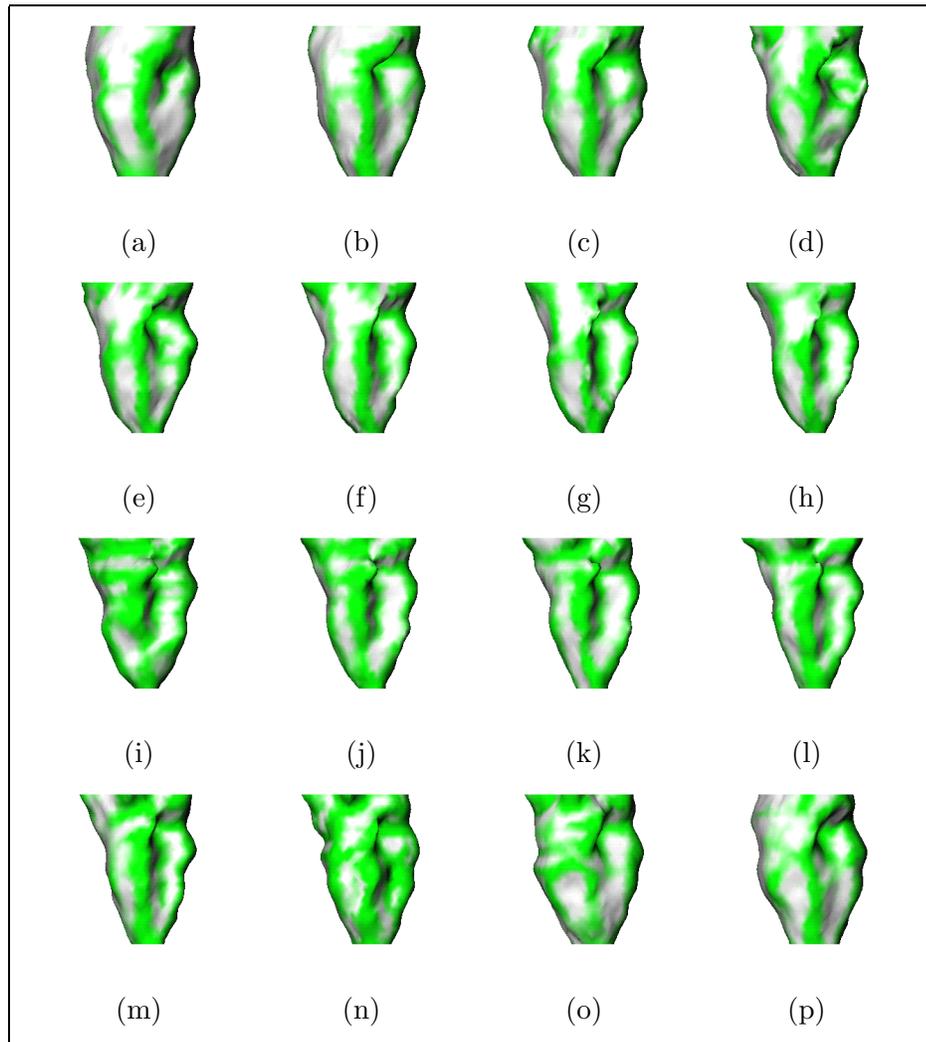


Figure 4.11: Potential energy maps of an endocardial surface over the entire cardiac cycle. The temporal sequence of the maps runs from top to bottom, left to right. The potential energy maps have the same color scale: green for larger values, white for smaller values.

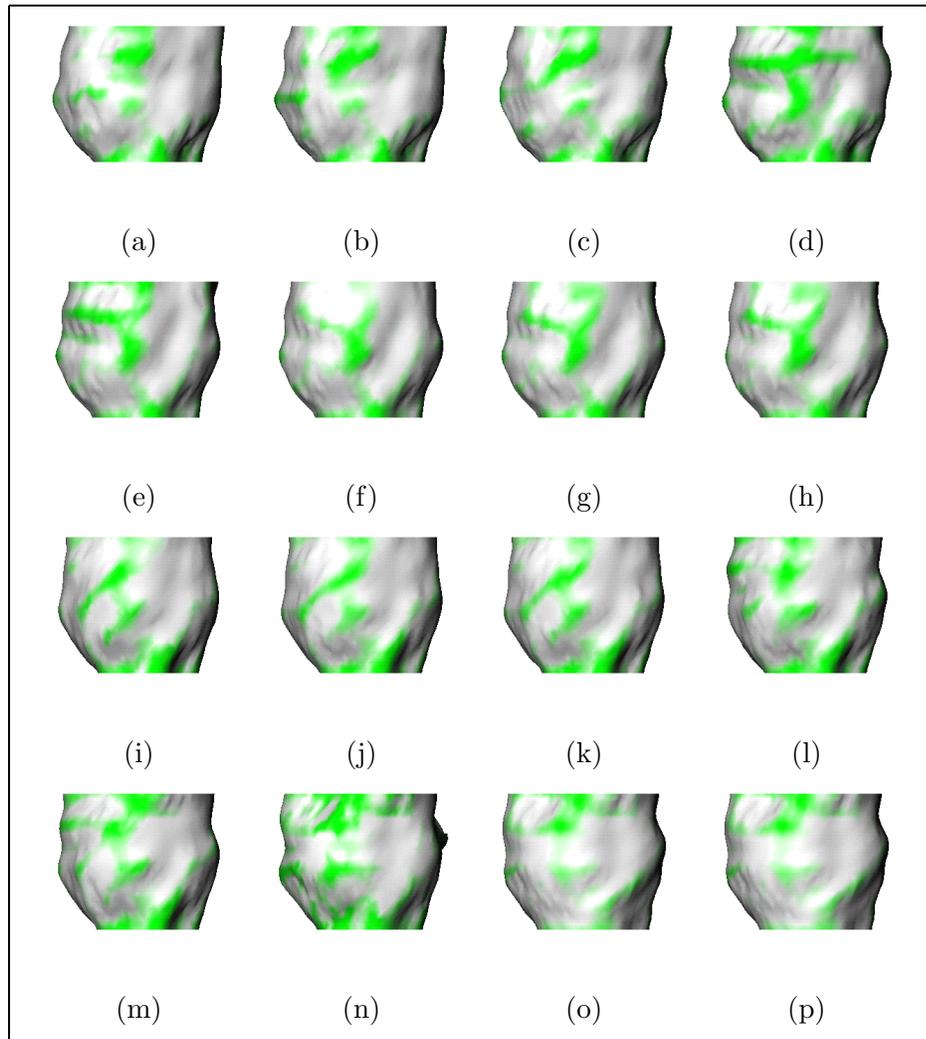


Figure 4.12: Potential energy maps of an epicardial surface over the entire cardiac cycle. The temporal sequence of the maps runs from top to bottom, left to right. The potential energy maps have the same color scale as that of Figure 4.11: green for larger values, white for smaller values.

We modify the idea of surface potential energy slightly to define the bending energy required to bend a curved plate or surface patch to a newly deformed state as:

$$\epsilon_{be} = A \frac{(\kappa_1 - \bar{\kappa}_1)^2 + (\kappa_2 - \bar{\kappa}_2)^2}{2} \quad (4.53)$$

The principal curvatures of the initial surface patch are κ_1 and κ_2 , while the same parameters of the deformed surface patch are $\bar{\kappa}_1$ and $\bar{\kappa}_2$. This equation assumes that the corresponding points on the surface patches are known, and arrives at a numerical value measuring the energy required to deform the initial surface patch to achieve a deformed shape. Obviously, if the surface patch undergoes rigid motion, there is no bending energy required for the movement since the shape of the patch does not change. Only non-rigid deformation requires bending energy which measures a form strain energy.

Another possible definition of bending energy is suggested in [1]:

$$\begin{aligned} \epsilon'_{be} &= \epsilon - \bar{\epsilon} \\ &= A \frac{\kappa_1^2 + \kappa_2^2}{2} - A \frac{\bar{\kappa}_1^2 + \bar{\kappa}_2^2}{2} \end{aligned} \quad (4.54)$$

The reason not to use this definition is that it cannot detect the large deformation where the principal curvatures change their signs but not their magnitudes. In this case, even though deformation happens, the value of this bending energy ϵ'_{be} is zero, which indicates no deformation.

4.4.2 Initial Surface Point Match

The bending energy of Equation 4.53 measures the required energy to deform a surface patch from one state to another. However, it is the goal of the motion tracking algorithm to find the point correspondences between temporally successive surfaces in the sequence. We will use the bending energy as the matching criterion to obtain the point correspondences. The essence of this matching criterion is that a surface patch deforms as little as possible between successive temporal frames, and the deformation can be fully characterized by the bending energy.

The motion of the surface patch surrounding each sample point consists of two distinctive parts: the rigid motion (global and local) and the non-rigid deformation. Since rigid motion does not change the shape properties of a surface patch, point correspondences with no deformation can be found by matching between surface patches requiring no bending energy. Hence, the bending energy measure can be used as the matching criteria for rigid motion. For the non-rigid deformation, we make the assumption that the surface patch is constrained to deform in a fashion such that the extent of the deformation is determined solely by the required bending energy. This assumption makes it reasonable to use the bending energy measure as the matching criteria for the non-rigid deformation.

Under the assumption that the surface patch surrounding each sample point deforms only slightly and locally within a small time interval, we construct a physically-plausible search region on the second surface at time t_{i+1} for each sampled point on the first surface at time t_i . For any point at time t_i which is a cup, trough, rut, ridge, dome, or cap point (defined by the shape index function), a search region W is defined as the area surrounding the intersection of normal vector of the point $\mathbf{x}(\mathbf{u})$ at t_i with the surface

at t_{i+1} . For any point at time t_i which is a saddle rut, saddle, or saddle ridge point, a search region W is defined as the area surrounding the nearest surface point at t_{i+1} to the point $\mathbf{x}(\mathbf{u})$ at t_i . W usually consists of the natural neighbor points of the intersected point, often the same orders of points as the surface patch fitting process, and the points inside W constitute a point set $\{\mathbf{x}_{W,i}, i = 0, \dots, N-1\}$. Bending energy measures between the surface patch surrounding point $\mathbf{x}(\mathbf{u})$ and surface patches surrounding points $\mathbf{x}_{W,i}$ are computed as:

$$\epsilon_{be}(\mathbf{x}, \mathbf{x}_{W,i}) = A \frac{(\kappa_1(\mathbf{x}) - \kappa_1(\mathbf{x}_{W,i}))^2 + (\kappa_2(\mathbf{x}) - \kappa_2(\mathbf{x}_{W,i}))^2}{2} \quad (4.55)$$

The point $\bar{\mathbf{x}}$ within the search window W that has the *minimum* corresponding bending energy is chosen as the point corresponding to point \mathbf{x} . The assumption for making this choice is that the surface patch deforms as little as possible in the short temporal interval, following the minimal bending energy criterion. Repeating the matching process for all the subsampled points of the surface at t_i , the results yield a set of sparse shape-based, best-matched motion vectors $\mathbf{d}_{init}(\mathbf{u}, t_i) = \bar{\mathbf{x}} - \mathbf{x}$ for pairs of surfaces derived from 3D image sequences.

An example of bending energy-based matching of an endocardial surface point is shown in Figure 4.13 and Figure 4.14. The potential energy map at beginning time t_0 (end diastole (ED)) is shown in Figure 4.13a, and the subsequent potential energy maps at t_0+2 , t_0+4 , and t_0+6 (end systole (ES)) are shown in Figure 4.13b, c, d. The displacement vectors of the point (in blue) are superimposed onto the potential energy maps of the endocardial surface. The complete trajectory of the point over the cardiac cycle (sixteen temporal frames) superimposed onto the endocardial surface at ES is shown in Figure

4.14a as an overview, and in Figure 4.14b as a more detailed blowup. Evidently, the point moves upwards during the contraction stage (ED to ES) and it moves downwards during the expansion stage (ES to ED). This out-of-plane motion demonstrates one important reason to use 3D images for LV motion analysis. It should be noted that the trajectory of this point is almost a complete loop, meaning the point moves back to where it begins. However, there are no periodic motion constraints imposed on the point correspondence tracking over the cardiac cycle, hence this cannot be guaranteed. In most cases, surface points usually move back near where they begin but not to the exact beginning positions.

The bending energy measures for all the points inside each search region are also recorded as the basis to measure the *goodness* and *uniqueness* of the matching choices. The value of the minimum bending energy in the search region between the matched points indicates the goodness of the match. This is because the matching criteria is based on the notion that the smaller the deformation between matching surface patches, the better the match. Denote this value as m_g , we have the following measure for matching goodness:

$$m_g(\mathbf{x}) = \epsilon_{be}(\mathbf{x}, \bar{\mathbf{x}}) = A \frac{(\kappa_1(\mathbf{x}) - \kappa_1(\bar{\mathbf{x}}))^2 + (\kappa_2(\mathbf{x}) - \kappa_2(\bar{\mathbf{x}}))^2}{2} \quad (4.56)$$

On the other hand, it is desirable that the chosen matching point is a unique choice among the candidate points within the search window. Ideally, the bending energy value of the chosen point should be an outlier (much smaller value) compared to the values of the rest of the points (much larger values). If we denote the mean values of the bending energy measures of all the points inside window W except the chosen point as $\bar{\epsilon}_{be}$ and

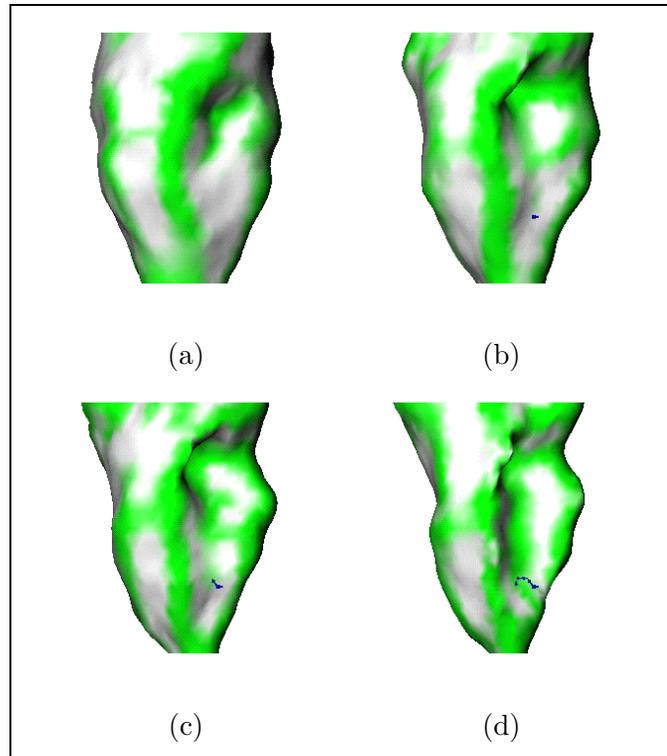


Figure 4.13: Trajectory of one endocardial point superimposed onto the potential energy map of an endocardial surface from end diastole to end systole. (a): at beginning time t_0 (ED); (b): at $t_0 + 2$; (c): at $t_0 + 4$; (d): at $t_0 + 6$ (ES). The displacement vectors of the point are shown in blue. The potential energy maps have same color scale as that of Figure 4.11: green for larger values, white for smaller values.

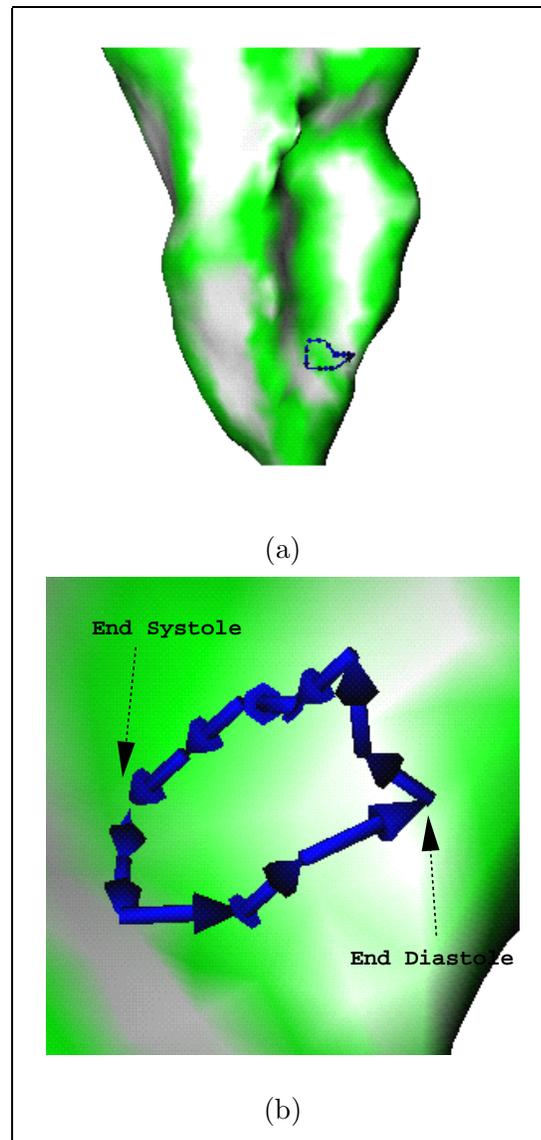


Figure 4.14: Complete trajectory of one endocardial point over the cardiac cycle (sixteen temporal frames), superimposed onto the potential energy maps of the endocardial surface at end systole. (a): an overview ; (b): a blowup of the trajectory. The potential energy maps have same color scale as that of Figure 4.11: green for larger values, white for smaller values.

the standard deviation as σ_{be} , we define the uniqueness measure as:

$$m_u(\mathbf{x}) = \frac{\epsilon_{be}(\mathbf{x}, \bar{\mathbf{x}})}{\bar{\epsilon}_{be} - \sigma_{be}} \quad (4.57)$$

This uniqueness measure means that if the bending energy of the chosen point is small compared to some smaller value (mean minus standard deviation) of the remaining bending energy measures, it is quite unique and reliable, otherwise it is not. Obviously for both goodness and unique measures, the smaller the values are the more reliable the match. Combining these two measures together, we arrive at one *confidence measure* for the matched point $\bar{\mathbf{x}}$ of point \mathbf{x} :

$$c(\mathbf{x}) = \frac{1}{k_{1,g} + k_{2,g}m_g(\mathbf{x})} \frac{1}{k_{1,u} + k_{2,u}m_u(\mathbf{x})} \quad (4.58)$$

where $k_{1,g}$, $k_{2,g}$, $k_{1,u}$, and $k_{2,u}$ are scaling constants for normalizing purposes. The confidence measures for all the surface matches are normalized to the range of 0 to 1. The matches with the highest confidence have the confidence measure value of 1, and the matches with the lowest confidence have the confidence measure value of 0. In the shape-based work on 2D contour matching[61, 92], a similar goodness measure is used. However, their uniqueness measure is based upon the assumption that the matching metric (the bending energy) is spatially distributed as Gaussian, centered at the matched point. We do not believe this is the situation in our case.

4.4.3 Optimal Dense Motion Field

A smoothing-interpolation process is needed for accurate estimation of the dense motion field of the surfaces. One reason is that even though surface motion of biological origin

often varies smoothly in direction and magnitude over space, the initial surface matching results are obtained by purely local processes, with no smoothness constraint between the motion of neighboring points enforced. Another reason is that because only the correspondences of a set of subsampled points are found, some sort of interpolation is needed to compute the dense motion field for every point on the surface. Under the assumption that the displacement fields of the LV surfaces are sufficiently smooth and that any changes of direction and magnitude take place in a gradual manner over space, a regularizing smoothing functional which includes both an initial estimate adherence term and a local smoothness term is constructed. Since the reliability of the initial correspondences vary based on their confidence measures, it should be clear that good, unique matches from the initial bending energy matching process should be preserved, while ambiguous matches should be smoothed over by their neighboring matches. The confidence measures from the initial match are used here as smoothing coefficients.

In the continuous domain, the regularizing smoothing function is constructed as

$$\mathbf{d}^*(\mathbf{u}) = \arg \min_{\mathbf{d}} \int \int_S \{c(\mathbf{u})[\mathbf{d}(\mathbf{u}) - \mathbf{d}_{init}(\mathbf{u})]^2 + (\frac{\partial \mathbf{d}(\mathbf{u})}{\partial \mathbf{u}})^2\} d\mathbf{u} \quad (4.59)$$

Here, S is the surface space, \mathbf{u} is the parameter vector representing a point in S , \mathbf{d}_{init} and \mathbf{d}^* are the initial and final displacement vectors, respectively, and $c(\mathbf{u})$ is the confidence measure.

Since we are dealing with a discrete polyhedral surface, the derivative of the displacement vector can be approximated by the weighted average finite differences per-

formed on the neighboring points:

$$\frac{\partial \mathbf{d}(\mathbf{u})}{\partial \mathbf{u}} = \sum_{i=0}^{N-1} \omega_i \{\mathbf{d}(\mathbf{u}) - \mathbf{d}(\mathbf{u}_i)\}, \quad i = 0, \dots, N-1 \quad (4.60)$$

$$\sum_{i=0}^{N-1} \omega_i = 1 \quad (4.61)$$

where $\{\mathbf{d}(\mathbf{u}_i)\}$ is the displacement vector set associated with the 1-order natural neighbor points, and $\{\omega_i\}$ is the natural neighbor weighting set associated with these neighbor points. Furthermore, the discrete version of the smoothing function can be conveniently posed as a series of linear equations, and can be solved iteratively:

$$\mathbf{d}(\mathbf{u})_{new} = (1 - c'(\mathbf{u}))\mathbf{d}(\mathbf{u})_{old} + c'(\mathbf{u}) \sum_{i=0}^{N-1} \omega_i \mathbf{d}(\mathbf{u}_i) \quad (4.62)$$

$$c'(\mathbf{u}) = \frac{1}{c(\mathbf{u}) + 1} \quad (4.63)$$

In the same spirit of the two-stage, non-shrinkage Gaussian smoothing of the triangulated surface described in Section 4.2, the regularization process can also be solved by a two-stage, non-shrinkage iterative procedure:

$$\mathbf{d}(\mathbf{u})_{new1} = (1 - c'_1(\mathbf{u}))\mathbf{d}(\mathbf{u})_{old} + c'_1(\mathbf{u}) \sum_{i=0}^{N-1} \omega_i \mathbf{d}(\mathbf{u}_i) \quad (4.64)$$

$$\mathbf{d}(\mathbf{u})_{new2} = (1 - c'_2(\mathbf{u}))\mathbf{d}(\mathbf{u})_{new1} + c'_2(\mathbf{u}) \sum_{i=0}^{N-1} \omega_i \mathbf{d}(\mathbf{u}_i) \quad (4.65)$$

The solution of this system of linear equations will yield a dense set of smoothed motion vectors that adhere to the reliable initial shape-based matches, yet vary smoothly on the surface space. Repeating the process for all the LV wall surfaces and assembling the

vectors end-to-end, we have a complete set of motion flow fields between pairs of surfaces during the cardiac cycle.

Figure 4.15 shows the dense endocardial displacement vector field from ED to ES, subsampled for visualization purposes. The trajectories are shown against the rendered endocardial surface at ES. Examples of the bending energy needed to deform surfaces from one state to another are given in Figure 4.16, with the endocardial surface on the right and the epicardial surface on the left. The top row shows the potential energy maps of the surfaces at their initial states, the middle row shows the potential energy maps at the deformed states, while the needed bending energy (the difference of potential energy between the original and deformation states) maps between matched surfaces are shown in the bottom row. Finally, the needed bending energy of a normal endocardial surface over the entire cardiac cycle are shown in Figure 4.17, with the similar maps for a normal epicardial surface shown in Figure 4.18. It is obvious from the figures that the endocardial surface has large bending energy values at some areas during some stages of the cardiac cycle, while the epicardial surface usually does not have large bending energy values. This is because the endocardial surface generally deforms more under normal conditions than the epicardial surface.

4.5 Experiments

Using the methodology described in the previous sections, experiments with the shape-based boundary motion tracking approach have been conducted. The results reported here are obtained from experiments using eight sets of canine magnetic resonance imaging (MRI) data under both baseline and post-infarction conditions, and five sets of canine Dynamic Spatial Reconstructor(DSR) data. The trajectories of surface points which

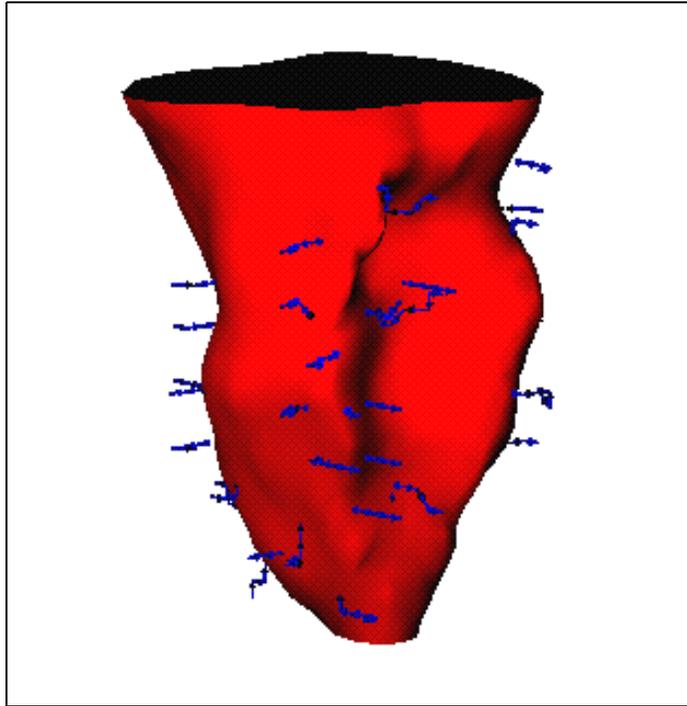


Figure 4.15: Dense (subsamped for visualization purposes) endocardial displacement vector field from ED to ES (MRI). The trajectory arrows are shown against the rendered endocardial surface at ES.

are near implanted imaging-opaque markers are compared to those of the markers for validation purposes. The changes of motion magnitudes between baseline data and post-infarct data are quantified to assess myocardial viability, and are compared to cardiac perfusion data (SPECT images and TTC-stained post-mortem optical photos).

The intent of the algorithm testing and evaluation processes is aimed at obtaining the most accurate and reproducible measures for characterizing *in vivo* measures that best predict *post mortem* myocardial injury. The first step has to do with validating the algorithm-derived motion versus the implanted-marker-derived motion (using both MRI

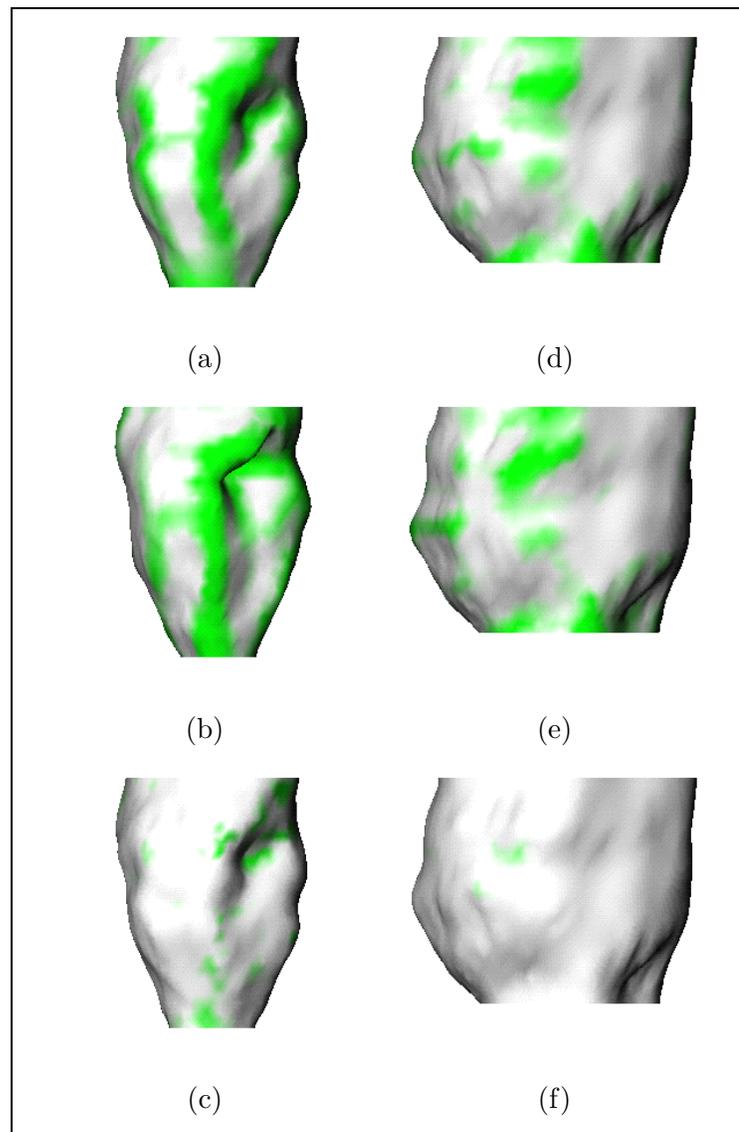


Figure 4.16: Bending energy maps between matched surfaces. The endocardial surfaces are on the left and the epicardial surfaces are on the right. Top row: potential energy maps of the surfaces at their initial states; Middle row: potential energy maps of the surfaces at their deformed states; Bottom row: needed bending energy maps between matched surfaces. All the energy maps have the same color scale as that of Figure 4.11: green for larger values, white for smaller values.

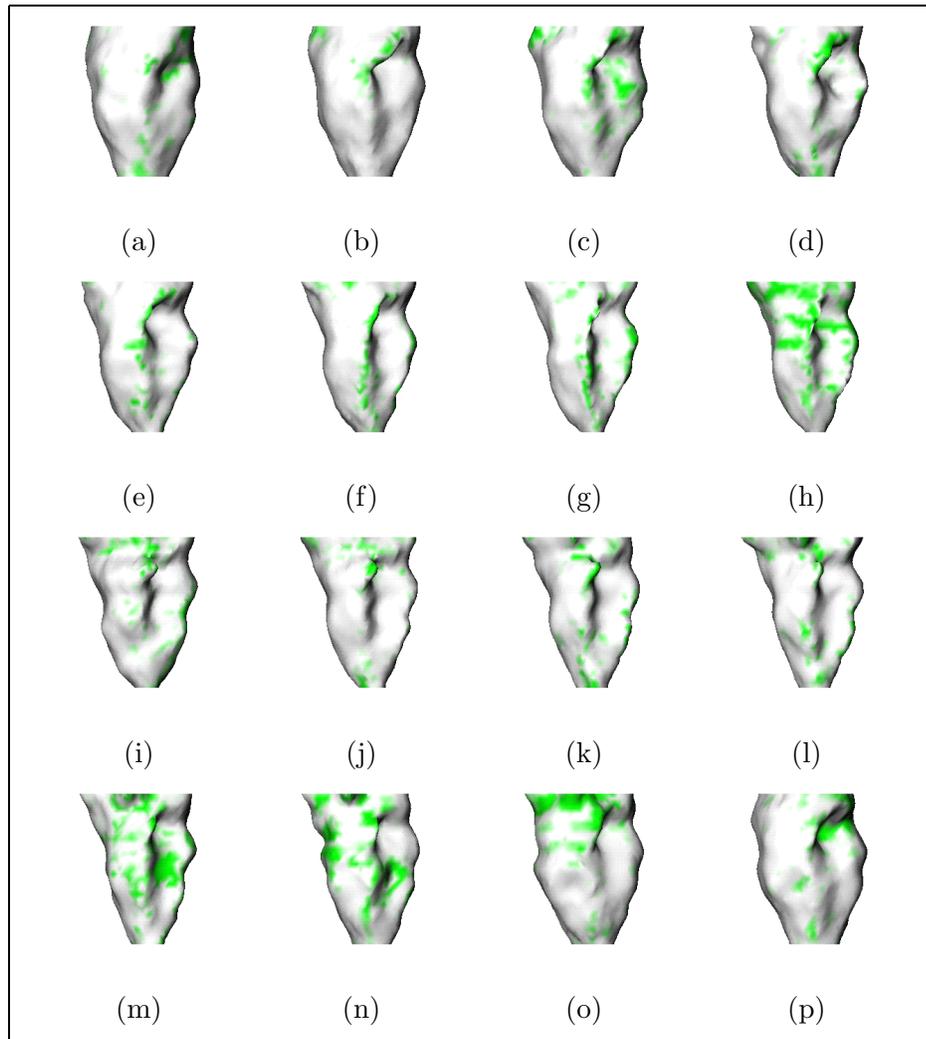


Figure 4.17: Bending energy maps of an endocardial surface over the entire cardiac cycle. The temporal sequence of the maps runs from top to bottom, left to right. The bending energy maps have the same color scale as that of Figure 4.11: green for larger values, white for smaller values.

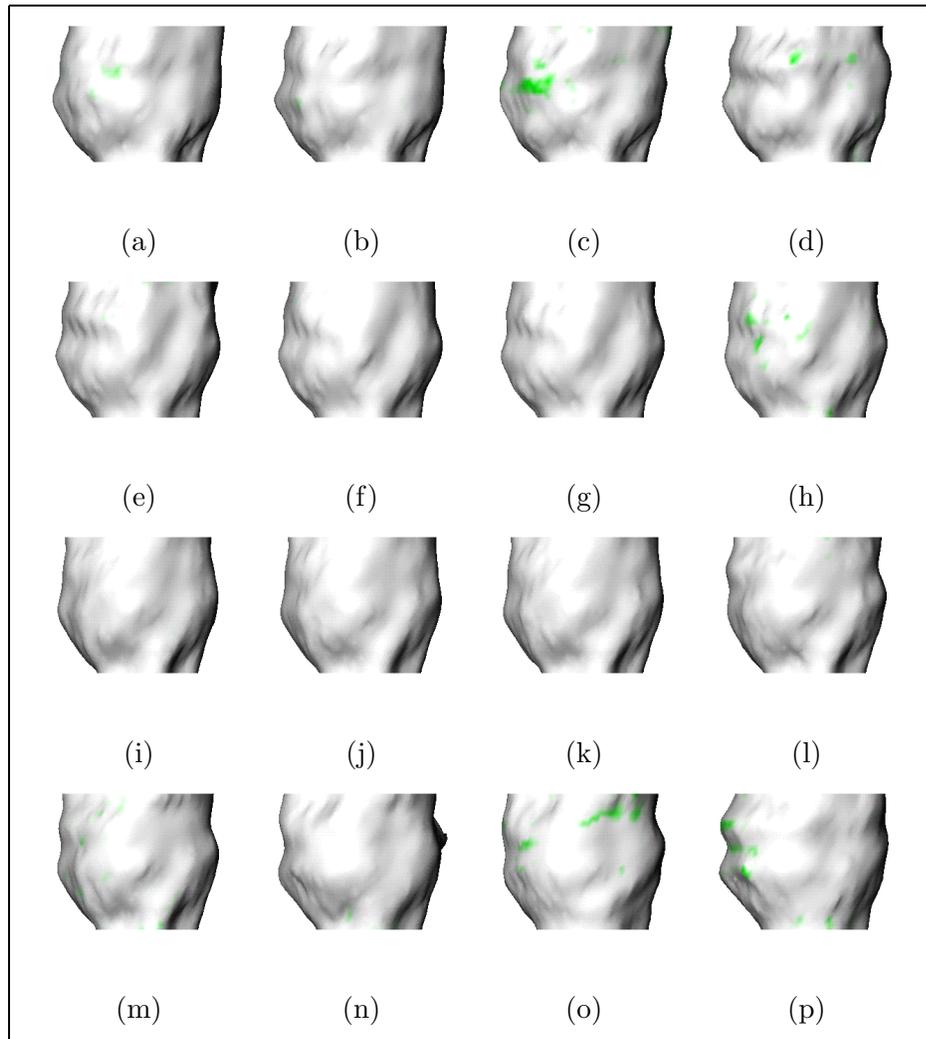


Figure 4.18: Bending energy maps of an epicardial surface over the entire cardiac cycle. The temporal sequence of the maps runs from top to bottom, left to right. The bending energy maps have the same color scale as that of Figure 4.11: green for larger values, white for smaller values.

and DSR data). The second step is to evaluate how well the algorithm-derived measures predict *post mortem* myocardial injury (MRI data only).

4.5.1 Magnetic Resonance Imaging Data

Since the use of implanted imaging-opaque markers will permit us to establish the a standard against which the validity of our non-invasive motion analysis algorithms can be evaluated, as well as permit us to study the efficacy of using image-derived *in vivo* measures of function for predicting regional myocardial viability, implanted marker experiments[118] were performed in fasting anesthetized, open chest, adult mongrel dogs by Dr. Albert Sinusas and his research group at Yale medical school.

The canine heart was exposed through a thoracotomy. The proximal portion of the left anterior descending coronary artery was isolated for placement of a snare occluder. Endocardial and epicardial pairs of markers were implanted for the validation of our non-invasive image analysis algorithms. They are loosely tethered, paired combinations of small copper beads (which show up as *dark* in the images) at the endocardial wall and small plexiglass capsules filled with a 200:1 mixture of water to Gd-DTPA at the epicardial wall (which show up as *bright* in the images). The markers within each pair were attached by an elastic string, which maintained the endocardial and epicardial markers on their respective surfaces during the entire cardiac cycle without restricting myocardial thickening. Marker pairs were placed in four locations on the canine heart: 1) central infarct zone, 2) normal zone, 3) peri-infarct border zone, and 4) the site of coronary occlusion. A picture of the MRI markers is shown in the top of Figure 4.19, with the copper bead on the left and the capsule on the right. The lower left diagram illustrates the procedure to insert the endocardial marker into the myocardium through a needle, and the lower right diagram shows the relative positions of the markers on the myocardium.

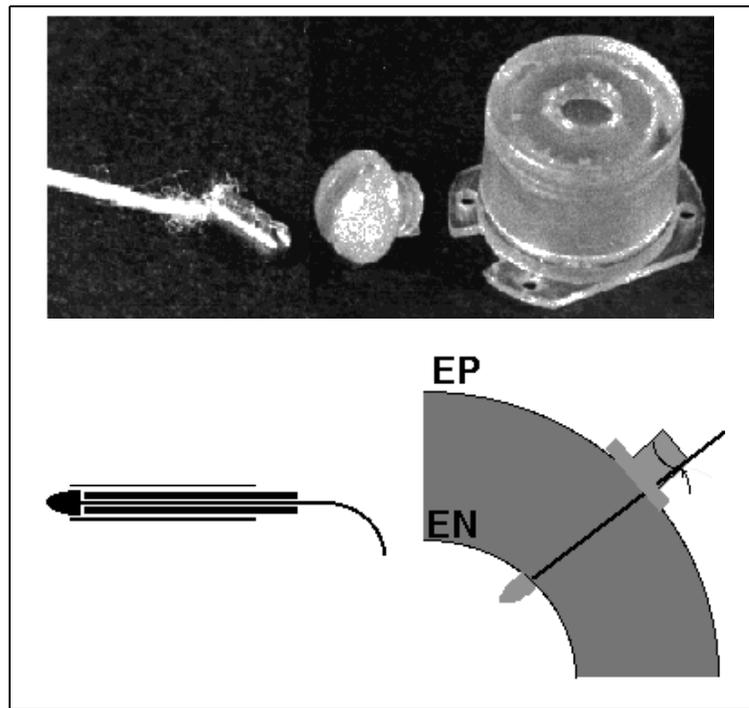


Figure 4.19: MRI markers and their relative positions. The upper picture shows the endocardial marker (copper bead on the left) and the epicardial marker (capsule on the right). The lower left diagram illustrates the procedure to insert the endocardial marker into the myocardium through a needle, and the lower right diagram shows the relative positions of the markers on the myocardium.

An example of an MRI image which contains both the endocardial and epicardial markers is shown in Figure 4.20.

Dogs were positioned in the magnetic resonance scanner for initial 4D imaging under baseline conditions, according to the MR imaging protocols described below. The left anterior descending coronary artery was then occluded, without movement of the dog relative to the imaging planes. Repeat 4D images were acquired after 10 minutes of

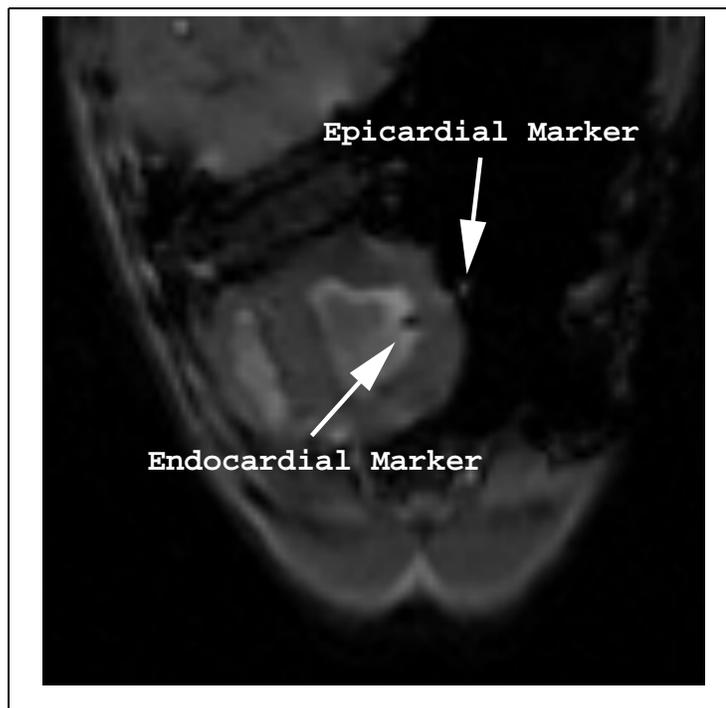


Figure 4.20: MRI image with endocardial and epicardial markers.

coronary occlusion. This way, we were assured that the images are registered with each other pre-occlusion and post-occlusion. Magnetic resonance imaging was performed on the GE Signa 1.5 Tesla scanner. Axial images through the LV were obtained with the gradient echo cine technique. This sequence provides images with an in-plane resolution of 1.64×1.64 mm and 5mm resolution perpendicular to the imaging planes. The temporal resolution depends on the dog's heart rate, and is triggered by ECG waves at each acquisition. The resulting 3D image frame at one time instant consists of sixteen 2D image slices, while within the cardiac cycle, we have sixteen temporal 3D frames. The MR images were acquired by Dr. Todd Constable of Yale MR center.

Figure 4.21 shows sixteen spatial slices which cover the entire left ventricle, from

apex to base. Sixteen temporal frames of a mid-ventricle slice are shown in Figure 4.22, from ED to ES to ED.

The location of each implanted marker is determined in each temporal frame by first manually delineating a point within the marker area in one of the 2D image slices, grouping all evidence of the brightest (or darkest) values in the vicinity of that point over all slices within the 3D frame using a connected components algorithm and then computing the 3D centroid of that cluster of points, weighted by the grey level. The markers are placed far enough apart spatially that trajectories can be formed by simple nearest Euclidean distance correspondence between centroids in adjacent temporal frames. It should be noted that because of the complexity of the implantation of the markers, not all the markers are found all the time. However, for the eight studies presented here, eighty percent (101 out of 128) of the markers have been found at all the sixteen time frames. This marker identification scheme has been validated on a 2D moving phantom. The trajectories traced out by tracking the marker from a cine gradient-echo MRI acquisition using the technique just described and the known physical trajectory of the phantom were virtually identical.

4.5.2 Dynamic Spatial Reconstructor Data

The Dynamic Spatial Reconstructor is a three-dimensional computerized tomography scanner[105, 104]. It can provide accurate, stop-action images of moving organs of the body. The canine data we are using is acquired at $33msec$ frame intervals in real time, with the spatial resolution of $0.91mm$ in all three dimensions. Again, four pairs of endocardial and epicardial markers, made from lead beads, are placed on the myocardium, which show up as bright spots in the images. The markers are hand-traced as the average positions of the most probable points. The DSR images are provided by Dr. Erik Ritman

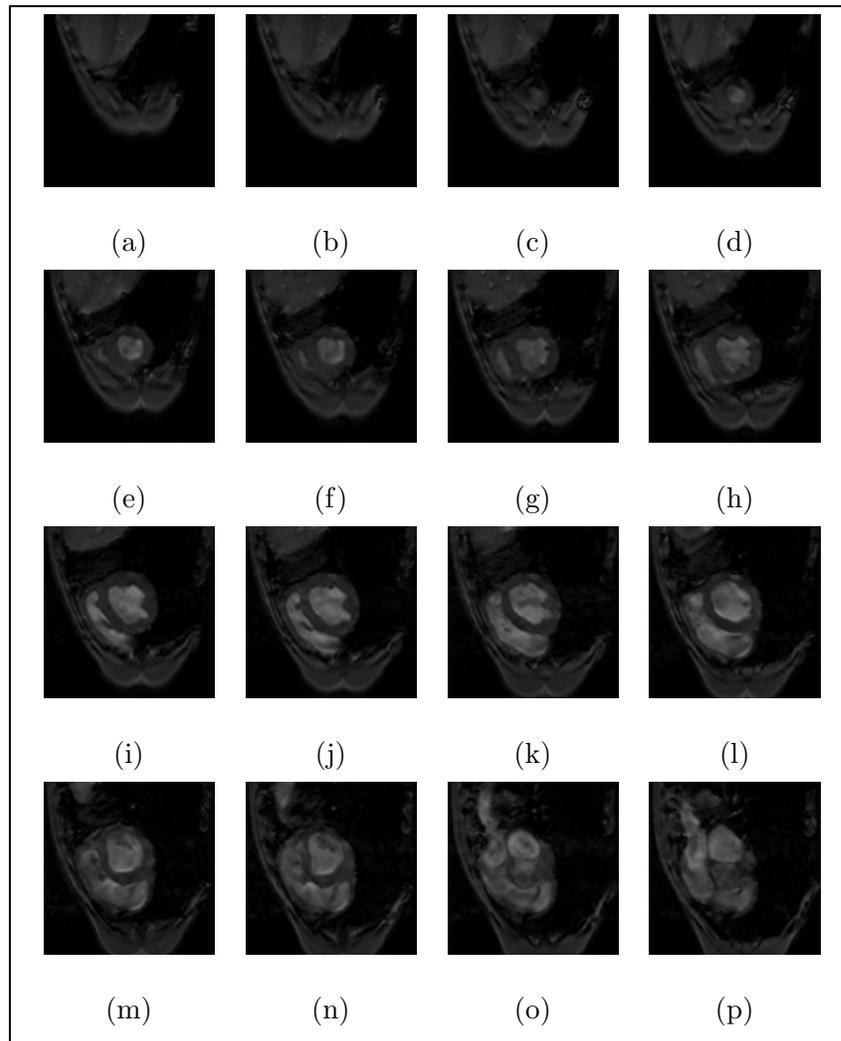


Figure 4.21: Sixteen spatial MRI images which cover the entire left ventricle. The images run from top to bottom, left to right to cover the LV from apex to base.

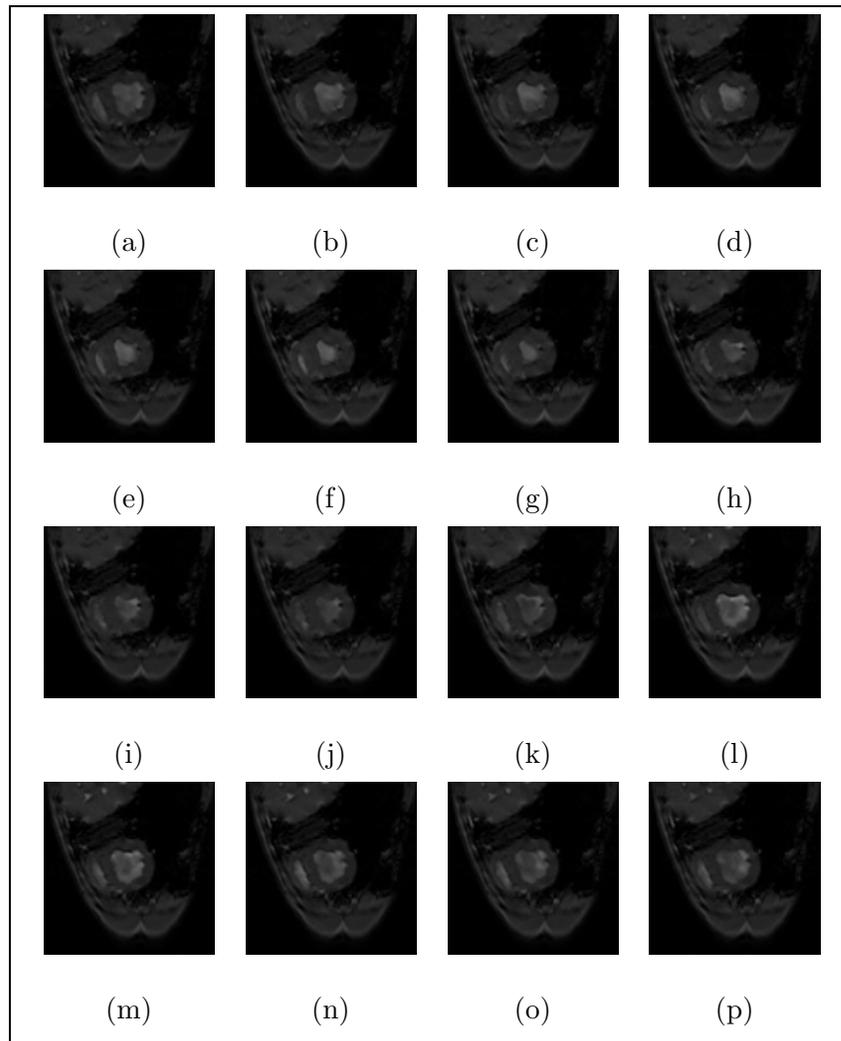


Figure 4.22: Sixteen temporal MRI images of a mid-ventricle slice. The images run from top to bottom, left to right for the temporal sequence of ED to ES to ED.

of the Mayo Clinic.

Sixteen sample spatial slices which cover the left ventricle are shown in Figure 4.23, with the sixteen temporal frames of a mid-ventricle slice shown in Figure 4.24. Again, the spatial slices cover the LV from apex to base, and the temporal frames cover the cardiac cycle from ED to ES to ED. Examples of DSR markers in the images are shown in Figure 4.25, with an endocardial marker on the left and an epicardial marker on the right. Figure 4.26 shows the dense endocardial displacement vector field from ED to ES for one DSR dataset. The trajectories are shown against the rendered endocardial surface at ES.

4.5.3 Motion Validation

In order to validate the motion trajectories formed from the shape-based tracking algorithm, the gold standard marker trajectories and the shape-based, algorithm-derived point trajectories are compared across the acute dog studies (8 MRI and 4 DSR). To avoid the possible distortion of the boundary surfaces by the implanted markers which may cause false shape features, the image intensity around each marker is *retouched* by a cardiologist after the markers' positions have been detected. This procedure is performed before the contour segmentation process.

Since the position of each marker is the 3D centroid of a cluster of candidate points in the image, the markers are usually not exactly on the myocardial surfaces. For both MRI and DSR studies, the point which is the nearest surface point to each marker is chosen as the *surface marker point* for the given physical marker. After offsetting the initial positional difference, the algorithm-derived trajectory of this surface marker point is considered as the algorithm-derived trajectory of the physical marker. Then, point-by-point positional errors between the algorithm and gold standard trajectories are compiled

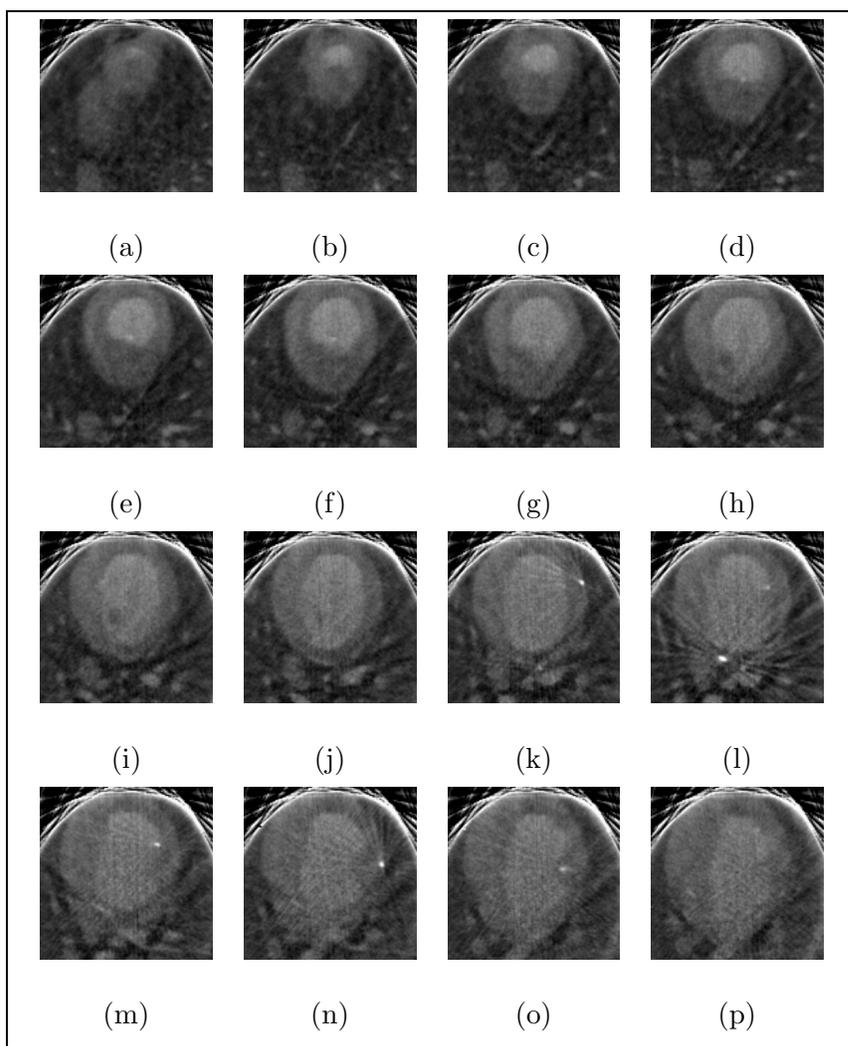


Figure 4.23: Sixteen spatial DSR images which cover the left ventricle. The images run from top to bottom, left to right to cover the LV from apex to base.

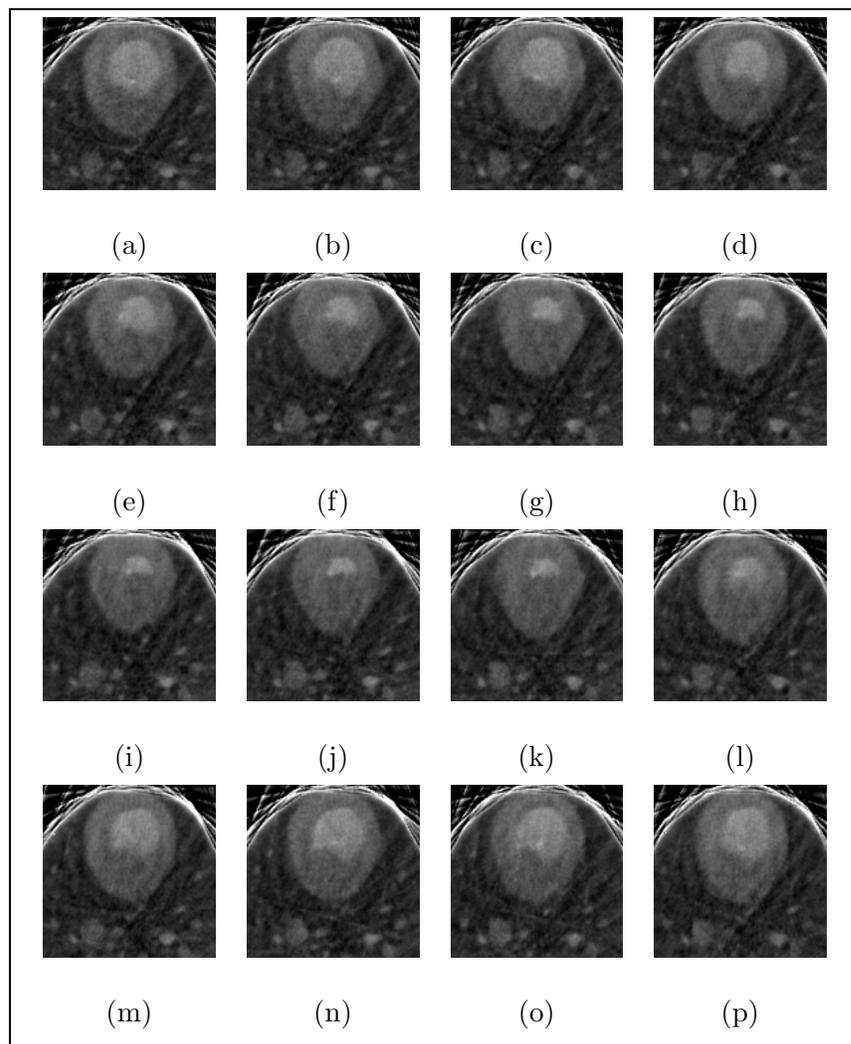


Figure 4.24: Sixteen temporal DSR images of a mid-ventricle slice. The images run from top to bottom, left to right for the temporal sequence of ED to ES to ED.

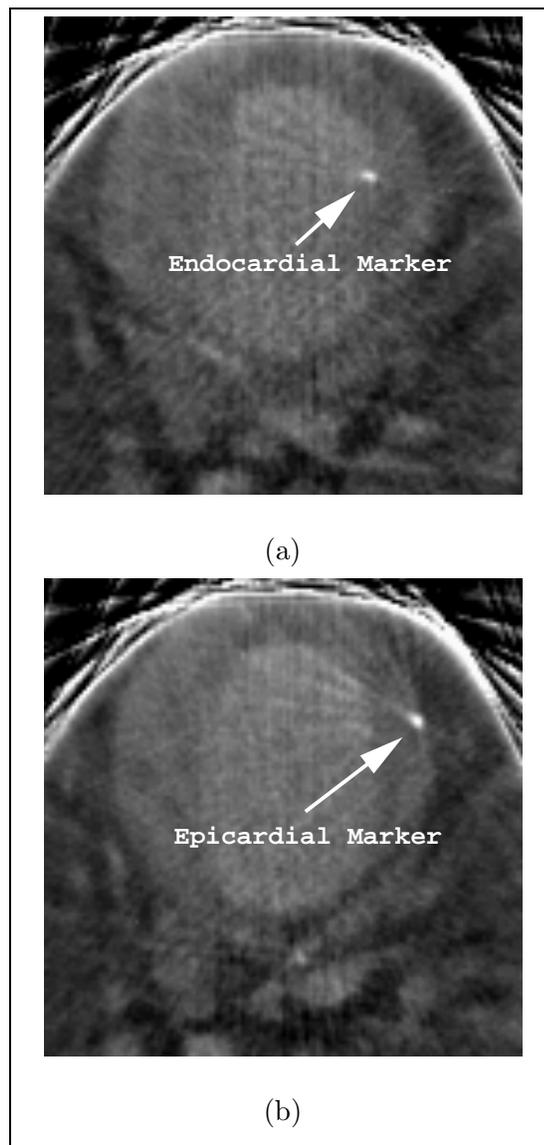


Figure 4.25: DSR images with endocardial and epicardial markers. (a): endocardial marker; (b): epicardial marker.

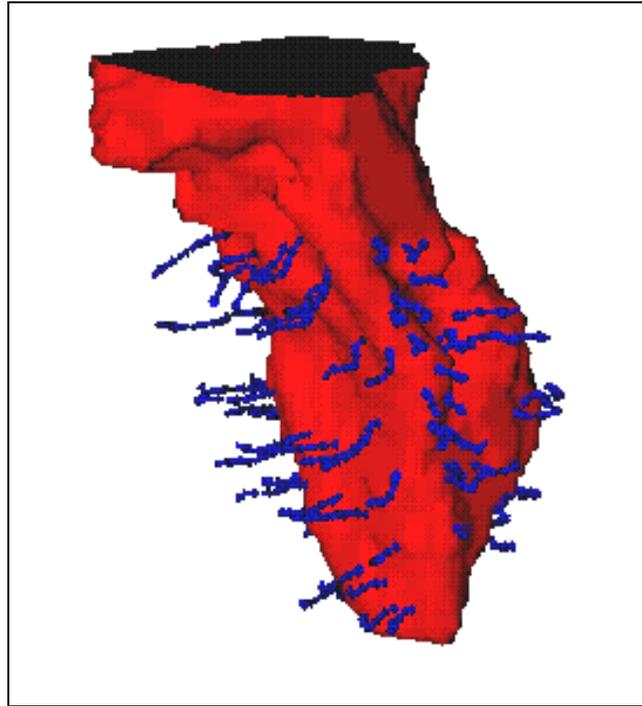


Figure 4.26: Dense endocardial displacement vector field from ED to ES for one DSR dataset. The trajectory arrows are shown against the rendered endocardial surface at ES.

across all 16 time frames for each marker. The mean and the standard deviations of the positional errors for all the markers are listed in the following tables.

Table 4.3 presents the error analysis for all the markers of both MRI and DSR data. For the baseline MRI studies, endocardial markers have a mean error of about one pixel and the epicardial markers have a mean error around two-thirds of a pixel. Since the endocardial points usually move two-to-three times the distance of the corresponding epicardial points, this mean error disparity is somewhat expected. However, the endocardial surface often has more shape features than the epicardial surface, which may explain that both of them have similar error standard deviations.

Study Type	Image Resolution. (<i>mm/pixel</i>)	Average Errors	
		Endocardial Markers	Epicardial Markers
MRI Baseline	1.64	0.993 ± 0.522 (<i>pixel</i>)	0.685 ± 0.509 (<i>pixel</i>)
		1.623 ± 0.856 (<i>mm</i>)	1.123 ± 0.835 (<i>mm</i>)
MRI Post-Infarct	1.64	0.488 ± 0.322 (<i>pixel</i>)	0.498 ± 0.339 (<i>pixel</i>)
		0.800 ± 0.528 (<i>mm</i>)	0.817 ± 0.556 (<i>mm</i>)
DSR	0.91	0.556 ± 0.305 (<i>pixel</i>)	0.645 ± 0.338 (<i>pixel</i>)
		0.506 ± 0.278 (<i>mm</i>)	0.587 ± 0.308 (<i>mm</i>)

Table 4.3: Average positional errors (in *pixel* units and in *mm*) between implanted markers and algorithm-derived point positions for eight MRI baseline, eight MRI post-infarct, and four DSR studies. Each data cell represents the mean \pm standard deviation errors for all the same type markers over the entire temporal frames.

For the post-infarct MRI studies, both endocardial and epicardial markers have mean errors in the half pixel range, with their error standard deviations also much smaller than those under baseline condition. This is because the infarction dramatically reduces the motion of the myocardium, especially endocardium (a thirty percent drop of average path length from baseline to post-infarct for the endocardial surface, a ten percent drop of average path length from baseline to post-infarct for the epicardial surface). This reduction of motion makes it less possible to make large matching errors. Even though it

still has larger motion, the feature-rich endocardial surface now has similar error statistics as the epicardial surface.

Since the motion tracking algorithm is based on matching local shape features, it is not surprising that the higher resolution DSR baseline studies produce better endocardial tracking results than the MRI studies. The high resolution DSR images pick up more local detail of the endocardium, thus have smaller mean errors as validated by the markers. Meanwhile, the accuracy of the relatively feature-less epicardium does not improve, in terms of pixel units, from the MRI studies, and it is slightly worse than the endocardial results. Evidently, the rich shape features of the endocardial surface is sufficient to track the larger motion presented in this case.

Overall, this table illustrates that the trajectories of motion predicted by the algorithm at points near the implanted markers are very close to the gold-standard motion of the markers, and are more accurate with better image resolution. Detailed mean error analysis for each of the MRI and DSR studies are presented in Table 4.4 through Table 4.9.

These error data are also examined as four groups of four time frames in the cardiac cycle. In this case, the sixteen positional errors of each marker within the cardiac cycle are sub-grouped into four groups, each with four error measures for each marker. The mean error and standard deviation of each group are computed to see if there is error bias over time, and is shown in Table 4.10 for all the studies. For MRI studies, the errors of the first group, measuring the errors of the first four matches, are generally smaller than the other three groups which are very similar among themselves. This may suggest that the algorithm-matched points often drift away from the real marker positions during the time period of the second group but not any further during later time frames. The baseline

MRI	Baseline Endocardial Markers			
Study	1	2	3	4
EB	0.892±0.376	1.472±0.354	0.983±0.460	1.348±0.433
FB	1.010±0.495	1.266±0.570	1.021±0.381	0.638±0.262
GB	0.165±0.091	0.447±0.189	*	0.704±0.255
HB	1.439±0.111	1.363±0.115	*	1.148±0.610
IB	*	*	1.405±0.642	*
JB	1.335±0.280	1.088±0.481	*	0.472±0.034
KB	0.505±0.288	*	0.729±0.305	1.178±0.294
LB	1.296±0.265	0.966±0.667	1.004±0.381	0.957±0.437

Table 4.4: Absolute positional errors (in pixels) between implanted endocardial markers and algorithm-derived point positions for eight canine MRI studies observed under baseline conditions. Each data cell represents the mean±standard deviation differences found over sixteen temporal frames for each of the four markers. * denotes that the implanted marker could not be found in all the temporal frames.

MRI Study	Baseline Epicardial Markers			
	1	2	3	4
EB	0.093±0.015	0.725±0.411	1.776±0.383	0.879±0.284
FB	0.758±0.419	0.836±0.488	0.694±0.179	0.464±0.200
GB	0.183±0.146	1.359±0.280	0.158±0.129	1.150±0.383
HB	0.212±0.139	0.108±0.109	*	0.517±0.146
IB	0.599±0.229	0.422±0.091	0.330±0.083	0.765±0.338
JB	0.293±0.141	*	*	1.062±0.255
KB	0.508±0.134	0.636±0.233	0.819±0.550	1.056±0.374
LB	0.480±0.258	1.444±0.240	0.192±0.097	1.337±0.134

Table 4.5: Absolute positional errors (in pixels) between implanted epicardial markers and algorithm-derived point positions for eight canine MRI studies observed under baseline conditions. Each data cell represents the mean±standard deviation differences found over sixteen temporal frames for each of the four markers. * denotes that the implanted marker could not be found in all the temporal frames.

MRI Study	Post-Infarct Endocardial Markers			
	1	2	3	4
EI	0.161±0.082	0.347±0.143	0.594±0.257	0.251±0.133
FI	0.448±0.373	0.494±0.272	0.458±0.205	0.073±0.046
GI	0.427±0.331	0.764±0.210	0.444±0.126	1.078±0.092
HI	0.365±0.340	0.571±0.245	*	0.461±0.084
II	0.449±0.292	*	*	*
JI	0.531±0.243	1.007±0.217	*	0.512±0.278
KI	0.829±0.154	*	0.517±0.194	0.643±0.177
LI	0.295±0.164	0.163±0.205	0.390±0.241	0.477±0.227

Table 4.6: Absolute positional errors (in pixels) between implanted endocardial markers and algorithm-derived point positions for eight canine MRI studies observed under post-infarct conditions. Each data cell represents the mean±standard deviation differences found over sixteen temporal frames for each of the four markers. * denotes that the implanted marker could not be found in all the temporal frames.

MRI Study	Post-Infarct Epicardial Markers			
	1	2	3	4
EI	0.450±0.156	*	0.151±0.131	0.542±0.304
FI	0.071±0.044	0/794±0.250	0.426±0.154	0.417±0.174
GI	0.233±0.269	0.515±0.363	0.352±0.220	*
HI	*	*	*	*
II	0.661±0.211	*	0.407±0.332	0.531±0.187
JI	1.284±0.222	*	*	0.495±0.222
KI	0.439±0.360	*	*	0.593±0.123
LI	0.787±0.161	0.336±0.178	0.426±0.289	0.557±0.269

Table 4.7: Absolute positional errors (in pixels) between implanted epicardial markers and algorithm-derived point positions for eight canine MRI studies observed under post-infarct conditions. Each data cell represents the mean±standard deviation differences found over sixteen temporal frames for each of the four markers. * denotes that the implanted marker could not be found in all the temporal frames.

DSR	Endocardial Markers			
Study	1	2	3	4
e146	0.331±0.160	0.531±0.117	0.858±0.232	0.941±0.332
e147	0.918±0.152	0.220±0.102	0.616±0.305	0.534±0.119
e181	0.219±0.099	0.404±0.125	0.518±0.334	*
c911	0.744±0.111	0.613±0.244	0.325±0.206	0.569±0.185

Table 4.8: Absolute positional errors (in pixels) between implanted endocardial markers and algorithm-derived point positions for four canine DSR studies observed under normal conditions. Each data cell represents the mean±standard deviation differences found over sixteen to eighteen temporal frames depending on the studies for each of the four markers. * denotes that the implanted marker could not be found in all the temporal frames.

endocardial markers have the largest increase of errors between the first group and the next three groups, which may be explained by the larger motion and deformation these markers undergo to cause mismatches. For DSR studies, the endocardial markers has consistently small errors over time. Once again, this suggests that the higher resolution, feature-rich DSR endocardial surface not only produces more accurate matches but also does so very consistently. The errors of DSR epicardial surfaces have similar patterns as the MRI ones.

Finally, a visual illustration of the marker position comparison for one MRI baseline study is shown in Figure 4.27. Here, the real physical marker (green) trajectory and

DSR Study	Epicardial Markers			
	1	2	3	4
e146	0.605±0.332	0.698±0.356	0.682±0.231	0.745±0.238
e147	1.103±0.355	0.406±0.095	0.383±0.122	0.522±0.456
e181	0.291±0.062	0.595±0.256	0.915±0.206	0.504±0.347
c911	0.853±0.372	0.567±0.255	0.782±0.215	0.769±0.133

Table 4.9: Absolute positional errors (in pixels) between implanted epicardial markers and algorithm-derived point positions for four canine DSR studies observed under normal conditions. Each data cell represents the mean±standard deviation differences found over sixteen to eighteen temporal frames depending on the studies for each of the four markers.

surface marker trajectory (blue), both from ED to ES, are plotted together, against the endocardial surface at ES. Similar figures for one DSR study are shown in Figure 4.28. From these figures, it is once again evident that the algorithm trajectories are usually very close to the corresponding marker trajectories.

4.5.4 Injury Validation

For five MRI studies under both baseline and post-infarct conditions, two *in vivo* measures (path length and wall thickening) computed from the algorithm-derived trajectories are used to evaluate how well the shape-based motion tracking approach can distinguish and predict myocardial regional injury.

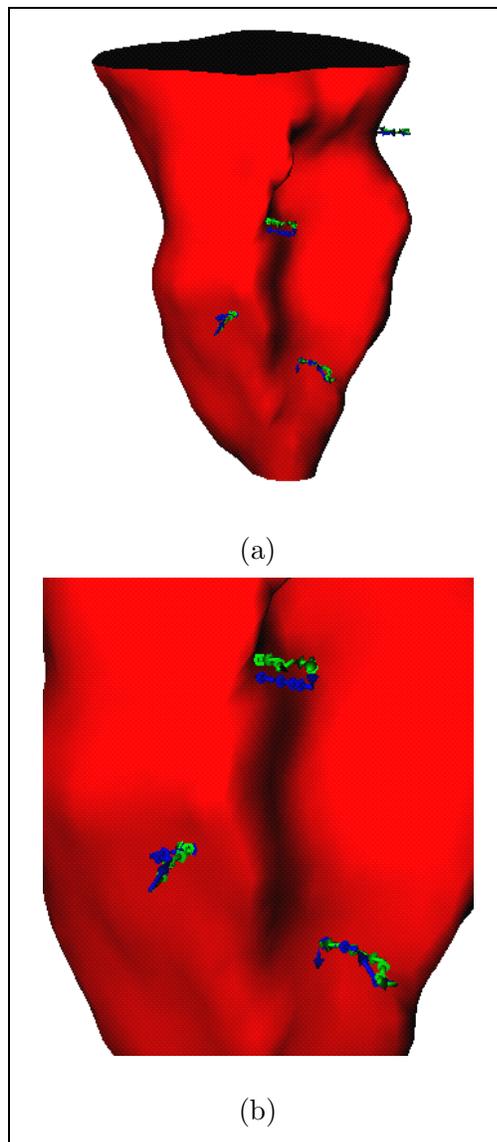


Figure 4.27: Comparison of algorithm and gold standard marker trajectories (MRI study). (a): overview of the algorithm trajectory (in blue) and the implanted marker trajectory (in green), against the endocardial surface at ES; (b): the blowup of the trajectories. The trajectories plotted are from ED to ES.

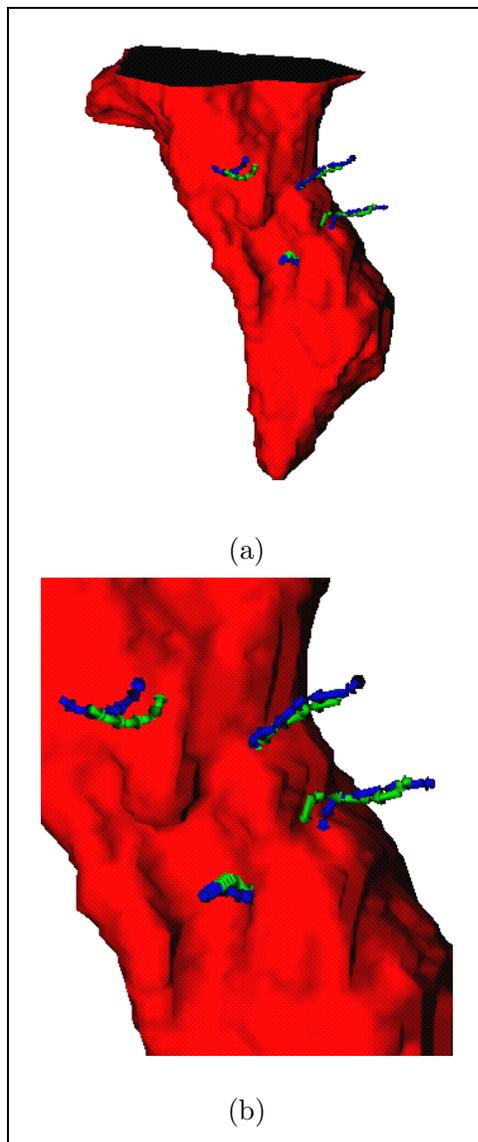


Figure 4.28: Comparison of algorithm and gold standard marker trajectories (DSR study). (a): overview of the algorithm trajectory (in blue) and the implanted marker trajectory (in green), against the endocardial surface at ES; (b): the blowup of the trajectories. The trajectories plotted are from ED to ES.

		Average Errors (<i>pixel</i>)			
		group 1	group 2	group 3	group 4
MRI Baseline	Endocardial	0.536±0.445	1.107±0.393	1.228±0.446	1.103±0.499
	Epicardial	0.506±0.401	0.749±0.511	0.725±0.553	0.758±0.515
MRI Post-Infarct	Endocardial	0.362±0.254	0.551±0.299	0.471±0.350	0.573±0.328
	Epicardial	0.390±0.300	0.517±0.348	0.533±0.380	0.547±0.304
DSR Baseline	Endocardial	0.570±0.291	0.586±0.381	0.573±0.306	0.495±0.211
	Epicardial	0.524±0.235	0.561±0.277	0.699±0.365	0.796±0.381

Table 4.10: Average positional errors over time. The cardiac cycle is divided into four sub-periods, beginning at the end of diastole. The average positional errors for all markers within each sub-period are computed to see the error pattern change over time.

4.5.4.1 Path Length

The complete trajectories of all the myocardial surface points are built by concatenating motion vectors between pairs of surfaces found from consecutive temporal frames. Flow vectors running through the surface points over time are connected to form trajectories that track each individual point's motion over the entire cardiac cycle. Then, motion and function indices for LV regional function analysis can be derived from these trajectories.

The path length of any surface point is the sum of the magnitudes of all sixteen displacement vectors of this point over the cardiac cycle, and it measures the overall

motion of the point. One physiological hypothesis of myocardial injury is that the post-infarct heart will have dramatically decreased motion in the injured zone from its baseline condition. Hence, it is reasonable to expect that we can measure myocardial regional injury from the comparison of the baseline and post-infarct path length maps of the myocardial surfaces.

Examples of endocardial surface path length maps are shown in Figure 4.29 for both baseline and post-infarct data, with the color scale representing the magnitude of the shape-tracked pixel-wise movement in pixel units. Here, the “O” sign denotes the site of the coronary occlusion, and the “I” sign denotes the central infarct zone predicted by a cardiologist. It is expected from the canine model that the surface region directly below the coronary occlusion site would be the infarct zone, and thus would have reduced motion as compared to the baseline data. Visually, it is obvious that the vast region below the occlusion site in the post-infarct path length map has very little motion.

These two surfaces, the baseline surface and the post-infarct surface at ED, are registered to each other by minimum distance mapping. The percentage change in path length for each point from baseline to post-infarct conditions is mapped onto the post-infarct surface, and is shown in Figure 4.30. Here, the unit of the color scale is percentage, with the positive values meaning increased path lengths and the negative values meaning decreased path lengths. As expected from the animal surgical model, the motion of the surface points under the coronary occlusion site is reduced by at least thirty percent. In addition, the map follows the expected pattern that while the motion of the central infarct zone has the largest decrease, the further away a point is from the central zone the smaller is its motion decrease.

Two validation tests are performed on the path length data. The first test ver-

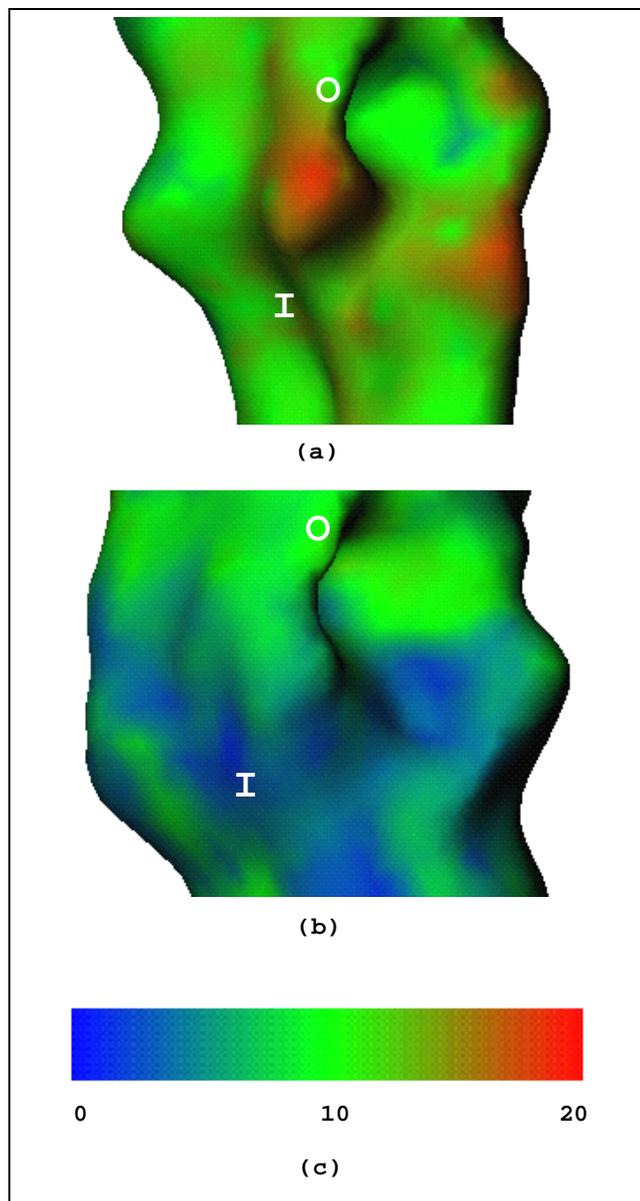


Figure 4.29: Baseline and post-infarct endocardial path length maps. (a): baseline path length map; (b): post-infarct path length map; (c): color scale (in pixel units). The “O” sign denotes the site of the coronary occlusion, and the “I” sign denotes the central infarct zone predicted by a cardiologist.

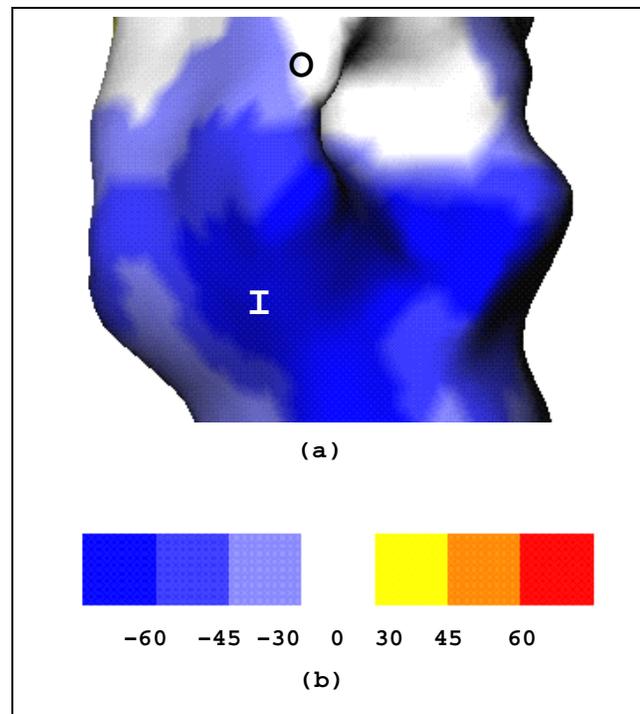


Figure 4.30: Change in endocardial path length from baseline to post-infarct condition. (a): map of percentage change of path length; (b): color scale (in percent), positive values mean increased path lengths and the negative values mean decreased path lengths). The “O” sign denotes the site of coronary occlusion, and the “I” sign denotes the central infarct zone predicted by a cardiologist.

	Path Length	a Factor		a		b		axb	
		Infarct Zone	Normal Zone	F	p	F	p	F	p
b Factor	Baseline	22.1 ± 3.8	21.7 ± 3.5	3.46	0.14	4.50	0.10	10.44	0.03
	Post-Infarct	11.0 ± 7.7	19.9 ± 4.5						

Table 4.11: Table of means and standard deviations of algorithm-derived *in vivo* path length measures (in *mm*), observed in the infarct zone and in a remote normal zone for five acute canine studies under both baseline and post-infarct conditions.

ifies the validity of using path length changes to differentiate the normal zone and the infarct zone motion behavior. For both the baseline and the post-infarct data of five MRI studies, the mean and standard deviation of the path lengths are computed for the antero-apical infarct zone and the remote normal zone from sampled points near the two implanted markers. These data are shown in Table 4.11. Two-way analysis of variance is performed for the path length measure, and the F-statistics and p values are computed for comparisons between a) baseline and post-infarct conditions, b) infarct zone and normal zone, and the interaction of a) and b). As can be seen in the table, the path length measure shows significant differences in the interaction term, indicating that the algorithm can discriminate the infarction and differentiate the normal zone and infarct zone. More detailed testing showed that the significance of the interaction is due to the difference of the measures in the infarct zone at baseline and post-infarct conditions ($p < 0.028$), and the difference between the infarct zone and the normal zone at post-infarct condition ($p < 0.022$).

The second test verifies the algorithm-predicted extent (area) of the infarct zone on the endocardial surface against other standard forms of myocardial regional viability measurement. Three-dimensional *post mortem* endocardial injury zones are found by digitizing color photographs of TTC-stained *post mortem* myocardium slices (5mm thick) of the excised hearts. The experiments were performed by Dr. Albert Sinusas of Yale medical school. The endocardial, epicardial and infarct zone boundaries of the *post mortem* left ventricle are hand-traced and stacked to reconstruct the LV volume representation. Figure 4.31 shows one 2D frame of the color photograph, the rendered LV volume (epicardial surface in transparent green, endocardial surface in red, and the infarct zone in blue), and the rendered endocardial surface along with the endocardial infarct zone. The areas of the endocardial infarct zones are computed and compared to the areas defined by thresholding the magnitudes of the *in vivo* algorithm-derived path length measures. Within a search window defined by a sphere centered at the central infarct marker I with radius being the distance between I and the occlusion marker O , points are considered to be inside the infarct zone if their post-infarct path length fell to levels below 80% of the mean infarct zone baseline value, computed from sample points near the infarct zone marker. The mean and standard deviation of both *post mortem* and *in vivo* infarct areas are reported in Table 4.12, as is their Pearson product-moment correlation. The high correlation value points to the utility of these measures for measuring the *extent* of endocardial injury.

Another form of myocardial regional viability measurement is Single Photon Emission Computed Tomography (SPECT), which measures myocardial blood flow and thus indicates tissue viability. Figure 4.32 shows an example of mapping the SPECT counts, of the same study as that in Figure 4.30 and 4.31, onto the MRI derived endocardial

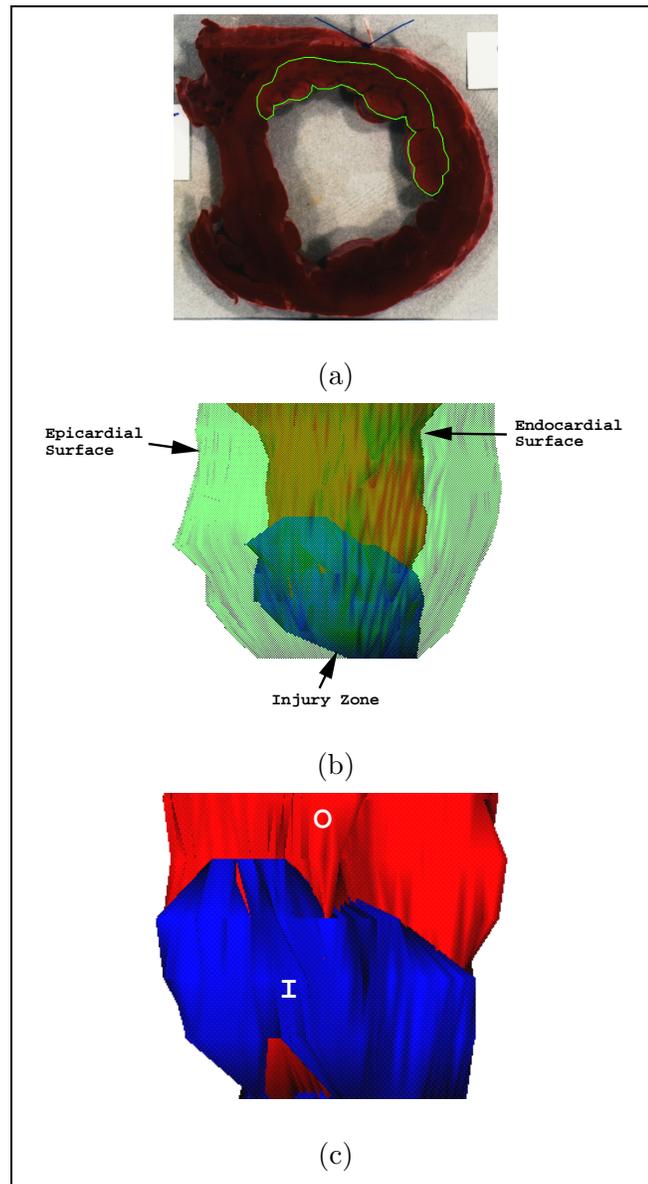


Figure 4.31: *Post Mortem* injury found from TTC staining. (a): 2D color photograph of TTC stained myocardial slice, with the injury region delineated by a green line; (b): rendered LV volume reconstructed from digitized and segmented 2D post mortem slices; (c): rendered endocardial surface along with the endocardial infarct zone (scaled to the same size as the path length map of Figure 4.30). The epicardial surface is in transparent green, the endocardial surface is in red, and the infarct zone is in blue.

Study	Infarct Area (mm^2)						Correlation
	1	2	3	4	5	average	
<i>Post Mortem</i>	963	811	833	749	623	796±124	0.968
<i>In Vivo</i>	939	855	807	710	602	783±131	

Table 4.12: Correlation between *post mortem* and *in vivo* infarct areas.

surface. Since surface points with SPECT counts under sixty percent are usually considered to be injury points, we can again compare the SPECT and path-length infarct areas to validate the ability of our shape-based motion tracking approach in predicting the extent of myocardial injury. (We should note that SPECT over-estimates low flow while it under-estimates high flow, thus often under-estimating the extent of injury region.)

4.5.4.2 Wall Thickening

In the previous section, we have shown that the algorithm-derived path length changes of the myocardial surface points predict the existence and extent of the infarct zone. However, the path length measure is a gross overall measure of local deformation *and* global motion, which may result in under-estimation of the injury. This is because the global motion of the injury zone does not decrease dramatically due the coupling between myocardial tissues. Meanwhile, myocardial thickening, measured by the change of thickness of LV wall between ED and ES, may provide additional insight into the myocardium viability since it is a more local measure similar to radial strain. For every epicardial

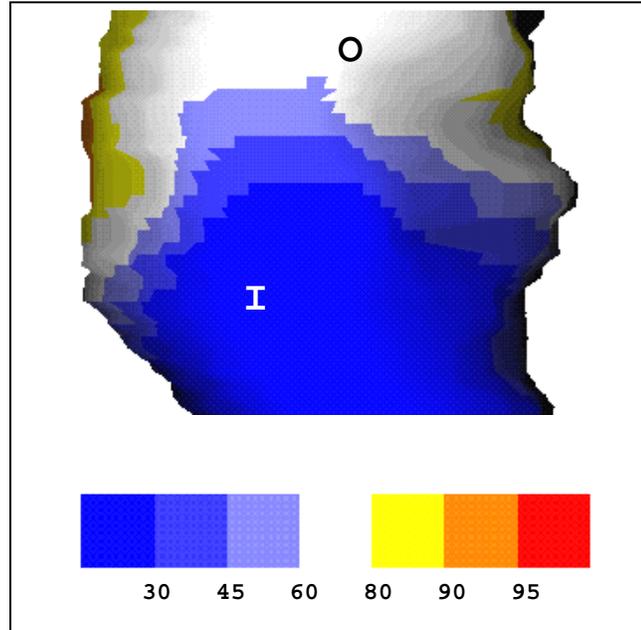


Figure 4.32: Myocardial injury zone from SPECT counts. (a): map of SPECT counts onto the MRI derived endocardial surface; (b): color scale (in percent), region with counts under sixty percent is often considered to be injury zone.

point, its thickening measure is defined as:

$$\tau' = \frac{\tau_{ED} - \tau_{ES}}{\tau_{ED}} \quad (4.66)$$

where τ_{ED} and τ_{ES} are the thickness of the LV wall at ED and ES. The thickness of the wall is computed by emitting a ray from the epicardial point in its inward normal direction until it intersects the endocardial surface, and the distance between the intersection and the epicardial point is considered to be the wall thickness. Thickening is a gross approximation to the radial strain of the wall.

	Thickening Measure(τ')	a Factor		a		b		axb	
		Infarct Zone	Normal Zone	F	p	F	p	F	p
b Factor	Baseline	44.6 \pm 26.2	34.7 \pm 19.5	0.82	0.42	4.90	0.09	44.7	0.003
	Post-Infarct	6.1 \pm 13.2	37.4 \pm 13.4						

Table 4.13: Table of means and standard deviations of algorithm-derived *in vivo* measure of radial thickness change (in percentage), observed in the infarct zone and in a remote normal zone for five acute canine studies under both baseline and post-infarct conditions.

Again, for both the baseline and the post infarct data of five MRI studies, the mean and standard deviation of the thickening measures are computed for the antero-apical infarct zone and the remote normal zone from sampled points near the two implanted markers. The data are shown in Table 4.13. Two-way analysis of variance is again performed for the change of thickening measure, and the F-statistics and p values are computed for comparisons between a) baseline and post-infarct conditions, b) infarct zone and normal zone, and the interaction of a) and b). As can be seen in the table, the thickening measure shows significant differences in the interaction term, indicating that the algorithm can distinguish infarction. More detailed testing showed that the significance of the interaction is due to the difference of the measure in the infarct zone at baseline and post-infarct conditions ($p < 0.010$), and the difference between the infarct zone and the normal zone at post-infarct conditions ($p < 0.045$). This shows the validity of using our algorithm-derived, point-tracked LV wall thickening measure to differentiate the normal zone and the infarct zone motion behavior.

4.6 Conclusion

A shape-based motion tracking approach has been developed in this chapter. It is our hypothesis that we can use the shape properties of the myocardial surfaces to track the motion trajectories of a dense field of points over the entire cardiac cycle, which can then be used to predict the existence and extent of myocardial injury.

Locally coherent surface representation is achieved by non-shrinkage Gaussian smoothing of the Delaunay triangulated surface, weighted by the natural coordinates of each surface point. The smoothed surface is characterized by its differential geometric properties through multi-order local surface fit, again using the natural neighbor relationships defined from the Delaunay triangulation. Surface points on successive temporal frames are matched based on differential geometric features and an ideal-thin-plate bending model of local surface patches. The optimal dense motion field is obtained using a mathematical optimization strategy to combine the data-derived initial matching information with a locally coherent smoothness model.

Experiments are been performed on eight MRI canine studies under both baseline and post-infarct conditions, and on four DSR canine baseline studies. The accuracy of the algorithm point tracking results has been validated against the gold-standard motion of the implanted imaging-opaque markers. The changes in motion parameters, path length and wall thickening measures, between baseline and post-infarct data are quantified to assess myocardial viability, and are validated using cardiac perfusion data.

Chapter 5

Volumetric Deformation Analysis

5.1 Introduction

In the previous chapter, we proposed a shape-based approach for computing point-wise myocardial surface motion fields between successive image frames. Even though purely surface motion characteristics, such as path length and displacements, do indicate the location and extent of injury reflected on the endocardial and epicardial surfaces, the most robust description of functional abnormalities of the myocardial wall should include measurement of the entire transmural motion and deformation of the myocardium. This is important, in part, in order to assess the transmural extent of myocardial injury which can be related to patient prognosis. Despite a number of recent attempts in the literature, it is not yet the case that transmural deformation of the complete LV can be accurately and reproducibly quantified in three dimensions over time. One critical limitation to the successful quantification of this information is the fact that the appropriate computational framework has not yet been developed for assembling the complex cues related to LV deformation that are available from image data sets. Furthermore, instead of using

proper biomechanical constraints of the myocardium to guide the motion and deformation recovery process, only empirical models have been employed to analyze the image data.

We propose here an integrated framework for the analysis of left ventricular motion and deformation. This unified approach is based upon the use of image analysis strategies and biomechanical modelling, and is embedded in a finite element framework for the integration of disparate sources of displacement and velocity information, heretofore used only separately, to help guide volumetric motion and deformation analysis. In this manner, noisy and complementary image information can be jointly utilized from both the LV epicardial and endocardial boundaries (where the shape-based estimated displacements are reliable) and the mid-wall (where measures such as MR phase velocity, MR tagging, and echocardiographic Doppler are reliable). In addition, the continuum mechanical properties of the myocardium provide physically meaningful constraints on the dynamic behaviors of the LV tissue. This, along with the finite element framework, enable us to incorporate naturally actual known cardiac physical parameters, such as pressures, into the motion/deformation estimation system.

5.2 Image-Derived Information

It is the goal of the unified motion and deformation analysis framework to characterize more completely the transmural function of the left ventricle. It takes advantage of the availability of several complementary image sources of LV anatomy and motion (displacement and velocity) information to quantify the dynamic behavior of the myocardium. In this section, we will briefly discuss several of the image sources which have been, or can be, used in our framework. Because of image availability, the remaining sections of this chap-

ter will focus on estimating motion and deformation by integrating shape-based boundary displacement and phase contrast velocity information from MR images. We should point out, however, that our unified framework can also use data from other imaging modalities include MR tagging, DSR, and echocardiography.

5.2.1 Shape-Based Boundary Displacement

As described in detail in the previous chapter, we have proposed that we can use the shape properties of the endocardial and epicardial surfaces to track the motion of a dense field of surface sample points over the entire cardiac cycle. This motion tracking method is based on locating and matching differential geometric landmarks and using a mathematical optimization reasoning strategy to combine a locally coherent smoothness model with data-derived information to obtain dense field motion vectors.

We will use these boundary displacement vectors as the shape-derived boundary information in our integrated framework. For computational stability and for not over constraining the boundary motion by shape information, however, only a subset of boundary displacement vectors in which we have the highest confidence will be used in the integrated estimation process. This subset of displacement vectors is often comprised of the vectors that begin from landmarks of the first surface or terminate at landmarks of the second surface. We will use this subset of boundary displacement vectors as the shape-derived boundary information in our integrated framework, and denote these displacement vectors as $\mathbf{U}_{boundary}$.

5.2.2 MR Phase Contrast Images and Mid-Wall Instantaneous Velocity

As discussed in Chapter 2, a new imaging technique[99, 98], *Phase Velocity Magnetic Resonance Imaging* recently, has been developed. It incorporates velocity phase encoding

into a conventional cine-MR sequence and produces images of myocardial instantaneous velocity throughout the cardiac cycle. Phase contrast methods can depict motion parameters with pixel precision and thus provide a high resolution technique for quantitative measurements[24].

The MR phase contrast velocity technique relies on the fact that a uniform motion of tissue in the presence of a magnetic field gradient produces a change in the MR signal phase, ϕ , that is proportional to its velocity[98]:

$$\phi = \nu\gamma M_1 = \nu\gamma \int_0^{TE} G(t)t dt \quad (5.1)$$

where $G(t)$ is the gradient strength as a function of time (the gradient waveform), ν the tissue velocity, M_1 the first moment of the gradient waveform, TE the echo delay time, and γ the gyromagnetic ratio. The gradient waveform can be modified to alter the first moment (motion sensitivity) while maintaining the same image localization characteristics. Images acquired with this altered waveform will have a different phase shift due to motion. The velocity in a particular spatial direction can be estimated by measuring the difference in phase shift between two acquisitions with different first gradient moments. Hence, instantaneous velocity maps encoded for motion in all three spatial dimensions may easily be obtained at multiple time instances throughout the cardiac cycle using a phase contrast cine-MR imaging sequence. The acquired velocity maps may then be used to provide information on tissue displacement, strain, strain rate, and other quantitative measures of motion and deformation. Figure 5.1 shows examples of phase contrast images of a canine mid-ventricle slice. In this dataset, three contiguous short axis slices were collected using the cine phase contrast gradient echo sequence. The imaging parameters

were: flip angle = 30° , $TE = 34msec$, $TR = 34msec$, $FOV = 28cm$, $5mm$ skip 0, matrix 256×128 , 4 nex, $venc = 15cm/sec$. It is important to note that the magnitude image and the three directional velocity images are perfectly registered since they are acquired from the same complex MR signal.

In theory, instantaneous velocity can be derived for each pixel in each image acquisition to provide a complete description of instantaneous movement of the LV at that moment. However, the phase contrast velocity estimates at interfaces between structures, e.g. near the endocardial and epicardial boundaries, are extremely noisy. It is difficult to obtain low noise estimates of velocity at the boundaries since some spatial averaging must occur, and thus pixels outside the myocardial wall (the blood pool for the endocardium and the air or other tissues for the epicardium) are sometimes included for the velocity estimates of the myocardial points. Thus, phase contrast images only provide reliable instantaneous motion information for the mid-wall region of the LV but not at the myocardial boundaries.

Since the velocity maps themselves only provide instantaneous motion information, efforts have been made to estimate the displacement and other measures to assess the motion and deformation of the myocardium[24, 75, 81, 96, 98, 97]. Assuming some constant velocity conditions between time frames, these approaches often use forward and/or backward integration of the velocity to track each point and estimate the displacement vector over time. More recently, a framework combining a spatially regularized velocity field with temporal Kalman filtering has been proposed to characterize the deforming LV in 2D[75], which takes into account the uncertainties in the velocity measurement near the boundaries.

We believe, however, that the weaknesses of the phase velocity image data, such

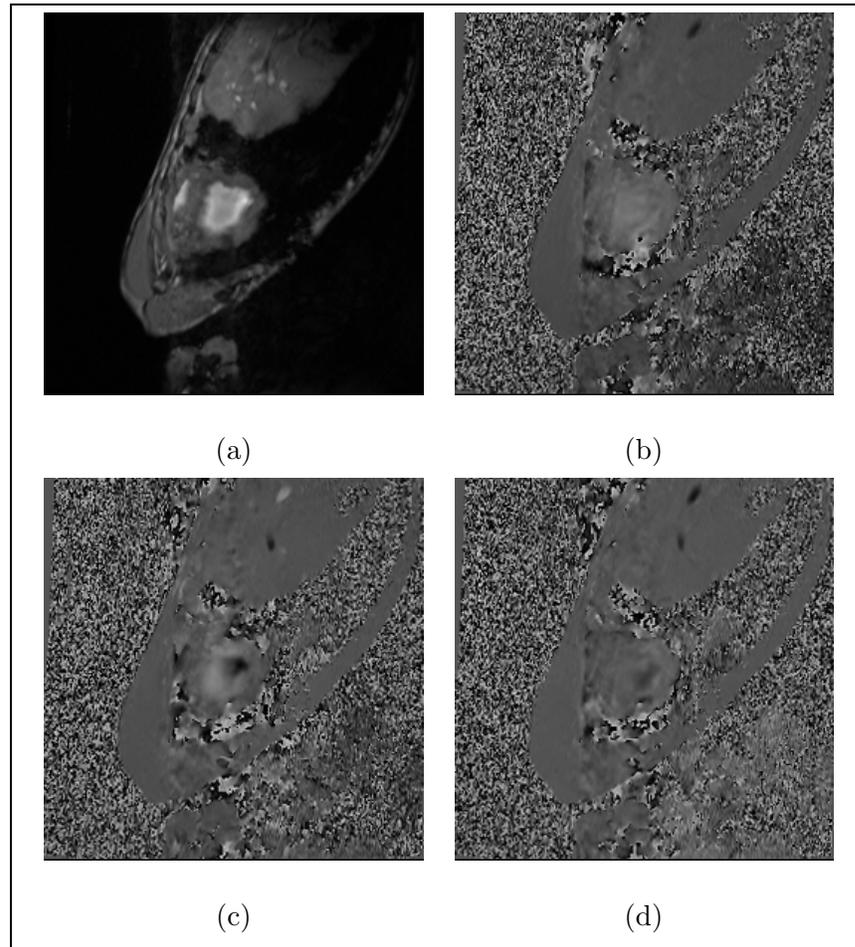


Figure 5.1: Phase contrast MR images. (a): the magnitude image; (b): the x direction velocity image; (c): the y direction velocity image; (d): the z direction velocity image. Please note that the velocity images show both positive and negative values of the velocity, with the dark colors representing negative values, the neutral grey for no motion, and bright colors for positive velocity values.

as noisy boundary data and uncertainty about point correspondences (constant velocity conditions between temporal frames are often assumed to compute displacements), makes it very difficult to obtain a reliable and robust assessment of myocardial motion and deformation over the entire LV and through the cardiac cycle using the data alone. It is more appropriate to use phase velocity information as only one source of data constraints within an integration framework, where it can be utilized without gross assumptions about the velocity conditions between temporal frames. Furthermore, since the phase image is derived from the same complex magnetic resonance signal as the regular magnitude MR image data upon which the shape-based boundary motion algorithm is based, these two image data are perfectly registered and can be used synergistically. In summary, we will use the reliable mid-wall MR phase velocity data as the mid-wall image information in our integrated framework, and we denote these mid-wall velocity vectors as $\dot{\mathbf{U}}_{mid-wall}$.

5.2.3 Other Image-Derived Data

5.2.3.1 MR Tagging and Tag Displacement

A review of MR tagging technique and tagged image based approaches of analyzing myocardial motion and deformation has been given in the Chapter 2. Here, we want to point out that the sparse MR tag displacement information can be easily incorporated into our integrated approach. If the MR tagging image can be derived from the same MR signal as the regular MR image and the phase contrast image, which is technically feasible, we can treat the tag displacement in the same way as the shape-based boundary displacement in the integration process, although these tag displacements can be for mid-wall points and/or boundary points. The integration results would be the optimal compromise between three complementary imaging data sources.

5.2.3.2 DSR Image and Optical Flow

The Dynamic Spatial Reconstructor, a three-dimensional computerized tomography scanner, provides high resolution, real-time images of the beating heart [104, 106]. We have applied and validated our shape-based boundary motion tracking algorithm on canine DSR data.

Even though the DSR does not directly provide tissue velocity or other motion information, we do note that velocities (optical flow) can be estimated from the spatio-temporal changes of the image intensity values[122]. Even though optical flow in general is not a good measurement for estimation cardiac motion, the estimated velocities should be fairly reliable for high resolution (both spatially and temporally), high quality image data such as DSR[75].

The integration of the shape-based boundary displacement and optical flow-based velocity would effectively use both image boundary information and grey level intensity information, which have only been used separately before.

5.2.3.3 Echocardiography and Doppler Velocity

There is a fairly long history of efforts aimed at trying to use echocardiographic information for quantitative analysis of the left ventricle, often aimed at extracting global parameters such as volume or volume differences (e.g. stroke volume and/or ejection fraction) [66, 119]. Historically, there have been few efforts that have been aimed at quantifying 3D motion and deformation. However, we note the work of McPherson[73] in the LV and, more recently, the interesting work of O'Donnell[86] and Raghavan[102] who are all exploring the use of ultrasound to measure strain and tissue elasticity.

Even though echocardiographic data often have low resolution, we believe that our

shape-based motion tracking approach would still be able to estimate the gross motion behavior of the LV boundary from these images. Furthermore, the use of color Doppler imaging of the velocities related to the movement of myocardial tissue fits nicely within our unified framework. Doppler imaging basically uses low pass filtering to extract information related to the lower frequency tissue motion, instead of the higher frequencies typically utilized when visualizing flow patterns in vessels or within the LV cavity. While only one component of the tissue velocity is available (orthogonal to the probe), this is nonetheless dense field information that is useful in our proposed integrated scheme.

The echocardiography based LV motion and deformation analysis will be undeniably very crude. However, we think it provides a relatively less expensive procedure to assess the state of health of the heart.

5.3 Continuum Mechanical Models

In this section, we discuss some of the basic concepts of continuum mechanics (see Fung[38] and Spencer[123] for more detail) and the models of myocardium based on these ideas[57, 59, 71, 84, 121]. It should be pointed out that our purpose is *not* to establish sophisticated constitutive models which best describe the mechanical properties of the myocardium. Instead, the emphasis is on using practical yet realistic models of the myocardium including relationships between the strain and stress, to guide the integrated framework to recover the motion and deformation of the LV from multiple, complementary image data.

5.3.1 Continuum Mechanics

Continuum mechanics deals with the mechanical behaviors of materials under the action of applied force, where the materials are continuous (or at least piecewise continuous) and deformable[38, 123]. The results of applying forces are often found in the changes of the kinematic variables such as displacement, velocity and acceleration fields of the object: each point moves a certain distance at a certain velocity and acceleration, each of which is dependent on both the point's position and the mechanical properties of the object.

5.3.1.1 Deformation Measure

A given particle of the object may be distinguished by its coordinates $\mathbf{X} = (X_1, X_2, X_3)$ at the undeformed state ($t = 0$). Thus the coordinates \mathbf{X} serve as labels with which to identify the particles of the object, and is called the *material coordinates*. Denoting the corresponding coordinates (the *spatial coordinates*) of the same particle at the deformed state (at time t) to be $\mathbf{x} = (x_1, x_2, x_3)$, then the equation

$$\mathbf{x} = \mathbf{x}(\mathbf{X}, t) \tag{5.2}$$

describes a motion of the body which gives the position of each particle at time t . Furthermore, the deformation gradient tensor \mathbf{F} relates the deformed and undeformed particle, and its nine components are defined as:

$$F_{iR} = \frac{\partial x_i}{\partial X_R} \quad i, R = 1, 2, 3. \tag{5.3}$$

In general, \mathbf{F} is not a symmetric tensor. Furthermore, although \mathbf{F} is important in the analysis of deformation, it is not itself a suitable measure of deformation. This is because a measure of deformation should have the property that it does not change when no deformation takes place; therefore it must be unchanged in a rigid-body motion. \mathbf{F} does not have this property; in fact in rigid-body motion, $\mathbf{x} = Q(t)\mathbf{X} + c(t)$, \mathbf{F} is equal to the rotation matrix Q . However, if there is only translation in the rigid-body motion, \mathbf{F} is equal to zero.

Hence, the Lagrangian strain tensor \mathbf{E} is defined:

$$\mathbf{E} = \frac{1}{2}(\mathbf{F}^T \mathbf{F} - \mathbf{I}) \quad (5.4)$$

where \mathbf{I} is identity matrix. It is a suitable measure of deformation since it reduces to the zero tensor when there is only rigid-body motion. If the deformation of the object is described by Equation 5.2 which gives the dependence of \mathbf{x} on \mathbf{X} , then it is straightforward to calculate the nine components of \mathbf{E} :

$$E_{RS} = \frac{1}{2}(F_{iR}F_{iS} - \delta_{RS}) = \frac{1}{2}\left(\frac{\partial x_i}{\partial X_R} \frac{\partial x_i}{\partial X_S} - \delta_{RS}\right), \quad i, R, S = 1, 2, 3. \quad (5.5)$$

where δ_{RS} is the Kronecker delta. This Lagrangian strain tensor \mathbf{E} has three invariants, the three principal strain invariants. Associated with the principal strains, the eigenvalues of \mathbf{E} , there also exist three principal strain directions, the corresponding eigenvectors. The principal strains and their directions are intrinsic to a given state of deformation.

The above definitions are valid in any arbitrary coordinate systems. In Cartesian coordinate system of (x, y, z) with displacement vector in the form of $[\mathbf{u}(x, y, z)]^T = (\mathbf{x} - \mathbf{X}) = (u(x, y, z), v(x, y, z), w(x, y, z))$, the Lagrangian strain tensor reduces to the

simple form:

$$E_{xx} = \frac{\partial u}{\partial x} + \frac{1}{2} \left[\left(\frac{\partial u}{\partial x} \right)^2 + \left(\frac{\partial v}{\partial x} \right)^2 + \left(\frac{\partial w}{\partial x} \right)^2 \right] \quad (5.6)$$

$$E_{yy} = \frac{\partial v}{\partial y} + \frac{1}{2} \left[\left(\frac{\partial u}{\partial y} \right)^2 + \left(\frac{\partial v}{\partial y} \right)^2 + \left(\frac{\partial w}{\partial y} \right)^2 \right] \quad (5.7)$$

$$E_{zz} = \frac{\partial w}{\partial z} + \frac{1}{2} \left[\left(\frac{\partial u}{\partial z} \right)^2 + \left(\frac{\partial v}{\partial z} \right)^2 + \left(\frac{\partial w}{\partial z} \right)^2 \right] \quad (5.8)$$

$$E_{xy} = \frac{1}{2} \left[\frac{\partial u}{\partial y} + \frac{\partial v}{\partial x} + \left(\frac{\partial u}{\partial x} \frac{\partial u}{\partial y} + \frac{\partial v}{\partial x} \frac{\partial v}{\partial y} + \frac{\partial w}{\partial x} \frac{\partial w}{\partial y} \right) \right] \quad (5.9)$$

$$E_{yz} = \frac{1}{2} \left[\frac{\partial v}{\partial z} + \frac{\partial w}{\partial y} + \left(\frac{\partial u}{\partial y} \frac{\partial u}{\partial z} + \frac{\partial v}{\partial y} \frac{\partial v}{\partial z} + \frac{\partial w}{\partial y} \frac{\partial w}{\partial z} \right) \right] \quad (5.10)$$

$$E_{zx} = \frac{1}{2} \left[\frac{\partial w}{\partial x} + \frac{\partial u}{\partial z} + \left(\frac{\partial u}{\partial z} \frac{\partial u}{\partial x} + \frac{\partial v}{\partial z} \frac{\partial v}{\partial x} + \frac{\partial w}{\partial z} \frac{\partial w}{\partial x} \right) \right] \quad (5.11)$$

In small deformation condition, if the components of the displacement are such that their first derivatives are so small that the squares and products of the partial derivatives are negligible, the Lagrangian strain tensor reduces to the infinitesimal strain tensor $[\epsilon]$:

$$[\epsilon] = \begin{bmatrix} \epsilon_{xx} \\ \epsilon_{yy} \\ \epsilon_{zz} \\ \epsilon_{xy} \\ \epsilon_{yz} \\ \epsilon_{zx} \end{bmatrix} = \begin{bmatrix} \frac{\partial}{\partial x} & 0 & 0 \\ 0 & \frac{\partial}{\partial y} & 0 \\ 0 & 0 & \frac{\partial}{\partial z} \\ \frac{1}{2} \frac{\partial}{\partial y} & \frac{1}{2} \frac{\partial}{\partial x} & 0 \\ 0 & \frac{1}{2} \frac{\partial}{\partial z} & \frac{1}{2} \frac{\partial}{\partial y} \\ \frac{1}{2} \frac{\partial}{\partial z} & 0 & \frac{1}{2} \frac{\partial}{\partial x} \end{bmatrix} \begin{bmatrix} u \\ v \\ w \end{bmatrix} = [B'][\mathbf{u}] \quad (5.12)$$

where $[B']$ is the strain-displacement matrix. For the convenience in further derivations, $[\epsilon]$ is expressed as a 6x1 vector instead of a 3x3 matrix. From Equation 5.12, it is evident that the strain tensor of a particle of an object is a function of its displacement vector, which in turn is a function of the spatial position of the particle.

5.3.1.2 Constitutive Equation

The strain measure of an object holds no matter what material the object is made of. It is insufficient to describe the *mechanical behavior* of any particular material, which means that by itself it cannot determine the changes of kinematic variables when forces are applied, or determine the changes of stress when strain is induced. The constitutive equations of a material specifies the dependence of the stress in an object on the kinematic variables such as the strain measure, and vice versa[38, 123].

Following the law of conservation of energy, the material time derivative of the sum of the kinetic energy and internal energy is equal to the sum of the rate at which mechanical work is done by the body and surface forces acting on the object and the rate at which other energy (heat flux, chemical energy, radiation energy, electromagnetic energy, *et al.*) enters the object[123]. If other energy is absent or neglected, then all the mechanical work done on an object either creates kinetic energy, or is stored as potential energy (called the *strain energy* W) which depends only on the deformation. For a linear elastic material, W may be approximated by a quadratic function of the infinitesimal strain components. For a general finite elastic deformation, W depends on an arbitrary manner on the deformation gradient \mathbf{F} . The specific manner of this dependence determines the mechanical behavior of any specific material.

Under the general finite elastic deformation theory[123], the strain-energy function $W(\mathbf{F})$ of an object depends on the deformation gradient tensor \mathbf{F} . While \mathbf{F} itself is not a zero tensor if the object is undergoing rigid-body rotation, there is a restriction on the value of the strain-energy function such that it is not changed if a rigid-body rotation is superimposed on the deformation. Suppose that a particle with initial position \mathbf{X} moves to \mathbf{x} . Further, a rigid rotation is superimposed on the particle to $\bar{\mathbf{x}} = \mathbf{M}\mathbf{x}$, where \mathbf{M} is

the rotation matrix. Let

$$F_{iR} = \frac{\partial x_i}{\partial X_R}, \quad \bar{F}_{iR} = \frac{\partial \bar{x}_i}{\partial X_R} \quad (5.13)$$

Then

$$\bar{F}_{iR} = M_{ij} \frac{\partial x_j}{\partial X_R} = M_{ij} F_{jR}, \quad \text{or} \quad \bar{\mathbf{F}} = \mathbf{M}\mathbf{F} \quad (5.14)$$

Thus, we require that

$$W(\mathbf{F}) = W(\mathbf{M}\mathbf{F}) \quad (5.15)$$

for all rotation matrices \mathbf{M} . A necessary condition for the strain-energy function to be independent of superimposed rigid motion is that it can be expressed in the form $W(\mathbf{F}^T \mathbf{F})$ [123].

In general, the constitutive equations for a finite elastic solid are defined as:

$$T_{i,j} = \frac{\rho}{\rho_0} F_{jR} \frac{\partial W(\mathbf{F})}{\partial F_{iR}} \quad i, j, R = 1, 2, 3. \quad (5.16)$$

where \mathbf{T} is the stress tensor, ρ_0 and ρ the initial and final material density respectively. The equation's apparent simplicity is deceptive, because W is a function of the nine components of \mathbf{F} , which makes it impractical to perform experiments to determine this function for any particular elastic material. In practice, various assumptions under different conditions have been made to derive practical yet realistic strain energy functions of the materials, from which the material constitutive laws can be derived.

5.3.2 Models of the Myocardium

The mechanical behavior of the myocardium is very diverse and complex, and it would be an admirable but extremely difficult goal to formulate its constitutive equations under all circumstances. Rather, we seek to establish equations which describe the most important features of the material while retaining physical plausibility. Ideally, the constitutive equations of the myocardium should characterize the non-linear, anisotropic material properties of the cardiac muscle in a compact way with as few parameters as possible. The relationship should also be formulated based on experimental measurements. There has been a fair amount active research in the biomechanics community in developing myocardial constitutive laws under different conditions and assumptions[57, 59, 71, 84, 121]. Since the stress tensor can be found from the derivatives of W with respect to the strain components[60], emphasis has been on the derivation of various strain energy functions for different myocardial models.

In general, two aspects of the mechanical properties of the myocardium have been considered: the passive tissue properties and the active muscle tension development. A constitutive law for passive tissue properties requires a fully three-dimensional relationship between the six components of the stress and the six components of the strain (assuming symmetric material), whereas the active muscle law requires only a one-dimensional relationship between the fiber strain and the active muscle tension[59]. Since the purpose of our system is to use the constitutive relationship to help recover motion and deformation from image data, not to model the forward activation of the left ventricle, we will only discuss the passive constitutive laws from now on. However, we do realize that the active muscle tension development largely determines the active contraction and expansion of the myocardium, and incorporating active muscle law into our framework

would add important actual physical constraints into the recovery process.

The simplest constitutive relationship is that of the linear elastic solid, or the *Hookean elastic solid*. In this case, the strain energy function has the form

$$W = \frac{1}{2} c_{ijkl} \epsilon_{ij} \epsilon_{kl} \quad (5.17)$$

where ϵ_{ij} and ϵ_{kl} are components of the infinitesimal strain tensor and c_{ijkl} are material specific elastic constants. Under this model, Equation 5.16 can be simplified to:

$$\sigma_{ij} = c_{ijkl} \epsilon_{kl} \quad (5.18)$$

where σ_{ij} is a stress tensor component. This is the constitutive equation for a linear elastic solid. It is evident that the stress components are linear functions of the infinitesimal strain components.

Under the assumptions that the strain and stress tensors are symmetric, and the material is isotropic (the elastic properties are identical in all directions), there are exactly two elastic constants which characterize the material and Equation 5.17 is further reduced to:

$$\sigma_{ij} = \lambda \delta_{ij} \epsilon_{kk} + 2\mu \epsilon_{ij} \quad (5.19)$$

where constants λ and μ are called the *Lame constants*.

In Cartesian coordinates, the linear isotropic constitutive law can be written as:

$$[\sigma] = [C][\epsilon] = [C][B'][\mathbf{u}] \quad (5.20)$$

$$[\epsilon] = [C]^{-1}[\sigma] = [D][\sigma] \quad (5.21)$$

where $[\sigma] = [\sigma_{xx} \ \sigma_{yy} \ \sigma_{zz} \ \sigma_{xy} \ \sigma_{yz} \ \sigma_{zx}]^T$ is the stress vector, $[C]$ is the stress-strain or *material* matrix:

$$[C] = \frac{E}{(1+\nu)(1-2\nu)} \begin{bmatrix} 1-\nu & \nu & \nu & 0 & 0 & 0 \\ \nu & 1-\nu & \nu & 0 & 0 & 0 \\ \nu & \nu & 1-\nu & 0 & 0 & 0 \\ 0 & 0 & 0 & 1-2\nu & 0 & 0 \\ 0 & 0 & 0 & 0 & 1-2\nu & 0 \\ 0 & 0 & 0 & 0 & 0 & 1-2\nu \end{bmatrix} \quad (5.22)$$

and $[D]$ is the strain-stress or *compliance* matrix:

$$[D] = \frac{1}{E} \begin{bmatrix} 1 & -\nu & -\nu & 0 & 0 & 0 \\ -\nu & 1 & -\nu & 0 & 0 & 0 \\ -\nu & -\nu & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1+\nu & 0 & 0 \\ 0 & 0 & 0 & 0 & 1+\nu & 0 \\ 0 & 0 & 0 & 0 & 0 & 1+\nu \end{bmatrix} \quad (5.23)$$

The *Young's modulus* $E = \frac{\mu(3\lambda+2\mu)}{\lambda+\mu}$ and the *Poisson's ratio* $\nu = \frac{\lambda}{2(\lambda+\mu)}$ in the equations are both material related constants. It should be noted that these linear, isotropic constitutive equations *do not* properly describe the mechanical behaviors of the myocardium because myocardium is non-linear and anisotropic. However, they are very simple to use in a computational framework, and are often treated as the first order approximations of more

sophisticated constitutive laws under small deformation conditions. An experimental method for evaluating a slightly modified model (isotropic exponential strain energy) *in vivo* has been performed on 2D MR tagging data[26]. The overall strategy of this study is based on the classical approach in which a particular model for the constitutive relation is fit to a set of experimental data that describe the displacement of the ventricles during diastolic expansion. The finite element method is used to recover the constitutive parameters from the pre-calculated 2D deformation derived from MR tagging data.

More sophisticated models of the myocardium often take into account the micro-structures of the cardiac muscle. The architectures and orientations of the myofibers, the organization of the myocardial sheets, and the collagen inter-connections between the micro-structures determine the non-homogeneous and non-linear stress-strain relationship throughout the myocardium[59, 71]. In one of the attempts to base the constitutive laws upon the micro-structures of the cardiac muscle, the myocardium is treated as a transversely isotropic material[71]. The constitutive equation for the passive tissue is given by an exponential strain energy function $W(E_{ij})$, where E_{ij} are Lagrangian strain components referred to the fiber coordinate system (fiber (F), cross-fiber (C), and transmural (T) coordinates):

$$W = \frac{1}{2} c(e^Q - 1) - \frac{1}{2} p(I_3 - 1) \quad (5.24)$$

where c is a constant and

$$Q = b_1 E_{FF}^2 + b_2(E_{CC}^2 + E_{TT}^2 + E_{CT}^2 + E_{TC}^2) + b_3(E_{FC}^2 + E_{CF}^2 + E_{FT}^2 + E_{TF}^2) \quad (5.25)$$

Here, p is the hydrostatic pressure Lagrange multiplier and I_3 is the third principal

invariant of the strain.

Because the composition of the myocardial tissue is often too complex to derive constitutive laws from a knowledge of the mechanical properties and layout of the microstructural components, simpler empirical relationships were proposed and constitutive parameters estimated from biaxial testing of the tissue were used. Characteristic features of the mechanical properties of passive myocardium include a). the stress-strain relationships along longitudinal, circumferential, and radial axes of the LV are quite different and nearly independent of each other, and b). the axial stress is very low at low axial strains but rises rapidly as the strain approaches a characteristic limiting value for that axis[121]. Based on these observations, a pole-zero strain energy function has been proposed by Hunter[59]:

$$\begin{aligned}
 W = & k_1 \frac{e_{11}^2}{(a_1 - e_{11})^{\alpha_1}} + k_2 \frac{e_{22}^2}{(a_2 - e_{22})^{\alpha_2}} + k_3 \frac{e_{33}^2}{(a_3 - e_{33})^{\alpha_3}} \\
 & + k_4 \frac{e_{12}^2}{(a_4 - e_{12})^{\alpha_4}} + k_5 \frac{e_{23}^2}{(a_5 - e_{23})^{\alpha_5}} + k_6 \frac{e_{31}^2}{(a_6 - e_{31})^{\alpha_6}}
 \end{aligned} \tag{5.26}$$

where e_{ij} are the strain components, a_m are the parameters expressing the limiting values for a particular type of deformation and are always larger than the corresponding strain components, α_m are the parameters expressing the curvature of the uniaxial stress-strain curves, and k_m are parameters giving the relative weighting of each strain energy term.

Similar simplified strain energy functions have been proposed by Humphrey *et al.* [57, 84], identified from biaxial tests on non-contracting canine mid-wall tissue:

$$\begin{aligned}
 W = & c_1(\alpha - 1)^2 + c_2(\alpha - 1)^2 + c_3(I_1 - 3) \\
 & + c_4(I_1 - 3)(\alpha - 1) + c_5(I_1 - 3)^2
 \end{aligned} \tag{5.27}$$

where $I_1 = \text{tr}[\mathbf{F}^T \mathbf{F}]$, and α_m are the stretch ratios at given muscle fiber directions.

While such non-linear models more appropriately describe the complex mechanical properties of the myocardium, they are often computationally very expensive. In the rest of this chapter, all the experiments have been conducted using the linear isotropic model, which is more feasible computationally. However, the different choices for the continuum models of the myocardium *do not* change the fundamental underlying concepts of the integrated framework to recover motion and deformation from image data, although we realize that more sophisticated non-linear models probably will produce more realistic and accurate results.

5.4 Finite Element Analysis

The finite element method (FEM) is a numerical analysis technique for obtaining approximate solutions to a wide variety of engineering problems, especially continuum mechanics problems[12]. Unlike the commonly used finite difference method, which envisions the solution region as an array of grid points, the finite element method envisions the solution region as built up of many small, interconnected subregions or *finite elements*. Its basic premise is that a solution region can be analytically modeled or approximated by replacing it with an assemblage of discrete finite elements, the finite element mesh, which can represent exceedingly complex shapes. In essence, a complex problem over a large solution region can be reduced to a series of greatly simplified problems over many finite elements. The solutions to a series of governing equations of the elements give a piecewise approximation to the solution of the governing equation of the original system[56]. For the analysis of left ventricular motion and deformation, the LV (the solution region) is represented by many small tetrahedra (the finite elements) constructed from the Delaunay

triangulation of the sampled points. Also, the displacement-based solutions of the governing equations give the approximate motion at the sampled points and the deformation of the elements.

5.4.1 Element and Interpolation Function

In a continuum mechanics problem, the field variable (the displacement in our case) possesses infinitely many values because it is a function of each generic point in the solution region. Consequently, the problem is one with an infinite number of unknowns. The finite element method reduces the problem to one with a finite number of unknowns by dividing the solution region into elements and by expressing the unknown field variable in terms of assumed approximating or interpolation functions within each element. These interpolation functions are defined in terms of the values of the field variable at specified *nodal points* (the sampled LV points in our case). The nodal values of the field variable and the interpolation functions completely define the behavior of the field variable within the element. In general, for any element e with r nodes, the field variable function $[\tilde{\delta}]^{(e)}$ within the element is related to its nodal values by r interpolating functions $N_i(x, y, z)$ such that the $[\tilde{\delta}]^{(e)}$ is expressed as:

$$[\tilde{\delta}]^{(e)} = \left\{ \begin{array}{l} \sum_{i=1}^r N_i(x, y, z)u_i \\ \sum_{i=1}^r N_i(x, y, z)v_i \\ \sum_{i=1}^r N_i(x, y, z)w_i \end{array} \right\} = [N][\delta]^{(e)} \quad (5.28)$$

where the interpolation function matrix $[N]$ and the nodal field variable vector (the vector representing the field values at the nodal points) are given by

$$[N] = \begin{bmatrix} N_1 & 0 & 0 & N_2 & 0 & 0 & \dots & N_r & 0 & 0 \\ 0 & N_1 & 0 & 0 & N_2 & 0 & \dots & 0 & N_r & 0 \\ 0 & 0 & N_1 & 0 & 0 & N_2 & \dots & 0 & 0 & N_r \end{bmatrix} \quad (5.29)$$

$$[\delta]^{(e)} = [u_1 \ v_1 \ w_1 \ \dots \ u_r \ v_r \ w_r]^T \quad (5.30)$$

Thus, the nodal values of the field variable become the unknowns for the finite element representation of a continuum mechanics problem. Once these unknowns are found, the interpolation functions define the field variable throughout the assemblage of elements. Clearly, the nature of the solution to the problem and the accuracy of the approximation depend not only on the number and size of the elements, but also on the interpolation functions being used. The finite element mesh must be accurate yet efficient in describing the geometrical structural details of the object, and it must also provide a suitable framework for enforcing the material constitutive laws. In Chapter 3, we discussed many optimal properties of using Delaunay triangulation as the geometrical representation of the left ventricle, and we will use this tetrahedral mesh as the finite element mesh for the linear isoparametric formulation (the element displacements are linearly interpolated in the same way as the geometry) of the system.

The procedure for formulating the individual element equations from variational principles and assembling these local equations to obtain system equations rely on the assumption that the interpolation functions satisfy certain requirements. Often functions are chosen such that the field variable or its derivatives are continuous across adjoining element boundaries. More generally, to guarantee monotonic convergence and to make

the assembly of the individual element equations meaningful, it is required that the interpolation functions satisfy[35, 89]:

- *The compatibility requirement:* at element boundaries, the field variable and any of its partial derivatives up to one order less than the highest-order derivative appearing in the variational functional must be continuous.
- *The completeness requirement:* all uniform states of the field variable and its partial derivatives up to the highest-order derivative appearing in the variational functional should have representation in the interpolated field variable function when, in the limit, the element size shrinks to zero.

In the case where the field variable is the displacement field of an object, the compatibility requirement ensures the continuity of displacement between adjacent elements, and the completeness requirement ensures that the displacement field representation allows for the possibility of rigid-body displacements and constant-strain states within the element. In an isoparametric linear formulation of the system with tetrahedral elements, a linear interpolation function is a suitable choice which ensures first-order continuity within the elements and zero-order continuity across the elements, and it yields zero strain within the element for rigid motion.

5.4.2 Finite Element Formulation

Most applications of the finite element method to continuum mechanics problems have relied on variational principles for the derivation of the element governing equations[12, 56]. Following this tradition, we will derive the governing equations using the minimum potential energy principle for the dynamics of the three-dimensional myocardium, based

on an isotropic linear elastic model. The unknowns for which we solve in this formulation are the nodal displacements or their derivatives, hence this is a *displacement formulation*.

5.4.2.1 Minimum Potential Energy Principle

For an elastic body of a given shape, its potential energy is defined as the energy of the deformation of the body (the strain energy) minus the work done on the body by the external forces. The theorem of minimum potential energy can be stated as following[133]: *The displacement $\mathbf{u} = (u, v, w)$ which satisfies the differential equations of equilibrium, as well as the conditions at the boundary surface, yields a smaller value for the potential energy than any other displacement which satisfies the same conditions at the bounding surface.* Hence, if $\Pi(u, v, w)$ is the potential energy, $U_p(u, v, w)$ is the strain energy, and $V_p(u, v, w)$ is the work done by the applied loads during the displacement changes, then we have at equilibrium

$$\begin{aligned}\delta\Pi(u, v, w) &= \delta[U_p(u, v, w) - V_p(u, v, w)] \\ &= \delta U_p(u, v, w) - \delta V_p(u, v, w) = 0\end{aligned}\tag{5.31}$$

In this equation, the variation is taken with respect to the displacements while all other parameters are held fixed.

The strain energy of a linear isotropic elastic body is a function of its strain and stress tensors, and can be expressed as (using Equation 5.12 and 5.20):

$$\begin{aligned}U_p(u, v, w) &= \frac{1}{2} \int \int \int_{\Omega} [\epsilon]^T [\sigma] dV \\ &= \frac{1}{2} \int \int \int_{\Omega} [\epsilon]^T [C] [\epsilon] dV\end{aligned}$$

$$= \frac{1}{2} \int \int \int_{\Omega} [\mathbf{u}]^T [B']^T [C] [B'] [\mathbf{u}] dV \quad (5.32)$$

where Ω is the volume of the body. The work done by the external forces, including the body forces $[F_b]$, the surface traction $[F_s]$ and the concentrated forces $[F_i]$, is given by:

$$V_p(u, v, w) = \int \int \int_{\Omega} [\mathbf{u}]^T [F_b] dV + \int \int_S [\mathbf{u}]^T [F_s] dS + \sum_i [\mathbf{u}]^T [F_i] \quad (5.33)$$

For the left ventricle, the body forces $[F_b]$ are mostly gravitational, surface traction $[F_s]$ and concentrated forces $[F_i]$ include forces arising from the ventricular blood pressure on the endocardium and the reaction forces from the adjoining structures such as the lung.

The displacement field \mathbf{u} that minimize Π and satisfies all the boundary conditions is the equilibrium displacement.

5.4.2.2 Element Formulation

Assume that the volume Ω of the linear elastic body is divided into M discrete elements. We may write the potential energy of the body (the assemblage of the elements) as the sum of the potential energies of all elements, provided that the interpolation functions expressing the displacement function within each element satisfy the compatibility and completeness requirements[56]:

$$\Pi(u, v, w) = \sum_{e=1}^M \Pi^{(e)}(u, v, w) \quad (5.34)$$

For a three-dimensional linear elastic object, polynomial interpolation functions satisfy the compatibility and completeness requirements when the polynomials contain at least the constant and linear terms. For tetrahedral elements, we need only the constant and

linear terms.

After the proper interpolation functions have been chosen, we may deal with the potential energy of an isolated element e . The displacements measured in a *local* coordinate system x, y, z (to be chosen conveniently) within element e are assumed to be a function of the displacements at its r nodal points:

$$[\mathbf{u}]^{(e)}(x, y, z) = [N]^{(e)}(x, y, z)[\mathbf{U}]^{(e)} \quad (5.35)$$

where $[N]^{(e)}$ is the displacement interpolation matrix, and $[\mathbf{U}]^{(e)}$ is a vector of the three displacement components U_i, V_i, W_i at all the nodal points:

$$[\mathbf{U}]^{(e)} = [U_1 \ V_1 \ W_1 \ \dots \ U_r \ V_r \ W_r]^T \quad (5.36)$$

It should be emphasized that $[\mathbf{U}]^{(e)}$ does not need to be expressed in the same local coordinate system as $[\mathbf{u}]^{(e)}$. In fact, it is often expressed in a global coordinate system for computational efficiency.

We can now calculate the corresponding element strain tensor as expressed in Equation 5.12:

$$[\epsilon]^{(e)} = [B']^{(e)}[\mathbf{u}]^{(e)} = [B']^{(e)}[N]^{(e)}[\mathbf{U}]^{(e)} = [B]^{(e)}[\mathbf{U}]^{(e)} \quad (5.37)$$

where $[B]^{(e)} = [B']^{(e)}[N]^{(e)}$ is the local element strain-displacement matrix. The stress tensor in the element is

$$[\sigma]^{(e)} = [C]^{(e)}[\epsilon]^{(e)} \quad (5.38)$$

By substituting Equations 5.35 and 5.37 into the potential energy functional, we obtain the potential energy of a single element in terms of the nodal displacement values:

$$\begin{aligned}
\Pi^{(e)} &= U_p^{(e)} - V_p^{(e)} & (5.39) \\
&= \frac{1}{2} \int \int \int_{\Omega^{(e)}} [\mathbf{U}]^{(e)T} [B]^{(e)T} [C]^{(e)} [B]^{(e)} [\mathbf{U}]^{(e)} dV \\
&\quad - \int \int \int_{\Omega^{(e)}} [\mathbf{U}]^{(e)T} [N]^{(e)T} [F_b]^{(e)} dV \\
&\quad - \int \int_{S^{(e)}} [\mathbf{U}]^{(e)T} [N]^{(e)T} [F_s]^{(e)} dS \\
&\quad - \sum_{i^{(e)}} [\mathbf{U}]^{(e)T} [N]^{(e)T} [F_i] & (5.40)
\end{aligned}$$

where the integrations are performed over the volume $\Omega^{(e)}$ and the surface $S^{(e)}$ of the element e . It is important to note that we may use different element coordinate systems in the calculations, which is the reason why each of the integrals can be evaluated very effectively in general assemblages.

The equilibrium of the potential energy of the entire elastic body assumes a minimum value when the first variation of the functional vanishes:

$$\delta\Pi = \sum_{e=1}^M \delta\Pi^{(e)} = 0 \quad (5.41)$$

where

$$\delta\Pi^{(e)} = \sum_{i=1}^r \frac{\partial\Pi^{(e)}}{\partial U_i} \delta U_i + \sum_{i=1}^r \frac{\partial\Pi^{(e)}}{\partial V_i} \delta V_i + \sum_{i=1}^r \frac{\partial\Pi^{(e)}}{\partial W_i} \delta W_i \quad (5.42)$$

Since δU_i , δV_i , and δW_i are independent (not necessarily zero) variations, we must have:

$$\frac{\partial \Pi^{(e)}}{\partial U_i} = \frac{\partial \Pi^{(e)}}{\partial V_i} = \frac{\partial \Pi^{(e)}}{\partial W_i} = 0, \quad i = 1, 2, \dots, r \quad (5.43)$$

for every element of the body. These equations express the conditions we use to find the element governing equations, and they are equivalent to minimizing the potential energy by differentiating $\Pi^{(e)}$ with respect to vector $[\mathbf{U}]^{(e)}$ and setting the result to zero:

$$\frac{\partial \Pi^{(e)}}{\partial [\mathbf{U}]^{(e)}} = 0 \quad (5.44)$$

Following this procedure and minimizing Equation 5.36 gives

$$\begin{aligned} & \int \int \int_{\Omega^{(e)}} [B]^{(e)T} [C]^{(e)} [B]^{(e)} [\mathbf{U}]^{(e)} dV \\ & - \int \int \int_{\Omega^{(e)}} [N]^{(e)T} [F_b]^{(e)} dV \\ & - \int \int_{S^{(e)}} [N]^{(e)T} [F_s]^{(e)} dS \\ & - \sum_{i^{(e)}} [N]^{(e)T} [F_i] \\ & = 0 \end{aligned} \quad (5.45)$$

or

$$[K]^{(e)} [\mathbf{U}]^{(e)} = [F]^{(e)} \quad (5.46)$$

where the element stiffness matrix is

$$[K]^{(e)} = \int \int \int_{\Omega^{(e)}} [B]^{(e)T} [C]^{(e)} [B]^{(e)} dV \quad (5.47)$$

and the element force vectors are

$$[F]^{(e)} = [F_B]^{(e)} + [F_S]^{(e)} + [F_I]^{(e)} \quad (5.48)$$

$$[F_B]^{(e)} = \int \int \int_{\Omega^{(e)}} [N]^{(e)T} [F_b]^{(e)} dV \quad (5.49)$$

$$[F_S]^{(e)} = \int \int_{S^{(e)}} [N]^{(e)T} [F_s]^{(e)} dS \quad (5.50)$$

$$[F_I]^{(e)} = \sum_{i^{(e)}} [N]^{(e)T} [F_i] \quad (5.51)$$

Equation 5.46 expresses the governing equilibrium equations of element e corresponding to the nodal displacements $[\mathbf{U}]^{(e)}$.

If inertial forces are needed to be considered in the element, a truly dynamic problem needs to be solved. Using d'Alembert's principle, we can simply include the element inertia force as part of the body forces. Assuming that the element accelerations are approximated by the interpolation functions in the same way as the element displacements, the contribution from the body forces is:

$$[F_B]^{(e)} = \int \int \int_{\Omega^{(e)}} [N]^{(e)T} \left[[F_b]^{(e)} - \rho^{(e)} [N]^{(e)} [\ddot{\mathbf{U}}]^{(e)} \right] dV \quad (5.52)$$

where $[F_b]^{(e)}$ no longer includes inertia forces, $[\ddot{\mathbf{U}}]^{(e)}$ lists the nodal point accelerations, and $\rho^{(e)}$ is the mass density of element e . The governing equilibrium equations are, in

this case,

$$[M]^{(e)}[\ddot{\mathbf{U}}]^{(e)} + [K]^{(e)}[\mathbf{U}]^{(e)} = [F]^{(e)} \quad (5.53)$$

where $[F]^{(e)}$ and $[\mathbf{U}]^{(e)}$ are time dependent. The matrix $[M]^{(e)}$ is the mass matrix of the element

$$[M]^{(e)} = \int \int \int_{\Omega^{(e)}} \rho^{(e)} [N]^{(e)T} [N]^{(e)} dV \quad (5.54)$$

In actually measuring the dynamic response of an elastic body, it is observed that energy is dissipated during vibration which is usually taken account of by introducing velocity-dependent damping forces. Introducing the damping forces as additional contributions to the body forces, we obtain

$$[F_B]^{(e)} = \int \int \int_{\Omega^{(e)}} [N]^{(e)T} \left[[F_b]^{(e)} - \rho^{(e)} [N]^{(e)} [\ddot{\mathbf{U}}]^{(e)} - \kappa^{(e)} [N]^{(e)} [\dot{\mathbf{U}}]^{(e)} \right] dV \quad (5.55)$$

In this case, $[F_b]^{(e)}$ no longer includes inertia and damping forces, $[\dot{\mathbf{U}}]^{(e)}$ is a vector of the nodal point velocities, and $\kappa^{(e)}$ is the damping property parameter of the element e . The governing equilibrium equations are, in this case,

$$[M]^{(e)}[\ddot{\mathbf{U}}]^{(e)} + [C]^{(e)}[\dot{\mathbf{U}}]^{(e)} + [K]^{(e)}[\mathbf{U}]^{(e)} = [F]^{(e)} \quad (5.56)$$

where $[C]^{(e)}$ is the damping matrix of the element

$$[C]^{(e)} = \int \int \int_{\Omega^{(e)}} \kappa^{(e)} [N]^{(e)T} [N]^{(e)} dV \quad (5.57)$$

In practice it is difficult to determine the damping parameters because they are frequency dependent. The damping matrix $[C]^{(e)}$ is often constructed using the mass and stiffness matrices together with experimental results on the amount of damping. One low-order approximation is Rayleigh damping where the damping matrix is of the form[12]:

$$[C]^{(e)} = \alpha[M]^{(e)} + \beta[K]^{(e)} \quad (5.58)$$

where α and β are constants to be determined from two given damping ratios that correspond to two unequal frequencies of vibration.

It is worth to pointing out that even though the element matrices $[M]^{(e)}$, $[C]^{(e)}$, and $[K]^{(e)}$ for any element e all take the same forms as derived above, the actual terms of the mass, damping, and stiffness matrices can vary even among elements with the *same geometry and same interpolation functions*. This is because different elements can have different material constitutive laws, different material densities, and different damping characteristics. This non-homogeneity gives us the flexibility to model different regions of the left ventricle differently, according to the prior knowledge about the tissue. It also, to certain degree, justifies the choice of the computationally efficient linear elastic model because each small piece of tissue can always be approximated to be linear isotropic elastic material if the size and the deformation of the element are small enough.

5.4.2.3 System Formulation

After the governing equilibrium equations of all the elements have been found, the next step in the finite element analysis of the left ventricle is to combine all these equations to form a complete set of system equations which govern the composite of elements. The procedure for constructing the system governing equations from the element equations is

the same regardless of the type of problem or the complexity of the system of elements. Even if an object is modeled with a mixture of several different kinds of elements or materials, the system equations are assembled from the element equations in the same way as described below[56].

The system assembly procedure is based on the insistence of *compatibility* at the element nodes. By this we mean that at any node where elements are connected the values of the unknown nodal variables are the same for all elements connecting at that node. The consequence of this rule is the basis for the assembly process. For the displacement-based formulation, the nodal variables are the displacements. When these displacements are matched at the nodes, the nodal stiffness, mass, damping, and loads for each of the elements sharing the node are added together to obtain the net stiffness, mass, damping, and loads at that node.

For the displacement-based finite element formulation, the general assembly procedure for the system governing equations from the element equations is summarized in the following steps:

- Set up the $3N \times 3N$ global stiffness matrix $[K]$, mass matrix $[M]$, damping matrix $[C]$, and $3N \times 1$ load matrix $[F]$, where N is the total number of nodes.
- After establishing the correspondence between local and global numbering schemes of the nodes and elements, the local indices of the coefficients of the element stiffness, mass, damping and load matrices are transformed into global indices.
- For all the elements, the local matrices are summed together to form the corresponding global matrices:

$$[M] = \sum_{e=1}^M [M]_t^{(e)} \quad (5.59)$$

$$[C] = \sum_{e=1}^M [C]_t^{(e)} \quad (5.60)$$

$$[K] = \sum_{e=1}^M [K]_t^{(e)} \quad (5.61)$$

$$[F] = \sum_{e=1}^M [F]_t^{(e)} \quad (5.62)$$

where $[M]_t^{(e)}$, $[C]_t^{(e)}$, $[K]_t^{(e)}$ and $[F]_t^{(e)}$ are the transformed element matrices in global indices.

The result of the above process would then be used to derive the system governing equations for the elastic body:

$$[M][\ddot{\mathbf{U}}] + [C][\dot{\mathbf{U}}] + [K][\mathbf{U}] = [F] \quad (5.63)$$

where $[\mathbf{U}]$ the nodal displacement vector field for the entire body.

It should be noted that while the finite element mesh provides the basis for approximating a continuous spatial model of the left ventricle, the governing equations in Equation 5.63 provide the basis of an appropriate temporal model for the motion and deformation analysis.

5.5 Integrated Motion/Deformation Analysis

Following the procedures described in Section 5.4, we can develop the finite element framework of the left ventricle, modeled as a linear isotropic elastic object. After the system nodal-displacement-based governing equations are assembled, we can use this system to pursue the integrated approach of quantifying LV motion and deformation. Complementary image derived information can be incorporated into one framework to

recover the true transmural deformation. For the remainder of this thesis, we will assume that the image-based sources include boundary constraints (shape-based displacements) and mid-wall constraints (instantaneous phase velocity), both from phase contrast MR images. However, as explained in Section 5.2, other types of image-based information can also be used in this unified framework. We should also point out that we are analyzing frame-to-frame motion and deformation, which means that the framework only attempts to quantify the LV tissue movement between pairs of temporally consecutive image frames. Even though we do analyze motion and deformation for all sixteen pairs of image frames, and changes between each pair can always be referred back to the chosen original undeformed state, we do not claim to have a temporal motion and deformation model beyond two image frames.

5.5.1 Initial Conditions

The integrated motion and deformation analysis framework is formulated such that the mid-wall velocity and the boundary displacements are used as data-based constraints. The unknown field variables are the displacement vectors at the nodal points, although the derivatives of the displacements (velocity and acceleration vectors at the nodal points) can also be derived from the system equations. Since we are only doing frame-to-frame analysis within the time interval T , we assume that the first image frame is sampled at time $t = 0$ and the second image is sampled at time $t = T$. For each pair of image frames at time $t = 0$ and $t = T$, the phase velocity data at $t = 0$ determine the initial conditions of the governing equations, while the shape-based displacements at the boundaries are treated as the boundary conditions of the system which impose prescribed displacements at certain boundary nodal points. Under these two image-based constraints, the integrated motion and deformation recovery can be performed within the finite element

framework.

At time $t = 0$, the initial conditions for the system governing equations are as follows:

- The initial displacements of all the points $[\mathbf{U}_{all}(0)]$ are always zero (the object has not moved).
- The three MR phase images provide the three components of the initial velocities $[\dot{\mathbf{U}}_{mid-wall}(0)]$ for the *true* mid-wall points (mid-wall point which are at least one pixel away from the boundaries). For all other points (boundary points and mid-wall points next to the boundaries), we could assume their velocities, $[\dot{\mathbf{U}}_{boundary}(0)]$, to be zero. (This could become a problem because the true mid-wall points and the boundary points now have discontinuity in their velocity values. To avoid this discontinuity problem, we may use the average of true mid-wall velocity values near each boundary point as its initial velocity.)
- The initial accelerations of all the points $[\ddot{\mathbf{U}}_{all}(0)]$ are assumed to be zero.
- The initial equivalent total loads $[F(0)]$ can be computed from the governing equations:

$$[F(0)] = [M][\ddot{\mathbf{U}}_{all}(0)] + [C][\dot{\mathbf{U}}_{all}(0)] + [K][\mathbf{U}_{all}(0)] \quad (5.64)$$

where $[\dot{\mathbf{U}}_{all}(0)]$ is the sum of $[\dot{\mathbf{U}}_{mid-wall}(0)]$ and $[\dot{\mathbf{U}}_{boundary}(0)]$.

It should be pointed out that since we will analyze pair-wise motion throughout the cardiac cycle, the estimated velocities and accelerations at time $t = T$ from the previous pair of images can be used as the initial conditions of velocities and accelerations at time $t = 0$ of the current pair of images. However, we must validate these estimates to be accurate before we can trust them. In this thesis, we do not use these estimates.

5.5.2 Boundary Conditions

From our shape-based boundary motion tracking algorithm, or other means of point tracking process such as MR tagging, the displacements of some nodal points from $t = 0$ to $t = T$ are known. Denoted as $[\mathbf{U}_{boundary}]$, these displacements are used as the boundary conditions of the system at time T . There are a number of ways to apply the boundary conditions to the governing equations. When the boundary conditions are applied, the number of nodal unknowns and the number of equations to be solved are effectively reduced. However, it is most convenient to introduce the known displacements in a way that leaves the original number of equations unchanged and avoids a major restructuring of the system equations[12, 56].

One way to include prescribed nodal displacements while retaining the original structure of system equations is to modify certain diagonal terms of the stiffness matrix $[K]$ and the corresponding terms of the load vector $[F]$. Let the prescribed displacement value of the displacement variable U_i (the i th term of the column vector $[\mathbf{U}]$) to be b , the following constraint equation

$$kU_i = kb \tag{5.65}$$

is added to the system governing equation (Equation 5.63), where $k \gg K_{ij}$. The modified governing equation for this displacement variable becomes:

$$\sum_{j=1}^{3N} M_{ij} \ddot{U}_j + \sum_{j=1}^{3N} C_{ij} \dot{U}_j + \sum_{j=1}^{3N} K_{ij} U_j + kU_i = F_i + kb \tag{5.66}$$

Therefore, the solution of this modified governing equation must now give[12]

$$U_i \approx b \tag{5.67}$$

Physically, this procedure can be interpreted as adding a spring of vary large stiffness, and specifying a load which produces the required displacement b for variable U_i . This procedure is repeated until all prescribed displacement variables have been treated. After these modifications have been made, we proceed with the simultaneous solution to the complete set of $3N$ differential equations.

In very strict terms, this modifying procedure will not give the exact values for the prescribed displacements at the corresponding nodal points because we have only modified the $[K]$ and $[F]$ matrices but not the $[M]$ and $[C]$ matrices. In addition, the left side of the i th governing equation includes the sum of the products of the ij th ($j = 1, \dots, 3N$) term of $[K]$ and the j term of $[\mathbf{U}]$. Even though the terms $K_{ij}U_j (j \neq i)$ are small comparing to $K_{ii}U_i$, they still make the solution of the prescribed displacement U_i inexact. However, if the chosen large multiplying factors are indeed very large compared to the values of the matrix terms, the errors will be negligible.

In addition, this inexactness provides a possible method for the incorporation of confidence measures into the displacement boundary conditions. From the discussion in Chapter 4, we know that the confidence of shape-based point matching between pairs of surfaces can be measured by a metric based upon the *goodness* and *uniqueness* of the match. Since we are using the displacement between these matched points as the prescribed displacements in the unified framework, we should treat these displacements differently based on their confidence measures. From this point of view, the large multiply-

ing factor should be weighted by the confidence measure for each prescribed displacement. The displacements with high confidence measures will have *really large* multiplying factors to enforce the system solution to give the exact prescribed values at these nodal points. The displacements with low confidence measures should have relatively small multiplying factors to have inexact solution values, which are the compromise of the prescribed conditions and the smoothness constraint which is implicitly enforced by the constitutive laws of the materials.

5.5.3 Numerical Solution

After setting up the initial and displacement boundary conditions, the finite element system is regarded as an elastic object in static conditions when some outside loads are applied to certain nodal points. Therefore, the object moves and deforms because of these forces. Mathematically, the governing equations represent a system of differential equations of second order and, in principle, the solution to the equations can be obtained by standard procedures for the solution of differential equations with constant coefficients. However, the procedure proposed for the solution of general systems of differential equations can become very expensive if the order of the matrices is large. In practice, these types of systems are almost always solved by numerical means.

In direct integration, the governing equations are integrated using a numerical step-by-step procedure. Instead of trying to satisfy Equation 5.63 at any time t , it is aimed to satisfy the governing equations only at discrete time intervals Δt apart. This means that equilibrium, which includes the effects of inertia and damping forces, is sought at discrete time points within the interval of solution. In addition, a variation of displacements, velocities, and accelerations within each time interval is assumed. It is the form of assumption on the variation that determines the accuracy, stability, and the

cost of the solution procedure[12].

In the Newmark method[82], the following assumptions about estimating displacement, velocity, and acceleration at time $t + \Delta t$ from the available data at t and $t + \Delta t$ are used:

$$[\dot{\mathbf{U}}(t + \Delta t)] = [\dot{\mathbf{U}}(t)] + [(1 - \delta)[\ddot{\mathbf{U}}(t)] + \delta[\ddot{\mathbf{U}}(t + \Delta t)]] \Delta t \quad (5.68)$$

$$\begin{aligned} [\mathbf{U}(t + \Delta t)] &= [\mathbf{U}(t)] + [\dot{\mathbf{U}}(t)]\Delta t \\ &+ \left[\left(\frac{1}{2} - \alpha \right) [\ddot{\mathbf{U}}(t)] + \alpha [\ddot{\mathbf{U}}(t + \Delta t)] \right] \Delta t^2 \end{aligned} \quad (5.69)$$

where α and δ are parameters that can be determined to obtain integration accuracy and stability. In addition to these two assumptions, for solution of the displacements, velocities, and accelerations at time $t + \Delta t$, the governing equations at time $t + \Delta t$ are also considered:

$$[M][\ddot{\mathbf{U}}(t + \Delta t)] + [C][\dot{\mathbf{U}}(t + \Delta t)] + [K][\mathbf{U}(t + \Delta t)] = [F(t + \Delta t)] \quad (5.70)$$

Solving from Equation 5.69 for $[\ddot{\mathbf{U}}(t + \Delta t)]$ in terms of $[\mathbf{U}(t + \Delta t)]$, and then substituting for $[\ddot{\mathbf{U}}(t + \Delta t)]$ into Equation 5.68, we obtain equations for $[\ddot{\mathbf{U}}(t + \Delta t)]$ and $[\dot{\mathbf{U}}(t + \Delta t)]$, each in terms of the unknown displacements $[\mathbf{U}(t + \Delta t)]$ only. These two relations for $[\dot{\mathbf{U}}(t + \Delta t)]$ and $[\ddot{\mathbf{U}}(t + \Delta t)]$ are substituted into Equation 5.70 to solve for $[\mathbf{U}(t + \Delta t)]$, after which, using Equations 5.68 and 5.69, $[\dot{\mathbf{U}}(t + \Delta t)]$ and $[\ddot{\mathbf{U}}(t + \Delta t)]$ can also be calculated.

The complete algorithm using Newmark integration scheme is given below[12]:

- Initial calculations:

1. Form mass matrix $[M]$, damping matrix $[C]$, and stiffness matrix $[K]$.
2. Initialize $[\mathbf{U}(0)]$, $[\dot{\mathbf{U}}(0)]$, and $[\ddot{\mathbf{U}}(0)]$ as the initial conditions.
3. Select time step size Δt , parameters α, δ , and calculate the integration constants $a_i, i = 0, \dots, 7$:

$$\delta \leq 0.5$$

$$\alpha \leq 0.25(0.5 + \delta)$$

$$a_0 = \frac{1}{\alpha \Delta t^2}$$

$$a_1 = \frac{\delta}{\alpha \Delta t}$$

$$a_2 = \frac{1}{\alpha \Delta t}$$

$$a_3 = \frac{1}{2\alpha} - 1$$

$$a_4 = \frac{\delta}{\alpha} - 1$$

$$a_5 = \frac{\Delta t}{2} \left(\frac{\delta}{\alpha} - 2 \right)$$

$$a_6 = \Delta t(1 - \delta)$$

$$a_7 = \delta \Delta t$$

4. Form effective stiffness matrix $[\hat{K}]$:

$$[\hat{K}] = [K] + a_0[M] + a_1[C]$$

5. Triangularize $[\hat{K}]$:

$$[\hat{K}] = [L][D][L]^T$$

- For each time step:

1. Calculate effective loads at time $t + dt$:

$$[\hat{F}(t + \Delta t)] = [F(t + \Delta t)]$$

$$\begin{aligned}
& + [M](a_0[\mathbf{U}(t)] + a_2[\dot{\mathbf{U}}(t)] + a_3[\ddot{\mathbf{U}}(t)]) \\
& + [C](a_1[\mathbf{U}(t)] + a_4[\dot{\mathbf{U}}(t)] + a_5[\ddot{\mathbf{U}}(t)])
\end{aligned}$$

2. Solve for displacements at $t + \delta t$:

$$[L][D][L]^T[\mathbf{U}(t + \Delta t)] = [\hat{F}(t + \Delta t)]$$

3. Calculate accelerations and velocities at $t + \Delta t$:

$$\begin{aligned}
[\ddot{\mathbf{U}}(t + \Delta t)] & = a_0([\mathbf{U}(t + \Delta t)] - [\mathbf{U}(t)]) \\
& \quad - a_2[\dot{\mathbf{U}}(t)] - a_3[\ddot{\mathbf{U}}(t)] \\
[\dot{\mathbf{U}}(t + \Delta t)] & = [\dot{\mathbf{U}}(t)] + a_6[\ddot{\mathbf{U}}(t)] + a_7[\ddot{\mathbf{U}}(t + \Delta t)]
\end{aligned}$$

The cost of a direct integration analysis is directly proportional to the number of time steps required for solution. On one hand, the time step must be small enough to obtain accuracy in the solution. On the other hand, the time step must not be smaller than necessary, because this would mean that the solution is more costly than actually required. In the selection of an appropriate time step Δt for direct integration, the two fundamental concepts to be considered are those of stability and accuracy of the integration scheme.

Stability of an integration method means that the initial conditions for the governing equations with a large value of $\Delta t/T$ must not be amplified artificially and thus make the integration of the lower natural vibration modes worthless. Stability also means that any errors in the displacements, velocities, and accelerations at time t do not grow in the integration. Stability is assured if the time step is small enough to integrate accurately the response in the highest frequency component of the natural vibration. An integration method is unconditionally stable if the solution for any initial conditions does not grow without bound for any time step Δt , in particular, when $\Delta t/T$ is large. The

Newmark method is unconditionally stable provided $\delta \geq 0.5$ and $\alpha \geq 0.25(\delta + 0.5)^2$ [12].

For an unconditionally stable integration method, the time step has to be chosen to yield an accurate and effective solution. It should only be small enough that the response in all modes which significantly contribute to the total structural response is calculated accurately. In practice, however, the vibration modes are often difficult if not impossible to calculate for a very complex object such as the left ventricle. Usually, computational experience is required to make the compromise between accuracy and efficiency. Empirically, we have chosen $\Delta t = \frac{T}{10}$ as the time step in our integration process. For the Newmark method, the two parameters α and δ can be varied to obtain stability and accuracy. The process corresponding to $\delta = 0.5$ and $\alpha = 0.25$ has the most desirable accuracy characteristics[12].

One additional step is also applied to make the integration process more stable and accurate. To reduce the oscillation of the elastic body of the left ventricle, the displacement boundary conditions are enforced gradually. If there are n integration steps between $t = 0$ and $t = T$, the enforced displacement U_i^k at step k of the integration is:

$$U_i^k = U_i \sin\left(\frac{\pi k}{2n}\right) \quad (5.71)$$

where U_i is the prescribed displacement at T . By enforcing the prescribed displacements this way, the elastic object makes larger movement at the beginning of the integration, and it moves less towards the end of the time interval. Hence, the system is more stable when it reaches time $t = T$.

The numerical solution obtained from the above described Newmark integration of the governing equations produces the estimated displacements, velocities, and acceler-

ations of the left ventricle at time $t = T$, the end time of the pair of image frames. These motion estimates are derived from an integrated framework which is based on a linear elastic mechanical model of the myocardium, and is constrained by the initial velocity information from the MR phase images and the shape-based boundary displacements. It takes advantage of the complementary nature of these image sources, and uses the material constitutive relationships to produce a mechanically plausible solution to the system governing equations. It should be pointed out that the motion analysis can be done for every pair of the images throughout the cardiac cycle. If the global coordinate systems are the same for all pair-wise operations, the displacements at any time frame can always be referred to the chosen initial state, usually the end of diastole. After the displacements have been calculated, the coordinate-dependent strain tensor $\epsilon^{(e)}$ for each tetrahedral element e can be computed from Equation 5.12. Furthermore, the principal strain tensor $\epsilon_p^{(e)}$ of each tetrahedral element e can be computed as the eigenvalues and eigenvectors of the tensor $\epsilon^{(e)}$.

In principle, using the finite element framework to track motion between temporal images can be regarded as a predictor from time $t = 0$ to time $t = T$. Since we already have data information at $t = T$ in terms of the segmented endocardial and epicardial surfaces, as well as the mid-wall velocities, we can refine the motion estimate between $t = 0$ and $t = T$ by comparing how close the image-driven, model-based prediction comes to the actual data. The differences between the data and the prediction can be used as a recursive feedback term to improve the matching process. Since we have only done some initial work regarding this feedback process in two-dimensional case[115], we present the mechanism in Appendix A.

5.6 Experiments

The integrated motion and deformation analysis framework proposed has been implemented. Experiments have been conducted with real cardiac MR phase contrast images from a normal canine study.

Figure 5.2 shows an example of phase contrast images of a canine mid-ventricle slice. In this dataset, three contiguous short axis slices were collected using the cine phase contrast gradient echo sequence for sixteen time frames. The imaging parameters were: flip angle = 30° , $TE = 34msec$, $TR = 34msec$, $FOV = 28cm$, $5mm$ skip 0, matrix 256×128 , 4 nex, $venc = 15cm/sec$. The in-plane resolution of the dataset is $1.09mm/pixel$, and the inter-plane resolution is $5mm$. The intensity values of the velocity images range from $-150mm/second$ to $150mm/second$, with the signs of the value indicating the directions of the velocities. The dog was infarcted to cause disconnected motion at the interventricular septum (the lower left part of the LV). The experiment was performed by Dr. Albert Sinusas of Yale medical school, and the images were provided by Dr. Todd Constable of Yale MR center.

Again, it is important to notice that the magnitude image and the three directional velocity images are perfectly registered since they are acquired from the same complex MR signal. It should also be noted that because of the technical difficulty still existing in the image acquisition, the image dataset only covers a small part of the left ventricle. However, this does not alter the validity of using this dataset to test the capability of the integrated framework except that there is 3D motion out of the field of view vertically.

Since it is more desirable to have roughly equal resolutions in all three dimensions to track surface motion as discussed in Chapter 3, some kind of interpolation is needed between the data contour slices. The shape-based contour interpolation is used to insert

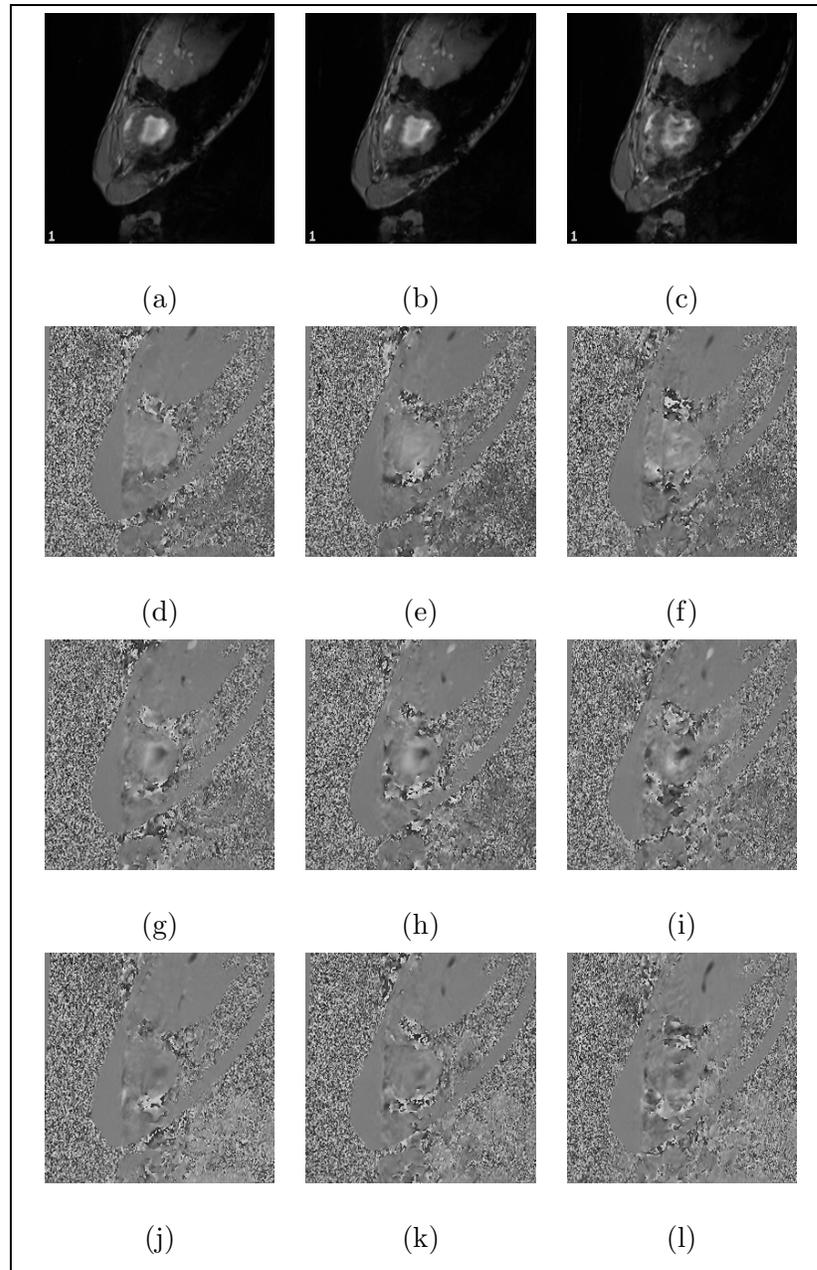


Figure 5.2: 3D MR phase contrast images at ED. (a)-(c): the magnitude images from lower to upper slices; (d)-(f): x dimension velocity images; (g)-(i): y dimension velocity images; (j)-(l): z dimension velocity images.

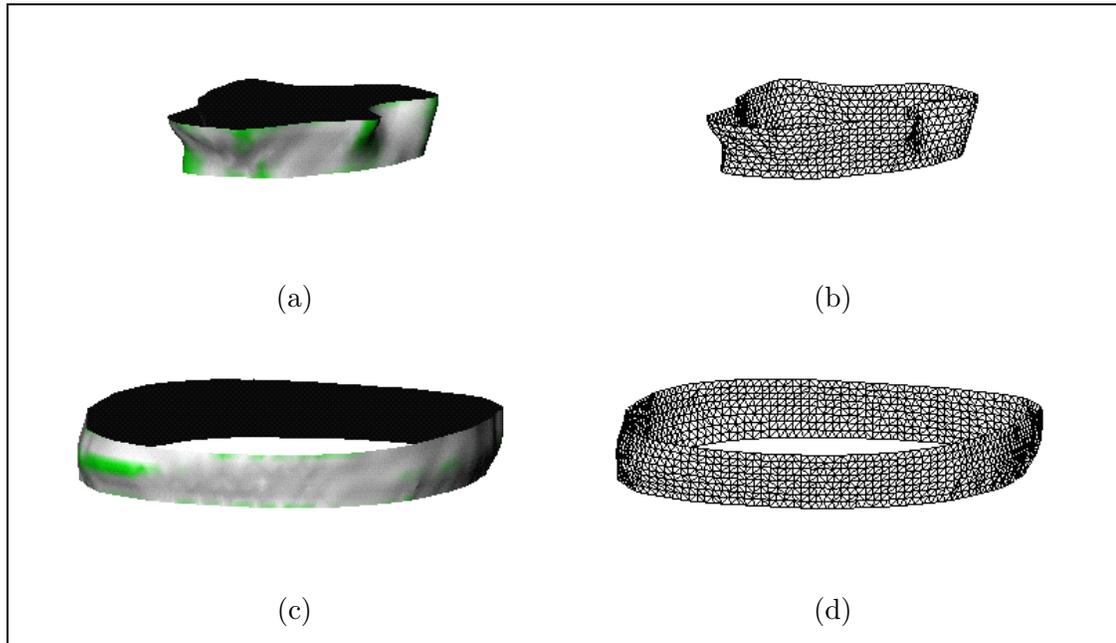


Figure 5.3: Myocardial Surfaces derived from phase contrast MR images. (a): the endocardial potential energy map; (b): the endocardial surface wireframe; (c): the epicardial potential energy map; (d): the endocardial surface wireframe.

three interpolated contours to every two consecutive data contours. Figure 5.3 shows the potential energy maps and the wireframes of the interpolated endocardial and epicardial surface at end diastole. The shape-based surface motion tracking process is then applied to the sixteen interpolated surface sequences, once for the endocardium and once for the epicardium. This way, the surface displacements have $1.09mm$ in-plane resolution and $1.25mm$ inter-plane resolution. A subset of the surface point displacements (ten percent) is used as the boundary displacement constraint in the integrated volumetric framework.

The velocity images still have $5mm$ inter-plane resolution. To deal with this problem, we have either inserted three tri-linearly interpolated velocity images into every

two data velocity images, or for computational reasons, we have coarsely re-sampled the in-plane images to reduce the in-plane resolution to $4.36mm$. In the example given in this section, the velocity images are re-sampled to lower resolution to save computation time. The mid-wall velocity of the phase contrast images is used as the initial velocity constraint in the integrated volumetric framework.

In the case where the velocity images are re-sampled to lower resolution, the myocardial surfaces are also re-sampled to the same lower resolutions of $4.36mm/pixel$ in-plane and $5mm/pixel$ inter-plane after the surface motion tracking has been performed. This way, even though the final re-sampled dataset has only $4.36mm$ in-plane and $5mm$ inter-plane resolutions to form larger tetrahedral elements to save computational expense, the boundary displacements still have $1.09mm$ in-plane and $1.25mm$ inter-plane resolutions. The myocardial sample points which are bounded by the endocardial and epicardial boundaries are Delaunay tessellated to form the finite element mesh of the myocardium. Figure 5.4 shows the low resolution tetrahedral finite element mesh of the mid-ventricle covered by the three-slice image set. In this case, there are 2147 tetrahedra in the mesh.

After the boundary displacement tracking process, the velocity image re-sampling process, and the finite element mesh construction process, we can now perform the integrated volumetric motion and deformation analysis. Following the procedures established in the previous sections, the governing equations of the myocardium are derived from the minimum potential energy principle. A linear isotropic elastic myocardial model is used, and the material-related constants that have been established experimentally for the myocardium in the biomechanics literature[138] are used, with Young's modulus set to be $75,000Pascal$, Poisson's ratio set to around 0.5, the myocardial mass density set to $1.5gram/mm^3$, and the damping parameter set to under 0.1. The velocity values at the

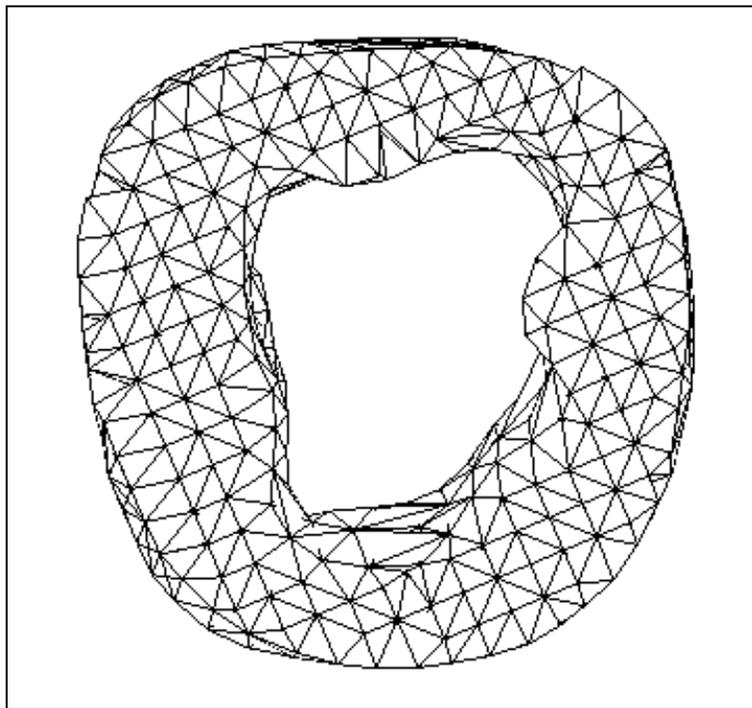


Figure 5.4: Volumetric finite element mesh of the mid-ventricle from phase contrast MR images.

mid-wall points are used as the initial velocity conditions, and the surface displacements are used as the displacement boundary conditions. Since the temporal resolution of the dataset is $0.03125\text{sec}/\text{frame}$, we choose the integration time step $\Delta t = 0.003125\text{sec}$ to have 10 integrated steps. Using these constraints and parameters, the motion and deformation parameters of the myocardium at all sixteen time frames are calculated using the Newmark integration process. In the experiment shown here, there are 2147 tetrahedra in the finite element mesh. The required computer memory for the system to handle this data set is around 60 MB. The computation time for each pair of images is about 10 hours on a Silicon Graphics Indigo2 workstation with 150 MHZ R4400 processor.

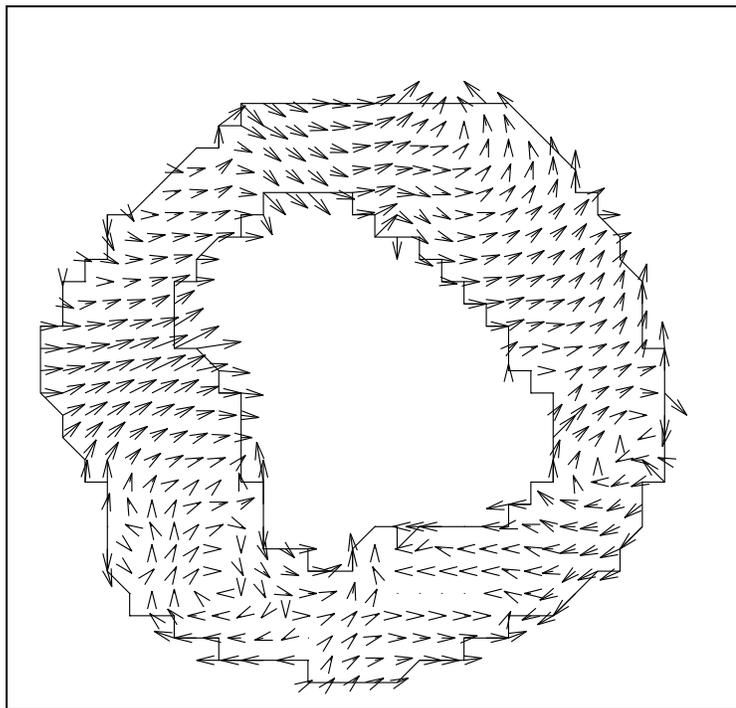


Figure 5.5: Dense field displacement vector map (2D projection) from the integrated framework. Note the non-homogeneous nature of the myocardial motion.

Figure 5.5 presents the two-dimensional projection of the three-dimensional dense field displacement vector map of the middle slice from ED to the next time frame, found from the integrated framework. The use of 2D projections instead of a true 3D vector map is only because of the ease of visualization. Here, a vector arrow begins from its position at present time (ED), and ends at its position in the next time frame. The non-homogeneous nature of the myocardial motion is very evident from this displacement map: different regions of the myocardium display very different motion characteristics in direction and magnitude.

While the displacements or path lengths of the myocardial points are useful for

predicting the state of health of the left ventricle, as discussed in Chapter 4, the element strain tensors of the myocardial tissues provide the non-homogeneous deformation information among regions which could be used to quantify transmural function, especially issues related to the extent of myocardial injury[43]. Even though we believe more detailed and sophisticated analysis on a range of image datasets under different physiological conditions is required to infer any useful information for clinical and research purposes, we still proceed to compute the strain measures on this particular dataset to test the capability of our integrated framework. To that end, we have calculated the strain tensors for each tetrahedral element of the finite element grid to depict the non-rigid deformation, excluding the rigid bulk motion of the elements. Figure 5.6 shows the three normal components (xx , yy , and zz components) and three shear components (xy , yz and zx components) of the strain tensor for the deformation between ED and ES. It seems that these three slices of mid-ventricle myocardium undergo very little z direction deformation. The large strain at lower left part of the LV may be explained by the disconnected motion caused by the infarction (we want to emphasize that this is a very intuitive explanation for these strain maps, there should be no conclusion drawn from this initial experiment). Figure 5.7 shows the more object-centered principal strain maps of the same deformation: the three principal components of the strain as well as the two-dimensional projections of the three-dimensional dense directions of the maximum principal strain (middle slice). Once again, large strain is observed at the lower left part of the LV. In both Figure 5.6 and 5.7, the strain values are mapped back to the myocardial grid at its original state (ED). In these figures, the negative strain values (contraction) are represent by different shades of blue, and the positive values (expansion) are represent by different shades of red.

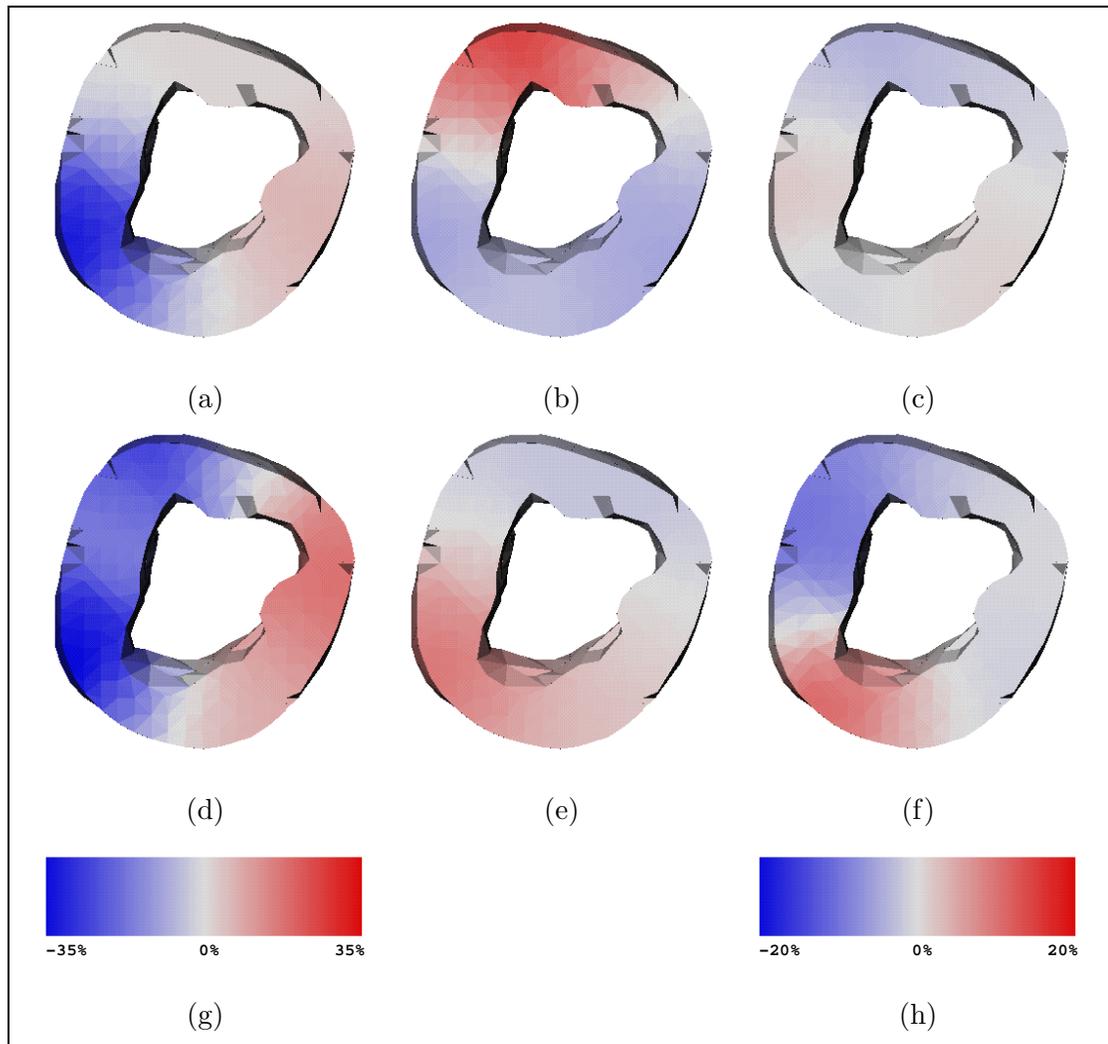


Figure 5.6: 3D strain maps of mid-ventricle (ED-ES). (a): x -direction normal strain; (b): y -direction normal strain; (c): z -direction normal strain; (d): xy -direction shear strain; (e): yz -direction shear strain; (f): zx -direction shear strain; (g): color scale for x -direction normal strain; (h): color scale for all other strains.

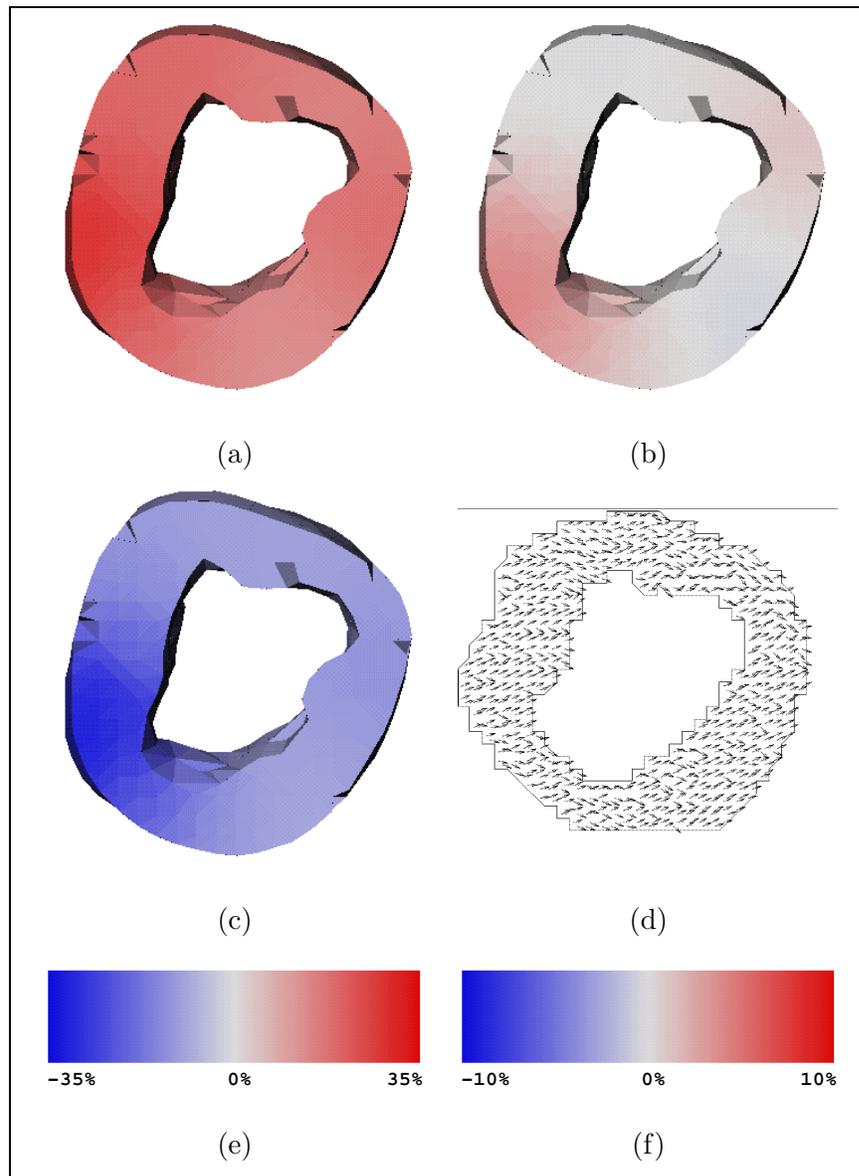


Figure 5.7: 3D principal strain maps of mid-ventricle (ED-ES). (a): the first (maximum) principal strain; (b): the second principal strain; (c): the third (minimum) principal strain; (d): two-dimensional projections of the three-dimensional directions of the maximum principal strain (middle slice). (e): color scale for the first and third principal strains; (f): color scale for the second principal strains.

The temporal changes of the strain tensors are investigated and compared to earlier observations available from biomechanics and cardiology literature [90, 132]. Since we have only three mid-ventricle image slices, it is difficult to reliably define the radial, longitudinal, and circumferential directions and the associated strain measures in those directions which are commonly used in the cardiology community. Instead, the temporal changes of the object-centered principal strains are compared to the data from literature. Previously, the available principal strain data are often observed at isolated positions of the myocardium varying from study to study. Here, we compare the average values of strains of all the elements to these isolated strain data. In the literature[90, 132], the values of the first (maximum) principal strain has been observed to reach a maximum strain of 30% to 40% at ES, the second principal strain has very small values, and the third (minimum) principal strain reaches an extreme value of -20% at ES. For our experiment, we observe that the average value of the first principal strain reaches a maximum strain of 32% at ES, the average second strain is very small and stable, and the third principal strain reaches -18% at ES. Obviously, these results are very consistent with previous studies. However, we should point out that our integrated motion and deformation framework can obtain *dense motion and strain fields* instead of only finding these information at isolated positions, as was done previously. In addition, the framework's ability to quantify the difference of motion and deformation characteristics between myocardial tissue elements makes it valuable to evaluate cardiac regional function. Figure 5.8 shows the temporal sequence of the first principal strain maps from ED to ES. Note the different strain values between different regions.

We want to point out that although the integrated framework is intended to integrate complementary image constraints within a unified system, it also can be used

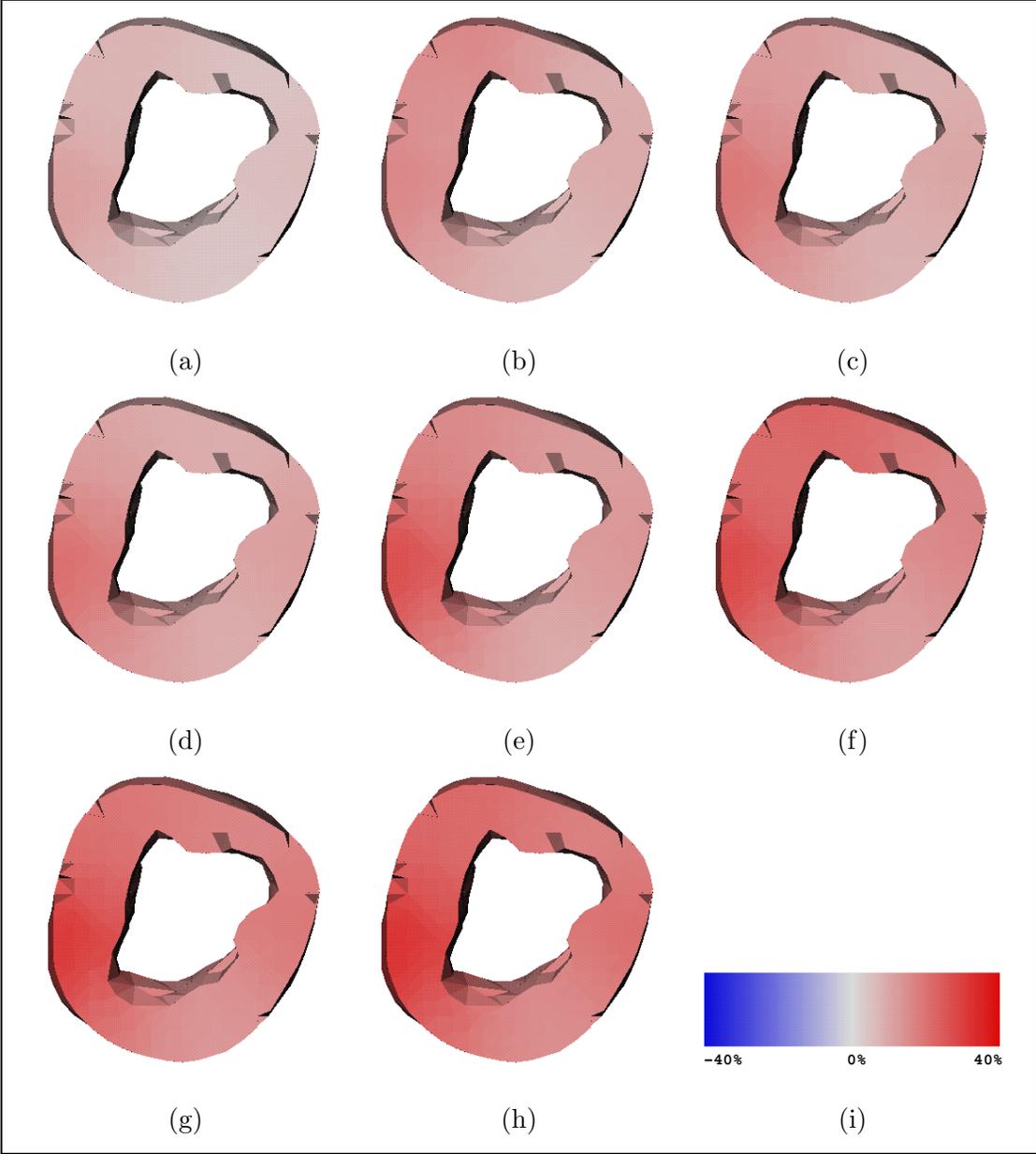


Figure 5.8: Temporal maps of the first principal strain (ED-ES) from phase contrast MR images. (a)-(h): the eight principal strain maps from ED to ES; (i): color scale.

for motion and deformation analysis using only one image source. The uniqueness of this framework is that it can take single or multiple image based data constraints, often very noisy by themselves, and estimate the best compromise motion and deformation parameters from these data and the mechanical model of the left ventricle, which provides a natural way to enforce the physically plausible potential energy functional and smoothness constraints. Further, the actual physical constraints related to known cardiac parameters such as pressure can also be incorporated into the system as external loads.

5.7 Conclusion

We have developed an integrated framework for the analysis of left ventricular motion and deformation. This unified approach is based upon the use of image analysis strategies and mechanical modelling of the myocardium, and is embedded in a finite element framework for the integration of complementary image sources.

This integrated motion and deformation analysis framework estimates the optimal motion and deformation parameters from noisy and complementary image data. Image-derived information from myocardial surfaces and the mid-wall are used in locations where they have the best signals. These data constraints are used as the initial and boundary conditions in the system governing equations of the finite element framework. A continuum mechanical model of the myocardium is applied to provide physically meaningful constraints on the dynamic behaviors of the LV tissue. Stability and accuracy are considered in seeking the solution to the system.

Experiments have been performed on one canine MR phase contrast image set. Motion and deformation parameters are estimated from the integration of boundary displacement information and mid-wall phase velocity information. Results have been com-

pared to previous studies in the literature.

Chapter 6

Summary

This thesis presents an integrated system for recovering motion and deformation of the left ventricle from three-dimensional image sequences. The goal of this work is to combine physical properties of the left ventricle with multiple, complementary sources of imaging data to depict temporal motion and deformation parameters. The algorithms have been implemented, and experiments have been conducted using real medical images of normal and infarcted canine hearts with favorable results.

The geometrical representation of the left ventricle is obtained using the three-dimensional constrained and bounded Delaunay tessellation of the myocardial sample points. The endocardial and epicardial surfaces are characterized by the differential geometrical properties of the multi-scale local surface patches, based on multi-order natural neighbor relationships. The surface displacement field is estimated by matching points of temporally consecutive surface frames based on geometrical similarity and a local smoothness constraint. The accuracy of the surface point tracking has been validated by the gold-standard of the implanted image-opaque physical markers. The MR phase images provide robust instantaneous velocity at the mid-wall region. A finite element frame-

work is established by using the Delaunay tessellation of the left ventricle as the finite element mesh. Continuum mechanical models of the myocardium are discussed, and a linear isotropic elastic model is adopted in the framework. Using the minimum potential energy principle, governing equations of system are established. The shape-based surface displacements are used as the boundary conditions, and the phase velocity images are used as the initial conditions in solving the governing equations. Displacement and strain measures are derived from the solution of the system, and are compared to the results in the literature.

We have exploited an attractive new research direction of using continuum mechanical models as a mean to guide dynamic information analysis from complementary imaging data. The approach provides a natural framework to integrate physical information of the object with visual image constraints. This model-based, integrated strategy should allow us to obtain more robust descriptions of motion and deformation of the myocardial wall.

There are, of course, several areas of potential improvement for this work. First of all, this work only deals with frame-to-frame motion and deformation. There has been no efforts in incorporating temporal motion and deformation models into the framework. The periodic nature of the cardiac motion should provide a basis to enforce some temporal constraints[61]. This work should also benefit from refining the motion and deformation estimation by minimizing the errors between the position and velocity predictions of the system equations and the image data position and velocity. We have done initial work in this regard using a recursive feedback mechanism in the two-dimensional case (see Appendix A). Extension to three-dimensions is needed.

Appendix A

2D Feedback Mechanism

When using the finite element framework to track motion between temporal images, it can be regarded as a predictor from time t_0 to time t_1 . Since we already have data information at t_1 in terms of the segmented endocardial and epicardial contours, as well as the mid-wall velocities, we can refine the mapping estimate between frames t_0 and t_1 by comparing how close the image-driven, model-based prediction comes to the actual data. The differences between the data and the prediction can be used as a recursive feedback term to improve the matching process. Here, we report our progress in using the boundary difference as the feedback force[115].

In the two-dimensional case, contour shape landmarks are defined as locally extreme curvature points or curvature zero-crossing points. Making the curvature zero-crossing points part of the landmark set ensures that any contour segment between two consecutive landmarks will not change curvature sign if we traverse the segment from one end to the other. In other words, all the contour segments constructed by the consecutive landmarks will be either constant convex, or constant concave, or a straight line.

In the integration of displacement and velocity process, the boundary displace-

ment constraint is only enforced at the matching vectors which terminate at the landmark points of the second contour. This way, the real and predicted contours at time t_1 intersect at these points. The contour segment defined by two consecutive landmarks of the real data will always be either constant convex, or constant concave, or a straight line. The corresponding predicted contour segment should be close to the real one in the same classification sense, if the initial shape-based boundary matching is reasonably good and the contour segment is not too large. In practice, these two requirements are readily satisfied. In the feedback process, predicted contour segments are compared to actual ones, based on a metric related to the similarity between pairs of actual and predicted contour segments. To date, two curve comparison metrics have been developed, and have shown similar effects in improving the matching process.

The first metric uses the shape matching idea that our initial boundary matching is based upon. We were using point-wise shape comparison in the matching process, but now we have to compare the entire curve segments. We define that the total tension for any curve segment \mathcal{C} equal to its normalized total curvature:

$$T(\mathcal{C}) = \int_{\mathcal{C}} |\kappa(s)| ds \tag{A.1}$$

Since we have stated that the real and predicted contour segments would be close in the sense of constant convexity or concavity, the total tension of any curve segment will indicate its total curvedness. Furthermore, since the whole real contour can be treated as if it were in an equilibrium state with respect to tension, the total tension difference (termed as expanding force $f(\mathcal{P})$) between the corresponding predicted segment \mathcal{P} and the real segment \mathcal{R} can be used as a target as to how much the predicted segment should

increase or decrease its tension:

$$f(\mathcal{P}) = T(\mathcal{P}) - T(\mathcal{R}) \quad (\text{A.2})$$

A positive $f(\mathcal{P})$ indicates that the segment has a tendency to expand along the outward tangent directions of the two end points, while negative $f(\mathcal{P})$ implies the shrinking tendency. Since the neighboring segments interact at their common end point, the net expanding force of the two segments determines the net expanding or shrinking tendency of the common landmarks.

The second comparison metric simply defines the total tension for any given curve segment equal to the normalized area of the segment (closed by the line connecting the two end points). The expanding force is again defined as the total tension difference between the corresponding predicted and real segments.

Figure A.1 illustrates the contour segment comparison idea described above. Here, the solid line represents the real contour, and the dotted line is the predicted contour. Segments A and C have an expanding tendency, while segment B is inclined to shrink. However, the net force at the common end of A and B causes that landmark expand (or shrink from B 's standpoint) into B , while the net force at the common end of B and C is minimal (no change).

After forming the net expanding force at each landmark point, adjustments are made for the initial boundary displacements. Displacement vectors emanating from the first image frame are modified so they will end on the boundary of the second image, at one side or another of the original matching landmarks, depending on the magnitude and direction of the net expanding force of each landmark. In Figure A.1, the common point

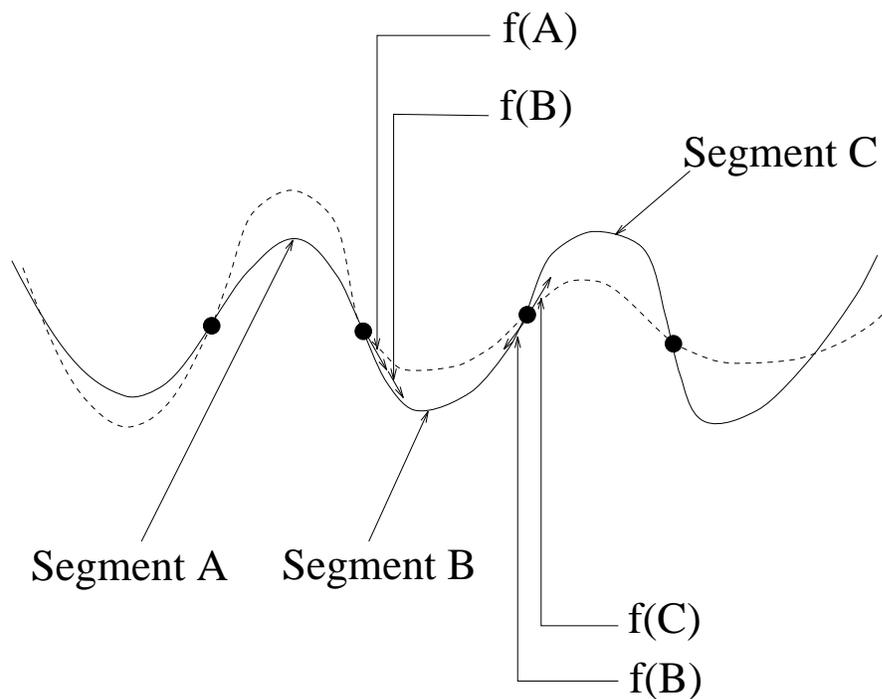


Figure A.1: Compute the landmark net expanding-shrinking force in the feedback mechanism.

of segments A and B has net expanding force (it is positive), hence it should move to the right (expanding from segment A 's view and shrinking from segment B 's view). The new displacement is then applied into the integrated finite element framework to compute refined motion information.

Figure A.2 illustrates the effect of the feedback mechanism. (a) is the original grid, (d) is the target data grid at the next time frame. (b) is the system predicted grid without any corrections, while (c) is the refined prediction after two steps of feedback correction at the boundaries. We can see the local and overall improvement of the refined prediction.

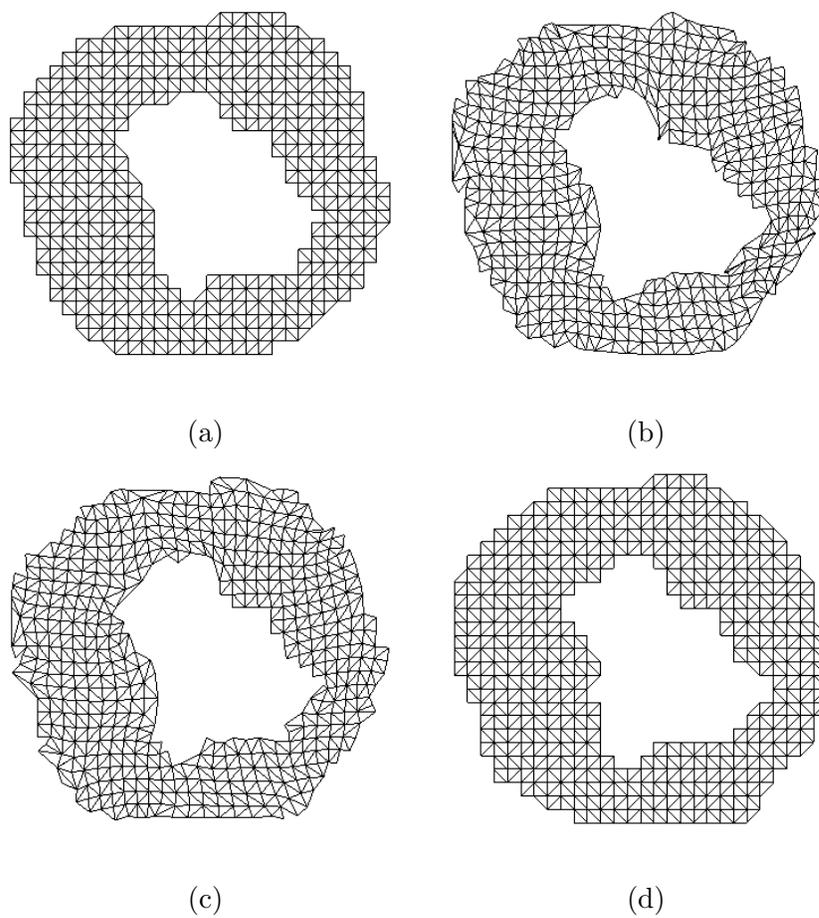


Figure A.2: Effect of the feedback mechanism. (a): original grid; (b): predicted grid without feedback; (c): predicted grid with two feedback iterations; (d): actual data grid.

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