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A Graph Theoretic Approach for Computing 3D+time Biventricular Cardiac Strain from Tagged MRI Data

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Abstract

Tagged magnetic resonance imaging (tMRI) is a well-established method for evaluating regional mechanical function of the heart. Many techniques have been developed to compute 2D or 3D cardiac deformation and strain from tMRI images. In this paper, we present a new method for measuring 3D plus time biventricular myocardial strain from tMRI data. The method is composed of two parts. First, we use a Gabor filter bank to extract tag points along tag lines. Second, each tag point is classified to one of a set of indexed reference tag lines using a point classification with graph cuts (PCGC) algorithm and a motion compensation technique. 3D biventricular deformation and strain is computed at each image time frame from the classified tag points using a previously published finite difference method. The strain computation is fully automatic after myocardial contours are defined near end-diastole and end-systole. An *in-vivo* dataset composed of 30 human imaging studies with a range of pathologies was used for validation. Strains computed with the PCGC method with no manual corrections were compared to strains computed from both manually placed tag points and a manually-corrected unwrapped phase method. A typical cardiac imaging study with 10 short-axis slices and 6 long-axis slices required 30 minutes for contouring followed by 44 minutes of automated processing. The results demonstrate that the proposed method can reconstruct accurate 3D plus time cardiac strain maps with minimal user intervention.

Graphical Abstract

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Keywords

Tagged magnetic resonance imaging (tMRI); Gabor filter bank; graph cuts; strain

1. Introduction

Magnetic resonance imaging is a non-invasive method for evaluating myocardial mechanical function (Zerhouni et al., 1988; Axel and Dougherty, 1989). Tagged MRI spatially modulates the longitudinal magnetization of the underlying tissue before image acquisition. This gives a periodic dark strip tag pattern that deforms with the heart tissue. Line tagged or grid tagged (using orthogonal modulation) MRI can be used to evaluate regional cardiac function by analyzing the motion pattern of the tag lines or grids.

Several techniques have been developed to either manually or automatically measure left ventricular myocardium deformation from the deformed tag pattern, including feature-based methods (Young and Axel, 1992; Moore et al., 1992; Guttman et al., 1994; Denney and McVeigh, 1997; Denney, 1999; Chen and Amini, 2002), optical-flow methods (Prince and McVeigh, 1992; Dougherty et al., 1999; Xu et al., 2010), non-rigid registration-based methods (Chandrashekar et al., 2004; Ledesma-Carbayo et al., 2008), and frequency-based methods like HARMONIC Phase (HARP) (Osman et al., 2000, 1999) and local sine wave modeling (SinMod) (Arts et al., 2010; Liu et al., 2014).

While most of this work has focused on the left ventricular (LV) wall, there is increasing interest in mechanical function of the right ventricular (RV) wall, particularly in conditions such as chronic obstructive pulmonary disease (COPD) (Wells et al., 2015; Kawut et al., 2014) and pulmonary arterial hypertension (Mauritz et al., 2012; Corona-Villalobos et al., 2015; Swift et al., 2015). While two-dimensional (2D) methods are often used for evaluating left ventricular mechanical function, these methods may not be as accurate in the RV wall due to the larger displacement of the tricuspid annulus (Zha et al., 2015; Auger et al., 2012) and its relatively irregular shape. In addition, the relatively thin wall of the normal RV makes detecting tags in the RV wall difficult and limits the number of tag lines that can be used for quantification.

Young et al. (Young et al., 1996) used a finite element model for 3D reconstructing deformation of the RV free wall mid-wall surface. Haber, et al. (Haber et al., 2000, 2005) later modeled the RV free wall as a solid and used a finite element model to obtain 3D biventricular strains. Tustison and Amini (Tustison and Amini, 2006) computed biventricular strains using volumetric deformable models with a nonuniform rational B-splines (NURBS)

basis. These 3D methods (Young et al., 1996; Haber et al., 2000, 2005; Tustison and Amini, 2006) used semi-automated tag line feature tracking to obtain displacements. Venkatesh et al. (Venkatesh et al., 2011) used a finite difference model (Denney and McVeigh, 1997) to reconstruct 3D biventricular strain from unwrapped HARP images with manual corrections to remove inconsistencies in the HARP images.

In this paper, we present a new method, called the point classification with graph cuts (PCGC) method, for detecting tag lines and computing 3D strains in both the LV and RV walls throughout the cardiac cycle from tMRI. In addition to the ability to detect tag lines and compute strains in the RV, strains are computed at each imaged phase in the cardiac cycle, which may allow for earlier detection of changes in ventricular structure and function and interventricular interaction.

HARmonic Phase (HARP) is a widely used technique for measuring 2D strain in both the LV and RV (Shehata et al., 2011; Mauritz et al., 2012; Khalaf et al., 2013). Since tagged images can be treated as AM-FM modulated 2D signals, local myocardial motion is encoded in the regional phase information. HARP computes this phase information from a complex image, which is produced by inverse Fourier transforming an isolated peak of the tagged MR image in the spatial frequency domain. The phase information is a material property and the same material point will retain the same phase value throughout the cardiac cycle, enabling tracking of the myocardium motion by tracking its phase value.

HARP is robust against noise, but, due to the bandpass filtering process, it constrains local variations in tag spacing and orientation because the location and shape of the bandpass filter are fixed. These constraints can cause artifacts such as branching and merging of the phase discontinuity when two tag lines get too close to each other in the original tag image, or breaking of the discontinuity when a large regional rotation is present. To address this issue, adaptive filtering methods such as Gabor filter banks (Qian et al., 2003; Chen et al., 2010) have been developed. A Gabor filter is a complexvalued filter that is convolved with the original image enabling local periodic strip features to be extracted from the complex response. A large magnitude response suggests a higher match between the filter parameters and the local tag spacing and orientation. Therefore, by convolving the original image with a bank of Gabor filters with different combinations of parameters, one can estimate local features from the parameters of the filters that have the largest magnitude responses, and obtain a phase image from the optimal local complex responses.

Myocardial deformation can be estimated by unwrapping the phase image or using the wrapped phase information directly. The phase unwrapping process reconstructs the absolute phase by adding multiples of 2π to each pixel. The algorithm in (Venkatesh et al., 2010, 2011) requires manual intervention to correct the unwrapping process in regions where the wrapped phase is inconsistent. Tracking methods like HARP tracking (Osman et al., 1999) avoid the unwrapping process and estimates the motion field by tracking the local phase information. However, tracking errors may happen when the material point is tracked to an inconsistent position from the present time frame to the next, due to the presence of phase artifacts, through-plane motion, or large interframe deformation. In addition, when through-plane motion occurs, the radial positions of the tracked points tend to drift either to the

epicardium or the endocardium, which can cause strain estimation errors (Tecelo et al., 2006).

An alternative to these phase based methods is to extract tag lines or tag line intersections first, by detecting edges in the phase image. Then the deformation field is estimated either by calculating the correspondence between detected tag lines and undeformed tag lines, or by tracking tag line intersection features between consecutive time frames as in (Chen et al., 2010), where a robust point matching algorithm (RPM) was used to match and track two intersection point sets in two consecutive time frames and an implicit deformable model was used to reconstruct a dense left ventricular deformation field. However, the RPM based method in (Chen et al., 2010) ignores information about the underlying deformation that is contained in tag line points not on tag intersections. While loss of this information may not be an issue in the relatively thick-walled left ventricle, where there are many tag intersections, it can cause problems in the right ventricular wall, where tag intersections are sparse or non-existent.

In this paper, we develop a deformation estimation method which uses Gabor filter banks to extract all tag line points in both the left and right ventricular walls and uses integer optimization to classify each point to a tag line. A deformation model is then fit to the tag points in each time frame of an image sequence and used to reconstruct dense motion field and strain in both the left and right ventricular walls. The classification algorithm assigns an integer tag line index to each tag point. It can be shown (Denney and Prince, 1995) that assigning a point to a particular tag line corresponds to a one-dimensional (1D) displacement of that point back to the undeformed tag line. The classification algorithm assigns indices to tag points so as to minimize the spatial variation in these 1D displacements between neighboring points. This smoothness constraint is formulated with a Markov Random Field (MRF), and the classification is performed iteratively with several binary optimization processes, which either change the index by 1 or keep it the same in each iteration. Binary optimization in each iteration is performed using a graph cuts method (max-flow/min-cut) (Bioucas-Dias and Valado, 2007; Kolmogorov, 2005). We refer to this proposed algorithm as the Point Classification with Graph Cuts (PCGC).

PCGC works best when the deformation field between a given time frame and the undeformed time frame is relatively small, which is not the case in many tagged cardiac imaging protocols, particularly near end-systole. To address this issue, we displace the extracted tag points in a given time frame by the inverse of the deformation field computed from the previous time frame. If the interframe motion is small, and the deformation field of the previous time is accurate, the tag points at a given time frame after compensation will be close to the undeformed tag line positions and can be accurately classified by the PCGC. After tag points from all tag groups (short-axis and long-axis view) are classified and the 1D displacements are computed, a 3D dense motion field and strains are reconstructed for both ventricles with the discrete model-free method (Denney and McVeigh, 1997).

This paper is organized as follows: the Gabor filter bank tag identification method, the PCGC method along with the motion compensation, and the strain reconstruction are

described in Section 2. Section 3 shows experimental results for *in-vivo* studies. Discussion and conclusion are presented in Section 4.

2. Methods

2.1. Gabor Filter Bank

To identify tag points in an image, we use Gabor filter banks similar to the ones used by (Chen et al., 2010). A Gabor filter is a linear filter composed of a Gaussian kernel modulated by a sinusoidal plane wave

$$h(x, y) = g(x', y') \cdot \exp(2\pi j \omega x') = A \cdot \exp(-\pi(a^2 x'^2 + b^2 y'^2)) \cdot \exp(2\pi j \omega x'), \quad (1)$$

where $(x', y') = (x \cos \theta + y \sin \theta, -x \sin \theta + y \cos \theta)$ are the coordinates (x, y) rotated by the tag line angle θ , ω is the spatial frequency of the sinusoidal carrier, A is the magnitude of the Gaussian envelope, and a and b control the shape of the envelope.

After 2D Fourier transform, the Gabor filter in frequency domain has a simpler form

$$\hat{h}(u, v) = \frac{A}{ab} \exp \left(-\pi \left(\frac{(u - u_0)^2}{a^2} + \frac{(v - v_0)^2}{b^2} \right) \right), \quad (2)$$

where $(u_0, v_0) = (\omega \cos \theta, \omega \sin \theta)$ are frequency components of the carrier in the spatial domain. In this paper, we chose $a = b = \sqrt{A} = \omega / \sqrt{2\pi}$.

The 5×3 array of Gabor filters shown in Fig. 1 defines a bank (Chen et al., 2010), where the frequency varies from $0.5\omega_0$ to $2\omega_0$ with an increment of $\sqrt{2}$ in scale and the orientation varies from $\theta_0 - \pi/8$ to $\theta_0 + \pi/8$ with an increment of $\pi/8$. Parameters of the filter in the center of the bank, (ω_0, θ_0) , are determined by tag line modulation frequency and orientation from the image acquisition protocol. In this example, where tag modulation is 45 degree and tag spacing (T) is 6.8 pixels, the Gabor filter bank is designed with $(\omega_0 = 1/T = 0.1467, \theta_0 = \pi/4)$. For image with -45° modulation and the same tag spacing, the Gabor filter bank applied is rotated by 90° with $(\omega_0 = 0.1467, \theta_0 = -\pi/4)$.

For grid-tagged images, Gabor filters could be applied directly to the image, but this sometimes results in the detection of spurious tag points near borders of the myocardium and near intersections. In this paper, we use strip filters of width $1/T$ to isolate tag lines in each orientation as shown in Fig. 2 and apply a Gabor filter bank to each resulting line-tagged image.

Since the filters in the bank are relatively coarsely sampled in frequency and orientation, the optimal frequency and orientation for a particular pixel must be interpolated from the parameters of the filters with the highest magnitude responses. In (Chen et al., 2010), the optimal parameters were computed using a weighted average of the parameters of the K highest magnitude response filters, where the weight for the k th filter at pixel i was defined

as $w_{i,k} = m_{i,k} / \sum_{k=1}^K m_{i,k}$ and $m_{i,k}$ is the magnitude response of the k th filter at pixel i . Similarly, the magnitude and phase response at each pixel was computed from a weighted average of the filter bank real and imaginary responses (Chen et al., 2010). (Chen et al., 2010) used $K = 3$. In this paper, we computed a weighted average over all filters ($K = 15$), which was a bit faster computationally since it was not necessary to sort the magnitude responses at each pixel.

Tag line points were identified inside the myocardium by detecting the locations where the phase response wrapped from $-\pi$ to π . The myocardium in both ventricles was segmented using endocardial and epicardial contours constructed with a dual-contour propagation technique developed by our group (Feng et al., 2009; Zha et al., 2015) and used in several clinical studies (Ahmed et al., 2012a; Pat et al., 2010b; Gupta et al., 2015; Ahmed et al., 2010; Dillon et al., 2012; Schiros et al., 2014, 2012; Ahmed et al., 2012b). This technique uses manually-drawn contours in time frames near end-diastole (ED) and end-systole (ES) to automatically propagate contours to all remaining time frames using non-rigid registration. ED and ES contours are typically drawn during clinical analysis of cardiac MRI data to compute functional parameters. A typical tag line point identification result near end-systole is shown in Fig. 3.

2.2. Point Classification with Graph Cuts (PCGC)

In this section, we describe the PCGC algorithm, which assigns an integer tag line index to each tag point assuming the underlying deformation is spatially smooth and small in magnitude.¹ We assume that each tag line was straight when originally applied to the tissue (i.e. undeformed) and each identified tag point belongs to only one tag line. We refer to tag lines at their undeformed position as reference tag lines.

Let Ω be the index set of all detected tag points, and each candidate reference tag line be labeled as $I \in \{0, 1, \dots, N-1\}$, where N is the number of all candidates. The classification problem can be framed as follows: for each tag point $p \in \Omega$ with coordinate vector $\mathbf{p} = [x_p, y_p]^T$ ($[\cdot]^T$ denotes transpose), it is assigned a label I_p indicating that the deformed tag point p moved from its original position, which was on the reference tag line with label I_p . The 1D displacement from p along the normal direction of the reference tag line is given by

$$u_p = \mathbf{n}^T \mathbf{p} + c_{I_p}, \quad (3)$$

where $\mathbf{n} = [\cos\theta, \sin\theta]^T$ is the reference tag line normal vector, and c_{I_p} is the offset of the reference tag line with label I_p , defined by the line equation: $x\cos\theta + y\sin\theta + c_{I_p} = 0$ for any point (x, y) on the reference tag line. c_{I_p} is a one to one function of label I_p . When all reference tag lines are separated by the same distance, which is the case in this paper, c_{I_p} is a linear function of I_p , and we have $c_{I_p} = c_0 + TI_p$, where $T > 0$ is the spacing between tag lines.

¹The small deformation assumption requires a motion compensation algorithm, which we describe in Section 2.4

From Equation 3 and Fig. 4 we can see that different labeling schemes result in different displacement patterns. We assume that spatially neighboring tag points should have similar 1D displacements and that the 1D displacement of a point is small. These two assumptions result in the following energy function of the label set for all tag points $L = \{l_p, p \in \Omega\}$:

$$E(L) = \sum_p \sum_{q \in \mathcal{N}(p)} V(u_p - u_q, d_{pq}; \eta_p) + \lambda \sum_p u_p^2 = \sum_p \sum_{q \in \mathcal{N}(p)} U_1(l_p, l_q) + \lambda \sum_p U_0(l_p), \quad (4)$$

where $p, q \in \Omega$ are two tag points in the domain. $q \in \mathcal{N}(p)$ indicates that q belongs to the neighborhood of p . $V(\cdot)$ is a convex pairwise potential function, which penalizes differences in displacement. $V(\cdot)$ and the neighborhood are defined below. u_p and u_q are 1D displacements defined in Equation 3 at point p and q with coordinate vectors $\mathbf{p}$ and $\mathbf{q}$. $d_{pq} = \|\mathbf{p} - \mathbf{q}\|_2$ is the Euclidean distance between the two tag points. λ is a weight that balances the influence of the pairwise and unary potentials. The pairwise term, U_1 , penalizes the displacement difference between two tag points. The unary term, U_0 , penalizes large displacements. The unary constraint is needed to obtain a unique solution for L . Without the unary term, when tag lines are evenly separated and c_p is a linear function of label l_p , there will be multiple optimal solutions of L differing from each other by an integer shift. Cardiac deformation, particularly near end-systole, involves large displacements, so we use the motion compensation technique described in Section 2.4 to reduce tag point displacements to a level where the small displacement assumption is valid.

The pairwise potential function $V(\cdot)$ in Equation 4 is defined as

$$V(a, b; \eta) = a^2 \phi(b; \eta) = a^2 \exp(-\eta^2 b^2), \quad (5)$$

where $\phi(\cdot)$ is a Gaussian radial basis function. This term serves as a membership weight to control the interaction between any two neighboring tag points. When two tag points are more separated, the membership weight decreases and the displacement difference is less penalized. The neighborhood $\mathcal{N}(p)$, for tag points p and q , is defined as $q \in \mathcal{N}(p)$ if and only if $\phi(d_{pq}) \geq \tau$. We set threshold $\tau = 0.1$ in this paper.

The radial basis function is defined such that, as η decreases, the Gaussian weighting pattern is wider. Typically, η (and the corresponding neighborhood size) is fixed. However, in this paper, we set $\eta = \eta_p = \omega_p$, the local tag frequency or the reciprocal of local tag spacing at point p , acquired from the estimated frequency map in Fig. 3(d). This allows the neighborhood to get smaller as the heart contracts and vice versa.

The energy function in Equation 4 conforms to a first-order Markov Random Field (MRF), which needs to be minimized over the label set L . This combinatorial optimization problem can be solved with several discrete optimization schemes (Cook et al., 1997; Kolmogorov, 2005). In this paper, we initialized the label set as $L^i = 0$ at step $i = 0$ and optimized L by iteratively adding binary values to it: $L^{i+1} = L^i + \delta_p$, where $\delta_p \in \{0, 1\}$, $p \in \Omega$. The optimal value of L at each iteration is obtained by minimizing the following energy function

$$\hat{E}(\Delta) = E(L^i + \Delta) = \sum_p \sum_{q \in \mathcal{N}(p)} U_1(l_p^i + \delta_p, l_q^i + \delta_q) + \lambda \sum_p U_0(l_p^i + \delta_p) = \sum_p \sum_{q \in \mathcal{N}(p)} E_1(\delta_p, \delta_q) + \sum_p E_0(\delta_p). \quad (6)$$

Similarly, the binary function $\hat{E}(\cdot)$ is composed of pairwise and unary terms, where $E_1(\cdot)$ is the first-order clique energy function of a pair of binary variables, and $E_0(\cdot)$ is the zeroth-order clique energy function of a single binary variable. It can be shown (Bioucas-Dias and Valado, 2007; Kolmogorov, 2005) that, when a submodularity condition is met, the binary energy at each step can be minimized globally by finding the minimum cut on the corresponding graph, and the optimal label set L can be obtained by iteratively optimizing Equation 6 $N-1$ times or until no potential improvement can be done to decrease the energy in Equation 4. The submodularity condition is

$$E_1(0, 1) + E_1(1, 0) \geq E_1(0, 0) + E_1(1, 1), \quad (7)$$

It is straightforward to show that this relationship holds for the energy function in Equation 6 for each pair of tag points (p, q) such that $q \in \mathcal{N}(p)$:

$$\begin{aligned} E_1(0, 1) + E_1(1, 0) &= \\ &\phi(d_{pq}; \eta_p) \cdot ((\mathbf{p} - \mathbf{q})^T \mathbf{n} + T(l_p^i - l_q^i) - T)^2 \\ &+ \phi(d_{pq}; \eta_p) \cdot ((\mathbf{p} - \mathbf{q})^T \mathbf{n} + T(l_p^i - l_q^i) + T)^2 \\ &\geq 2\phi(d_{pq}; \eta_p) \cdot ((\mathbf{p} - \mathbf{q})^T \mathbf{n} + T(l_p^i - l_q^i))^2 \\ &= E_1(0, 0) + E_1(1, 1). \end{aligned} \quad (8)$$

Since the submodularity condition is met, the binary energy function is *graph representable* (Kolmogorov and Zabini, 2004). Let $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ be a directed graph with vertices $\mathcal{V} = \{v_1, \dots, v_n, s, t\}$, where $n = |\Omega|$ is the number of all tag points. $v_1, \dots, v_n$ represent the binary variables, and s (source) and t (sink) are terminals. Note there is only one source and one sink. Each s - t cut on graph $\mathcal{G}$ corresponds to a configuration of the variables such that $\delta_p = 0$ when $v_p \in S$ and $\delta_p = 1$ when $v_p \in T$, where S and T are sets of vertices including source s and sink t , respectively. By properly constructing the graph, the cost of the graph cut corresponds to the binary energy in Equation 6, and the binary energy is minimized by computing of the minimum s - t cut on graph $\mathcal{G}$, which can be accomplished efficiently using the max-flow/min-cut algorithm (Kolmogorov and Zabini, 2004; Bioucas-Dias and Valado, 2007).

The graph construction consists of two steps (Kolmogorov and Zabini, 2004). First, an elementary graph is constructed for the unary energy term at each point p (Fig. 5 (a) and Fig. 6(a)) and an elementary graph is constructed for the pairwise energy term for each pair of

points (p, q) such that $q \in \mathcal{N}(p)$ (Fig. 5(b) and Fig. 6(b)). Then, all the elementary graphs are merged by adding up weights for directed edges to yield the final graph $\mathcal{G}$, like in Fig. 5(c). The details of elementary graph construction is illustrated in Fig. 6.

After the binary set is optimized by minimizing the energy function using max-flow/min-cut algorithm, the label set L is updated with $L^{i+1} = L^i + 1$. This process repeats until no potential improvement can be done to decrease the energy, or the maximum label $N-1$ is reached. Note that the set of candidate tag lines should cover as many probable reference tag lines as possible, in order to prevent a situation where the optimal labels of some of the tag points are outside the range of the set. On the other hand, the set should cover as few candidates as possible to reduce processing time, because, at each step, a new graph is constructed and the max-flow/min-cut algorithm is run. In this paper, for an image sequence the candidate tag lines are selected in following ways: we first determine the region of interest (ROI) covering the left and right ventricular myocardium at the time closest to end-diastole (ED), with an extra extension of 5 pixels; we then select candidate tag lines passing through the ROI at their undeformed positions. The pseudo code of PCGC is provided in Algorithm 1.

Algorithm 1

Point Classification with Graph Cuts

```

Input : Tag line labels  $\{0, \dots, N-1\}$ ; neighborhood  $\mathcal{N}(p)$  and
 $\phi(d_{pq})$  for each  $p$  and  $q \in \mathcal{N}(p)$ .
Output: Optimal label set  $L$ .
initialize  $i = 0$ ,  $L^i = \mathbf{0}$ , improvement possible = true;
while improvement possible and  $i + 1 < N$  do
    Compute binary energies for each tag point and pair of tag points.;
    Construct graph  $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ .;
    Compute  $s-t$  cut based on  $\mathcal{G}$  and get  $L^i$ .;
    if  $E(L^{i+1}) < E(L^i)$  then
         $L^{i+1} = L^i + 1$ ,  $i = i + 1$ ;
    else
        improvement possible = false;
    end
end

```

2.3. Auxiliary Points for Biventricular Data

The PCGC algorithm described above works well for the relatively thick-walled LV because any tag point will typically have a sufficient number of tag points in its neighborhood to enforce smoothness through the pairwise energy term. The RV wall, however, is relatively thin and tag lines can be so sparse that a tag point will have no points in its neighborhood, or a small set of tag points will be isolated and have no interaction with other points.

To address this issue in biventricular studies, we introduce a set of auxiliary points to increase the point density and improve pairwise interaction in the RV wall. Auxiliary points are computed by adding π to the Gabor filter bank phase map, wrapping the resulting phase, and detecting points where the phase wraps from $-\pi$ to π . This results in a set of points in lines with the same undeformed separation (T) as the original tag points but are shifted by one-half tag spacing as shown in Fig. 7. In the PCGC, label assignments to the original tag points and auxiliary points are distinct but both range from 0 to $N-1$. This scheme allows original tag point displacements to be computed relative to original reference tag lines and auxiliary point displacements to be computed relative to auxiliary reference lines. However, there is no distinction between these two point sets when computing the pairwise energy term in Equation 6. This means that the neighborhood of each point can contain points from both of these two sets. The auxiliary points are only used to assist in classification and labeling the original tag points. Auxiliary points are discarded after the PCGC algorithm completes and are not used for final displacement and strain reconstruction.

2.4. Motion Compensation and Strain Reconstruction

As mentioned earlier, the PCGC algorithm assumes small displacements from the undeformed tag line, which is a poor assumption in cardiac motion. To make the PCGC algorithm applicable to tagged images with large displacements, we use a motion compensation technique, which transforms tag points at a deformed time frame to new positions that are close to the reference tag line positions. Fig. 8 is an illustration of this process. The 1D tag point displacements in Equation 4 are computed from the motion compensated tag point positions, whereas the distance between tag points d_{pq} in Equation 4 and the neighborhood system are determined from the original (not motion compensated) tag point locations.

Several methods can be used for motion compensation. In this paper, we used a 2D version of the discrete model-free (DMF) algorithm (Denney and McVeigh, 1997) to reconstruct a dense deformation field from sparse displacement measurements. The DMF algorithm uses a finite difference based technique to map tag points in a deformed configuration back to their (undeformed) reference position. In the PCGC algorithm, tag points in the first imaged time frame are assumed to have small displacements, so they are classified with no motion compensation. In subsequent time frames, each tag point location is compensated with the dense deformation map computed from the classified tag points at the previous time frame using the 2D DMF algorithm.

After all tag points were detected and classified using the PCGC, 1D displacement measurements are computed from the classified tag points. At each time frame, there are 1D displacement measurements from all tag line orientations. We use the original 3D DMF method to estimate a 3D dense deformation field and to compute 3D biventricular Lagrangian strain. This process is repeated for each time frame to compute 3D+time biventricular strain as was done in previous work (Venkatesh et al., 2011).

3. Experiments and Results

In this section, we evaluate the performance of the PCGC and validate the reconstructed biventricular strains with *in-vivo* data. A total of 40 human studies were used, including images from normal volunteers (NL) and patients with pathologies including diabetes with infarction (DMI), resistant hypertension (HTN) and pulmonary arterial hypertension (PAH). 10 studies (4 NL, 3 DMI, and 3 HTN) out of the dataset were selected randomly and used to optimize the parameter λ . The proposed method was tested on the remaining 30 studies (10 NL, 5 DMI, 8 HTN, and 7 PAH) and then validated by comparing the reconstructed strains to those obtained with a feature-based method with tracked and edited tag points (Denney and McVeigh, 1997; Denney, 1999; Denney et al., 2003) and a manually unwrapped phase-based method (Venkatesh et al., 2011).

All participants underwent the MRI scan on a 1.5 Tesla machine (GE Healthcare, Milwaukee, WI) optimized for cardiac application. 8 – 12 short-axis slices and 6 radially-prescribed long-axis slices were imaged with a fast gradient-echo cine sequence using the following parameters: field of view = 40×40 cm, scan matrix = 256×128 , flip angle = 10° , repetition/echo time = 8.0/4.2 ms, views per segment = $8 \sim 10$, 20 time frames per cardiac cycle with a typical temporal resolution of 50 ms, slice thickness = 8 mm. Grid spatial modulation of magnetization (SPAMM) was applied to short-axis slices, while line tags were applied to long-axis slices. All tag lines were separated with a tag spacing (T) of 7 pixels. The validation dataset with 30 human studies covered a wide diversity of human hearts including both geometries and motion patterns, and was also used in (Venkatesh et al., 2011) to test the manually unwrapped phase-based method.

Preparation of these cardiac studies included myocardium segmentation, for which we used the dual-contour propagation method (Feng et al., 2009; Zha et al., 2015) introduced previously in Section 2.1. First, we manually drew epicardial and endocardial contours for both left ventricle (LV) and right ventricle (RV) near end-diastole (ED) and end-systole (ES). Then contours were automatically propagated to all other time frames with the dual-contour method. The contouring and propagation took approximately 30 minutes for each study. Contouring was the only manual intervention used in the study. Once the contours near ED and ES were specified, the remaining processing was fully automatic, and no editing of tag points was performed in this paper.

All programs were implemented with MATLAB (Mathworks, MA) on a laptop computer with Intel Core i5 CPU (2.27 GHz). We used a Quadratic Pseudo-Boolean Optimization (QPBO) algorithm (Hammer et al., 1984; Boros et al., 1991; Kolmogorov and Zabini, 2004; Kolmogorov and Roth, 2007) for the max-flow/min-cut computation, the code of which was publicly available. Though the algorithm was implemented for Markov random field problems with nonsubmodular terms, it also can be used for submodular problems. The processing time with the proposed method (including Gabor filtering, PCGC and motion compensation) was 1 minute for a typical cardiac slice composed of $20 \times 256 \times 256$ pixel images with grid tags. 3D+t strain computation using the DMF method for a typical cardiac study was 30 min. A typical cardiac imaging study with 10 short-axis slices and 6 long-axis slices required 30 minutes for contouring followed by 44 minutes of automated processing.

3.1. Optimization of λ

We optimized the parameter λ in Equation 4 on a set of 10 human studies which were not part of the validation dataset. For different choices of λ values ($\lambda \in \{10^{-4}, 10^{-3}, 10^{-2}, 10^{-1}, 1\}$), we compared 1D displacements of tag points identified and classified with the PCGC to those from manually identified tag points at the time frame closest to end-systole. Fig. 9 shows the mean and standard deviation of the displacement measurement differences for LV short-axis groups, LV long-axis groups, RV short-axis groups, and RV long-axis groups. We conclude that the PCGC algorithm is not sensitive to choices of λ values less than or equal to 0.1. We used $\lambda = 0.01$ for the following validation experiment.

3.2. In-Vivo Validation Experiment

In order to validate the proposed method on the set of 30 human subjects described previously, tag points were manually identified and edited at the time frame nearest end-systole in each study by an expert user. Accuracy of tag points detected and classified by the PCGC was evaluated by comparing the 1D displacement measurements from classified tag points to those from the manually identified tag points. Fig. 10 shows plots of the differences for short- and long-axis slices in both the RV and LV. The displacement measurement differences were -0.002 ± 0.442 (pixels) for LV short-axis groups, -0.061 ± 0.69 (pixels) for LV long-axis slices, -0.009 ± 0.880 (pixels) for RV short-axis slices, and -0.337 ± 1.879 (pixels) for RV long-axis slices. The classified tag point locations were notably less accurate for RV than for LV. There are multiple reasons for this difference in accuracy. First, due to the thinness of the RV free wall, accuracy of the detected tag points can be largely affected by the noisy signal present over the myocardium. Second, the endocardial and epicardial boundaries of the RV can sometimes look like tag lines. Third, the interframe deformation of RV free wall, especially at long-axis view, is larger in the RV relative to the LV.

Strains were computed in regions defined by the American Heart Association (AHA) 17 segment model (Cerqueira et al., 2002) excluding the apex. RV free wall strains were computed on a similar model adapted to the RV. LV and RV cardiac strain parameters (unitless) were averaged over the mid-ventricular segments. We also computed LV twist (in degrees), which was defined as the rotation angle difference between LV apex and base (Young and Cowan, 2012).

We compared the resulted strain parameters from the proposed method (PCGC tag point classification and DMF strain reconstruction) to those from two other methods. The first method used tracked and manually corrected tag points at end-systole (ES) as described above (Denney and McVeigh, 1997; Denney, 1999; Denney et al., 2003). The second method used unwrapped HARP images from all time frames with manually placement branch cuts and quality-guided phase unwrapping for 1D displacement measurements (Venkatesh et al., 2011). For both of these methods, the DMF strain reconstruction was used, resulting in 3D cardiac strains at ES for the first one and 3D+time strain curves for the second. We refer to the first method as the Feature-Based method (FB) and the second as the manual Strain from Unwrapped Phase (mSUP) method.

ES strain parameters from the proposed method were compared to those from the feature-based method (FB) using paired t-tests. The results are shown in Table 1. A P-value equal to or less than 0.05 was considered statistically significant. Strains and twists from these two methods were not significantly different. Correlations were quite high except for RV tangential strains and RV longitudinal strains for the reasons described above. The maximum coefficient of variance (CV) of the LV strain parameters was 2.33% and that of the RV strain parameters was 4.66%. The CV for twist was 1.61%.

In Table 2 we compared peak strains (twists) and strain rates (twist rates) from the reconstructed strain time curves using the proposed method to those reconstructed using mSUP. Parameters except for systolic twist rates were not significantly different using these two methods. Correlations were high except for $E_{tt}RV$ and $E_{min}RV$ strain rates. CV for RV strain rates and twist rates were higher than LV strain rates.

Fig. 11 shows the minimum principal strain at end-systole for a representative from each of the subject groups (normal volunteers (NL), diabetic patients with myocardial infarction (DMI), resistant hypertensive patients (HTN), and patients with pulmonary arterial hypertension (PAH)) using the FB, mSUP and the proposed method. Qualitatively, the strain maps from all three methods are similar.

Minimum principal strains averaged over each subject group using the proposed method, mSUP and 2D HARP strain (Osman et al., 2000), are shown in Fig. 12. Because different subjects have different heart rates, the strain curves were normalized in time by dividing the QRS delay time of each time point by the systolic interval in that subject and multiplying the result by 100%. This resulted strains versus % systolic interval, which were averaged and plotted in Fig. 12. PCGC strain curves were similar to those from the mSUP method and were smoother. Because the HARP algorithm computes 2D Eulerian strain, there were some differences between the strain curves from HARP strain and those from mSUP or the PCGC. As expected, strain magnitudes from all three methods were lower in the DMI and PAH groups than in NL and HTN.

4. Discussion and Conclusion

In this paper, we presented a method, called the PCGC, for measuring 3D cardiac deformation and strain from tagged MR images in both the LV and RV walls through mid diastole with no manual correction of the tag line points - even in the later frames where there is considerable fading of the tag lines and in the RV free wall where the myocardium is relatively thin. We used Gabor filter banks for tag point extraction, and a graph cuts based algorithm to classify each of the detected tag points for displacement measurement. We also introduced a motion compensation technique with the discrete model-free method to improve the classification accuracy. The resulting algorithm required 30 minutes for manual contouring followed by 44 minutes of fully automated processing for a typical study with 10 short-axis slices, 6 long-axis slices, and 20 time frames.

For validation with in vivo data, we used a method similar to prior papers by our group (Venkatesh et al., 2010, 2011), which used three different methods for extracting

displacement information from the tMRI data: feature-based (FB) tag tracking (Denney, 1999; Denney et al., 2003) followed by manual correction, manually-edited strain from unwrapped phase (mSUP) (Venkatesh et al., 2011), and HARP (Osman et al., 2000, 1999). mSUP and HARP are not tag detection methods, but the wrapped (HARP) or unwrapped (mSUP) phase is a measure of myocardial deformation that is either used to fit a deformation model (mSUP) or used to compute Eulerian strain directly (HARP).

We used the FB method for validation because strains computed with this method have been reported by our group in the clinical literature (Ahmed et al., 2010; Pat et al., 2010a; Ahmed et al., 2012a,b; Gupta et al., 2015; Schiros et al., 2015; Zha et al., 2015). We also used mSUP for validation because it can measure 3D strains through the cardiac cycle as opposed to FB, which can practically only measure a single time frame (usually ES). Note that while theoretically, the FB method could be used for other time frames to get strain in the entire cycle, this is extremely time consuming (4 ~ 8 hours) due to the need to manually correct tag line points particularly past end-systole. The PCGC can accomplish the same thing in 44 min of fully automated processing with similar strains as shown in Fig. 12. The second method, mSUP, can measure 3D strains in the LV and RV through the cardiac cycle, but it requires manual correction of residues caused by phase inconsistencies in the HARP image (joining of tag lines, spurious tag lines, etc.). The PCGC does not have this requirement. As shown in Tables 1 and 2 and Figs. 11 and 12, the PCGC, which required no manual intervention after contouring, computed 3D strains in both the LV and RV walls that were similar to those computed with manual intervention (FB and mSUP).

The motion reconstruction accuracy from tagged MR images largely depends on the performance of the tag point extraction method. In our work, we used a bank of Gabor filters to detect the tag points, which adjust parameters to fit to the local tag features, and potentially perform better than the bandpass filter with fixed window. However, the tag points were detected pixel-wise. Tag detection accuracy could potentially be improved by fine tuning the tag locations to sub-pixel resolution or spatially smoothing the tag points in a given tag line.

We used a graph cuts based method for tag point classification (PCGC), which assumes the 1D displacement field is spatially smooth. For computing the neighborhood of the tag point and the membership weight, we used the local frequency map which is a by product from the Gabor filter bank, and a Gaussian type radial basis function. Other types of neighborhood functions could potentially be used.

One modification we made for the PCGC is that we generated auxiliary points to improve the classification accuracy. The phase shifted map was used with half a cycle difference. Theoretically, we can generate any times dense auxiliary points by changing the shifted phase. For example, shifting the phase map with $2\pi/3$ and $4\pi/3$ will generate auxiliary points at one-third and two-third positions between neighboring tag lines, thus giving a two times denser point set. However, more auxiliary points will increase computation time of the PCGC algorithm.

We used the discrete model-free method for motion compensation. However, there are more options that can be adopted, such as non-rigid registration, which aligns two images by warping one with parametric transformation. One of the future research topics is an investigation of other motion compensation techniques.

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Highlights

- A new method for computing 3D+time biventricular cardiac strain from tagged MR data.
- Gabor filter banks extract tag features from left and right ventricular walls.
- A graph cut algorithm optimally assigns tag features to tag lines.
- Fully automated processing after segmentation step takes 44min for a typical study.
- Validation on 30 human studies including normals and a range of pathologies.

Figure 1.

Gabor filter bank in the (a) spatial domain (real part) and (b) frequency domain (magnitude) for a 256×256 pixel tag image with a 45° modulation and tag spacing of 6.8 pixels. The Gabor filter in center of (a) and denoted with red circle in (b) has parameters $\omega = 0.1467$, $\theta = \pi/4$.

Figure 2.

Illustration of pre-filtering process for grid tagged images. (a) Short-axis cardiac tagged image near mid-ventricle and end-systole. (b) Fourier transform magnitude of the image in (a). The strip filter enclosed with red lines preserves tag line with 45° orientation and removes tag lines of -45° as shown in (c). The filter enclosed by yellow lines does the opposite as shown in (d).

Figure 3.

Example of feature extraction. White borders are myocardial contours. (a) is the tagged MR image at end-systole. (b) is the phase map computed after interpolation of the complex responses from the Gabor filter bank centered at $(0.1467, \pi/4)$. (c) shows the detected tag points using the phase map from (b). Only points within contours were displayed. (d) is the estimated tag frequency map using the optimal interpolated filter parameters. The frequency ranges from 0.13 pixel^{-1} (blue) to 0.18 pixel^{-1} (yellow).

Figure 4.

Two examples of label configurations - one resulting in a smooth deformation pattern (a) and one resulting in a nonsmooth deformation pattern (b). Two dotted reference tag lines are labeled as l_1 and l_2 . $\mathbf{n}$ is the normal vector of the reference tag lines. p , q_1 , and q_2 are detected tag points with coordinate vectors $\mathbf{p}$, $\mathbf{q}_1$, and $\mathbf{q}_2$.

Figure 5.

Illustration of elementary graphs and the final graph. s and t are terminal source and sink, respectively. v_p and v_q are two vertices corresponding to the binary variables δ_p and δ_q . (a) is the elementary graph of a unary term, for the case of $E_0^p(1) > E_0^p(0)$. (b) is the elementary graph of a pairwise term, for the case of $E_1^{pq}(1,0) > E_1^{pq}(0,0)$, and $E_1^{pq}(1,0) \geq E_1^{pq}(1,1)$. (c) is the final graph after merging all elementary graphs. The cut divides vertices into two sets S (white) and T (dark).

Figure 6. Construction of elementary graphs for (a) unary terms and (b) pairwise terms.

Figure 7.

Illustration of auxiliary points for tag angle of 45° (top row) and -45° (bottom row). White borders are myocardium contours. (a) Tagged images after pre-filtering. (b) Phase maps from the Gabor filter bank. (c) Phase maps shifted by π . (d) Tag points (red) and auxiliary points (yellow) from the phase maps and phase shifted maps, respectively.

Figure 8.

Illustration of motion compensation. (a) shows tag lines at their initial positions without deformation. (b) shows the deformed tag lines. (c) is the result after motion compensation. Dashed lines are reference positions.

Figure 9.

Mean 1D displacement measurement differences at ES with different choices of λ for (upper left) LV short-axis groups, (upper right) LV long-axis groups, (lower left) RV short-axis groups, and (lower right) RV long-axis groups from the 10 human studies. Manually identified tag points were used for comparison. Error bar represents one standard deviation.

Figure 10.

Mean displacement measurement differences at ES for LV short-axis, LV long-axis, RV short-axis, and RV long-axis groups from the 30 validation studies. Manually identified tag points were used for comparison. Error bar represents one standard deviation.

Figure 11.

Representative end-systolic minimum principal strains ($E_{\min}$ and $E_{\min RV}$) computed using (top to bottom) FB, mSUP and the proposed method for (left to right) a normal volunteer (NL), and patients with myocardial infarction and diabetes (DMI), resistant hypertension (HTN), and pulmonary arterial hypertension (PAH). Strain ranges from blue (25% contraction) to yellow (no change).

Figure 12.

(a) LV minimum principal strains ($E_{\min}$) and (b) RV minimum principal strains ($E_{\min RV}$) with the proposed method (blue), mSUP (red) and HARP strain technique (black) averaged over 10 normal volunteers (NL), 5 diabetic patients with myocardial infarction (DMI), 8 resistant hypertensive patients (HTN), and 7 patients with pulmonary arterial hypertension (PAH). Strains were plotted against the percentage of the systolic cycle. Error bar represents one standard error.

Table 1

Statistics of differences between end-systolic strains (unitless) and twists (degrees) from the proposed method and FB method for 30 validation studies.

Strain	Differences	<i>p</i>	ρ	CV
E_{rr}	0.0034 ± 0.0019	0.65	0.94	2.03%
E_{cc}	0.0047 ± 0.0023	0.52	0.90	2.33%
E_{ll}	0.0037 ± 0.0018	0.68	0.96	1.57%
E_{min}	0.0004 ± 0.0010	0.96	0.99	0.70%
<i>Twist</i>	-0.1539 ± 0.0787	0.82	0.99	1.61%
E_{rrRV}	0.0076 ± 0.0022	0.40	0.94	2.57%
E_{ttRV}	0.0102 ± 0.0044	0.27	0.79	4.66%
E_{llRV}	0.0125 ± 0.0044	0.18	0.77	4.14%
E_{minRV}	0.0003 ± 0.0019	0.98	0.96	1.32%

Differences = Mean $\pm$ Standard Error. ρ = Correlation Coefficient. For all correlation coefficients, $p < 0.001$. CV = Coefficient of Variance. E_{rr} = LV radial strain. E_{cc} = LV circumferential strain. E_{ll} = LV longitudinal strain. E_{min} = LV minimum principal strain. E_{rrRV} = RV radial strain. E_{ttRV} = RV tangential strain. E_{llRV} = RV longitudinal strain. E_{minRV} = RV minimum principal strain.

Table 2

Comparison of peak strains and strain rates (twists and twist rates) computed using the proposed method and mSUP.

Strain	Differences	p	p	CV
E_{cc} Peak	-0.0055 ± 0.0003	0.44	<0.001	1.86%
Sys Rate	0.0023 ± 0.0032	0.96	<0.001	3.34%
E Dia Rate	0.0274 ± 0.0067	0.67	<0.001	6.92%
E_{min} Peak	-0.0037 ± 0.0004	0.65	<0.001	1.55%
Sys Rate	-0.0196 ± 0.0040	0.75	<0.001	3.42%
E Dia Rate	-0.0502 ± 0.0046	0.38	<0.001	5.46%
$Twist$ Peak	1.2900 ± 0.0541	0.22	<0.001	3.37%
Sys Rate	13.5935 ± 0.6530	0.04	<0.001	8.05%
E Dia Rate	-9.6224 ± 0.5940	0.11	<0.001	7.90%
$E_{t}RV$ Peak	-0.0058 ± 0.0007	0.52	<0.001	4.02%
Sys Rate	-0.0637 ± 0.0084	0.30	0.44	8.42%
E Dia Rate	0.0081 ± 0.0102	0.93	<0.001	9.74%
$E_{min}RV$ Peak	-0.0095 ± 0.0005	0.29	<0.001	1.94%
Sys Rate	-0.1211 ± 0.0092	0.10	0.53	7.40%
E Dia Rate	-0.0631 ± 0.0094	0.35	0.43	10.76%

Differences = Mean $\pm$ Standard Error. p = Correlation Coefficient. CV = Coefficient of Variance. E_{cc} = LV circumferential strain. E_{min} = LV minimum principal strain. $E_{t}RV$ = RV tangential strain.

$E_{min}RV$ = RV minimum principal strain. Peak = peak strain (unitless) / twist (degrees) during the cycle. Sys Rate = systolic strain rate (sec^{-1}) / twist rate (degrees/sec). E Dia Rate = early diastolic strain rate (sec^{-1}) / twist rate (degrees/sec).