Three-Dimensional Myocardial Tissue Tracking and Strain Calculation for Volumetric Cine DENSE Data

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Introduction. Cine DENSE (Displacement ENcoding with Stimulated Echoes) is a quantitative myocardial motion imaging technique that encodes tissue displacement into the phase of the stimulated echo through multiple time frames of the cardiac cycle (1-5). This abstract introduces novel automatic algorithms for myocardial tissue tracking and strain calculation for three-dimensional (3D) cine DENSE data.

Methods. In DENSE, the displacement of each voxel is encoded as a phase shift that accrued since the displacement encoding time t_0. The acquired data inherently measure the Eulerian displacement field. However, to better visualize and interpret that data, the frame-to-frame trajectory of the Lagrangian displacement field is typically desired. To compute the Lagrangian displacement trajectories, tissue tracking needs to be performed. In this work, scattered data interpolation using radial basis functions (RBF) was developed for Lagrangian tissue tracking (6).

Suppose a function $T(u)$ needs to be interpolated, where u is a vector given by Eq. [1], and the value of $T(u)$ is a scalar. Let $p_1, \ldots, p_N$ be a given set of nodes in the n-dimensional space R^n, and the corresponding function values are $y_1, \ldots, y_N$. The goal of interpolation is to use an equation consisting of all p_i and y_i to give a close estimation of $T(u)$. The general definition of a set of RBF is given by Eq. [2], where $\|u-p_i\|$ denotes the Euclidean distance defined in Eq. [3]. In this work, the linear splines function (Eq. [4]) was chosen. Using RBF, the desired equation can be expressed by Eq. [5], where β_i is the interpolation expansion coefficient. In order to obtain β_i, Eq. [6] needs to be solved. Introducing the notations in Eq. [7] through [11], Eq. [6] can be simplified as Eq. [12], and then be solved by Eq. [13].

$$\textbf{[1]}\ u=[u_1 \ \cdots \ u_n]^T \quad \textbf{[2]}\ g_i(u)\equiv g(\|u-p_i\|)\ \ i=1,\cdots,N \quad \textbf{[3]}\ d(u,w)=\sqrt{(u_1-w_1)^2+\cdots+(u_n-w_n)^2}$$

$$\textbf{[4]}\ g_i(u)=\|u-p_i\| \quad \textbf{[5]}\ T(u)=\sum_{i=1}^{N}\beta_i g_i(u)+\beta_{N+1} \quad \textbf{[6]}\ \begin{cases}\sum_{k=1}^{N}\beta_k g_k(p_i)+\beta_{N+1}=y_i, & i=1,\cdots,N\\ \sum_{k=1}^{N}\beta_k=0\end{cases}$$

$$\textbf{[7]}\ q=\begin{bmatrix}1\\ \vdots\\ 1\end{bmatrix}\in R^N \quad \textbf{[8]}\ G=\begin{bmatrix}g_1(u_1) & \cdots & g_N(u_1)\\ \vdots & \vdots & \vdots\\ g_1(u_N) & \cdots & g_N(u_N)\end{bmatrix}\in R^{N\times N} \quad \textbf{[9]}\ H=\begin{bmatrix}G & q\\ q^T & 0\end{bmatrix}\in R^{(N+1)\times(N+1)}$$

$$\textbf{[10]}\ B=\begin{bmatrix}\beta_1\\ \vdots\\ \beta_{N+1}\end{bmatrix}\in R^{N+1} \quad \textbf{[11]}\ Y=\begin{bmatrix}y_1\\ \vdots\\ y_N\\ 0\end{bmatrix}\in R^{N+1} \quad \textbf{[12]}\ HB=Y \quad \textbf{[13]}\ B=H^{-1}Y$$

$$\textbf{[14]}\ q_i=p_i-u\ \ (i=1,\cdots,N_n) \quad \textbf{[15]}\ A=[q_1 \ \cdots \ q_{N_n}] \quad \textbf{[16]}\ A'=[q_1' \ \cdots \ q_{N_n}']$$

$$\textbf{[17]}\ A'=FA \quad \textbf{[18]}\ F=A'A^T(AA^T)^{-1} \quad \textbf{[19]}\ AA^T=USV^T$$

$$\textbf{[20]}\ \begin{cases}S_{i,k}^0=S_{i,k} & i\neq k\\ S_{i,i}^0=1/S_{i,i} & else\end{cases} \quad \textbf{[21]}\ F=A'A^TVS^0U^T \quad \textbf{[22]}\ E=\frac{1}{2}(F^TF-I)$$

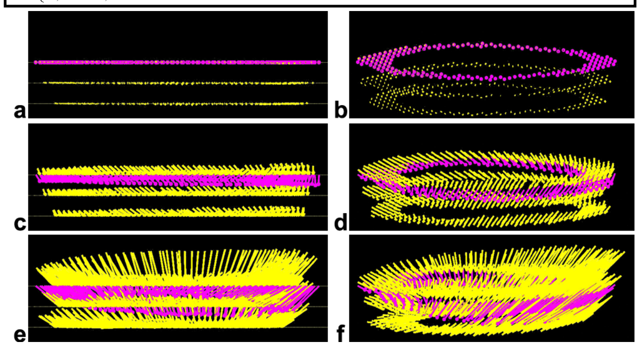

Fig. 1 Tissue tracking illustration of 3D cine DENSE data in 2D view (a,c,e) and 3D view (b,d,f). The top, middle and bottom rows are at end-diastole, through-systole and end-systole, respectively.

Fig. 1 shows a tracking example of one slice. The three slices of yellow arrows are measured Eulerian displacement vectors. Their heads lie on the mesh grid of imaging planes indicating the tissue positions at this cardiac phase, whose coordinate values in each direction correspond to $y_1, \ldots, y_N$. Their tails indicate the corresponding tissue positions at $t = t_0$, which correspond to $p_1, \ldots, p_N$. Solving β_i, the RBF interpolation Eq. [5] can be established. The tails of purple arrows correspond to the voxels to be tracked at $t = t_0$, which overlap with one slice of yellow arrow heads (Fig. 1a and 1b) and serve as the input vectors of u. For each direction, the interpolated coordinate values are calculated using Eq. [5]. Combination of the interpolated coordinates in all directions generates the heads of purple arrows which correspond to the tissue positions at the current cardiac phase.

The frame-to-frame trajectory is obtained by connecting the pathline of the Lagrangian displacement vector head, and is then slightly smoothed using a 10th order polynomial fitting to each coordinate of the tissue position as a function of time.

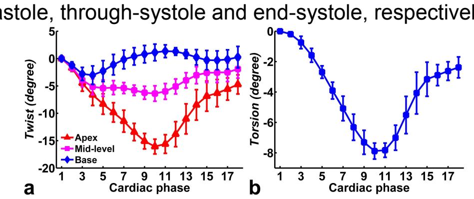

Fig. 2 (a) Twist angles as a function of time at the apex, mid-level and base of the LV. (b) LV torsion as a function of time.

Next, the Lagrangian strain tensor E was calculated as follows. For a given voxel point u, suppose there are N_n arbitrary neighboring points, p_1 through p_{N_n}, and suppose the deformation characteristics of the region where these points are located is uniform. The distance vectors between u and the neighboring points are calculated as Eq. [14], then these vectors are recorded as Eq. [15], where A is an $n \times N_n$ matrix. After tissue deformation, the corresponding deformed distance vectors are expressed by A' in Eq. [16]. The relationship between A and A' can be described by Eq. [17], where F is the deformation gradient tensor, an $n \times n$ matrix characterizing the local deformation at the point u. Usually F can be solved by Eq. [18]. However, in ill-condition cases, singular value decomposition (SVD) may be needed to compute Eq. [18]. In detail, SVD is performed to AA^T as Eq. [19], then S^0 is calculated as Eq. [20], and Eq. [18] can be re-written as Eq. [21]. Finally, E can be calculated as Eq. [22], where I is the identity matrix.

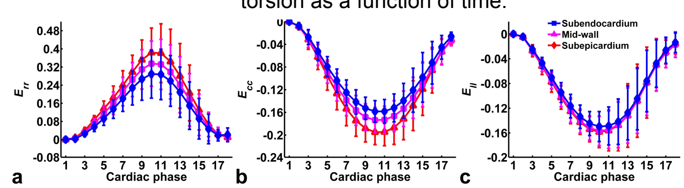

Fig. 3 Example mean strain-time curves for E_{rr}, E_{cc}, and E_{ll}.

Under protocols approved by institutional review board of the University of Virginia, a free-breathing ECG- and navigator-gated 3D spiral cine DENSE sequence with imaging parameters described in (4) was applied in five healthy volunteers on a 1.5T MRI system (Avanto, Siemens Medical Solutions, Germany). The above algorithms were performed using a MATLAB program (Mathworks Inc., Natick, MA, US). After 3D Lagrangian trajectories were obtained, twist, defined as the counterclockwise rotation angle of one slice viewed from the base of the left ventricle (LV), was calculated. Torsion was also calculated as the difference between the twist angles of the apex and the base of the LV, normalized by the ratio of the long-axis length to the average short-axis radius of the LV. In addition, E was decomposed into the local radial, circumferential and longitudinal (RCL) coordinate system (7) to obtain normal strains E_{rr}, E_{cc}, and E_{ll}, respectively.

Results. Twist angles for the most basal, the mid-ventricular, and the most apical levels are plotted vs. time in Fig. 2a. The evolution of LV torsion as a function of time is shown in Fig. 2b. The twist and torsion results in this study are consistent with previous results from myocardial tagging in healthy volunteers (8,9). Mean strain-time curves of the subendocardial, mid-wall and subepicardial layers of the myocardium for E_{rr}, E_{cc}, and E_{ll} from the mid-ventricular slices are shown in Fig. 3a-3c, respectively. Strain results in this study are very similar to previous results (7,8).

Conclusion. Using the automatic algorithms of tissue tracking and strain calculation in this study, reliable 3D results of myocardial mechanics including strain, twist and torsion can be obtained using 3D cine DENSE data.

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