Fast Tracking of Cardiac Material Points from SF-CSPAMM Images Using 3D SF-HARP

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Introduction: MR tagging is a powerful technique to assess the regional myocardial function. However, since conventional SPAtial Modulation of Magnetization (SPAMM) images are obtained at a fixed imaging plane, the images acquired at different timeframes do not represent the true motion of specific myocardial material points. Slice Following Complementary SPAMM (SF-CSPAMM)[1], proposed by Fischer *et al*, avoided through-plane motion effects by tagging the desired slice of the myocardium and applying a subtraction imaging technique to image just that part of the myocardial tissue. Sampath *et al* proposed a method, called SF-Harmonic Phase (SF-HARP)[2], which can perform 3D tracking of material points from SF-CSPAMM images. This technique is very promising due to the nature of ultrafast HARP-based motion tracking[3]. A limitation of this method includes that two-dimensional tagging is applied on both the short-axis (SA) and long-axis (LA) images. This approach obviously incorporates redundant data acquisition which will unnecessarily prolong the acquisition time. In this study, we propose an improvement of SF-HARP that can track the cardiac material points from SF-CSPAMM images with two-dimensional tagging on SA images and one-dimensional tagging on long-axis images. This technique abbreviates the imaging time by 25% and the computational motion tracking is around 1s per timeframe.

Method: The motion tracking was restricted to those material points located on the intersections of SA and LA tagged planes at the reference time. Using SF-CSPAMM, these material points will stay on the intersections of SA and LA tagged planes through the cardiac cycle even though both tagged planes are deformed. The 3D harmonic phase values ($[\phi_1\ \phi_2\ \phi_3]^T$) of these material points can be obtained at the reference time and the phase time-invariance property of material points is used for motion tracking. Assume an intersection point, $\underline{q}_n$, is located on the intersection of the deformed SA tagged plane $\boldsymbol{S}$ and the LA tagged plane $\boldsymbol{L}$ at timeframe $\boldsymbol{n}$ (see Fig. 1). The acquired slice-followed images, $\boldsymbol{S_p}$ and $\boldsymbol{L_p}$, can be viewed as the projection of $\boldsymbol{S}$ and $\boldsymbol{L}$ respectively in a 3D coordinate system. In the 2D coordinate system on the $\boldsymbol{S_p}$ plane, the projection of the point $\underline{q}_n$ is marked as $\boldsymbol{p_n}$. Similarly, on the $\boldsymbol{L_p}$ plane, the projection of the point $\underline{q}_n$ is marked as $\boldsymbol{r_n}$. The goal of motion tracking is, starting from $\underline{q}_n$ at timeframe $\boldsymbol{n}$, to find $\underline{q}_{n+1}$ at timeframe $\boldsymbol{n}+1$. The algorithm of motion tracking is as following (see Fig.1):

Step 1 On $\boldsymbol{S_p}$, find $\boldsymbol{p_{n+1}}$, who has the same phase value $[\phi_1\ \phi_2]^T$ as $\boldsymbol{p_n}$ using 2D-HARP. ($\boldsymbol{p_n}$ and $\boldsymbol{p_{n+1}}$ are the projection points of $\underline{q}_n$ and $\underline{q}_{n+1}$ on $\boldsymbol{S_p}$, respectively).

Step 2 Find the line $\boldsymbol{l_n}$, which is perpendicular to plane $\boldsymbol{S_p}$ and intersecting with $\boldsymbol{S_p}$ on point $\boldsymbol{p_{n+1}}$.

Step 3 Project $\boldsymbol{l_n}$ onto $\boldsymbol{L_p}$ and find the intersection line $\boldsymbol{l_{np}}$.

Step 4 On plane $\boldsymbol{L_p}$, project point $\boldsymbol{r_n}$ onto line $\boldsymbol{l_{np}}$. The point projected on $\boldsymbol{l_{np}}$ is marked as $\boldsymbol{r_{np}}$.

Step 5 Starting from $\boldsymbol{r_{np}}$, on line $\boldsymbol{l_{np}}$, search for the closest point that has the same phase value ϕ_3 as point $\boldsymbol{r_n}$ using 1D-HARP. (starting from $\boldsymbol{r_{np}}$, to find $\boldsymbol{r_{n+1}}$).

Step 6 Find $\underline{q}_{n+1}$ by combining both the information of $\boldsymbol{r_{n+1}}$ and $\boldsymbol{p_{n+1}}$.

Experiment: MR imaging was performed on clinical 1.5T Philips MR whole body systems. The SF-CSPAMM images were acquired from one normal human subject using a spiral acquisition[4]. 6 SA slices with horizontal and vertical tags and 8 LA slices with horizontal tags only were acquired. The imaging parameters were: FOV=380mm, matrix size=160×160, ramped flip angles=7-25°, slice thickness=8mm, NSA=2, Spiral Interleaves=12, Acquisition Window=20ms, and TR=32.5ms. The cine images for each tagging direction on each slice were acquired in a 23s breath-hold (BH) and the complete dataset was acquired in 20 BHs. A total of 10 cardiac phases were acquired (from end-diastole to end-systole). This dataset was post-processed by 3D SF-HARP which was implemented using MATLAB in a software program with a graphic user interface. A one-layer mesh (6 SA circles and 16 LA lines, a total of 96 material points) was built inside the midwall of left ventricle in the first timeframe and was tracked until end-systole. Ecc was computed on 16 segments from each of 6 SA levels.

Result: The total processing time for 3D SF-HARP was around 8 minutes and the motion tracking time was 1s per timeframe. Fig. 2 shows the tracked mesh, superimposed by the computed Ecc strain map, from end-diastole to end-systole. There is evidence of circumferential contraction and longitudinal shortening towards the apex as expected. Simultaneously, base-to-apex torsion can be appreciated at timeframe 10 of Figure 2.

Conclusion: 3D SF-HARP can track 3D true motion of the material points located on the intersections of SA and LA tagged planes. The phase time-invariance property of material points was used for motion tracking. This technique is faster than earlier approaches and shows its potential to be used in clinical applications.

References: [1] Fischer SE, *et al.*, Magn Reson Med 1994;31:401-413.
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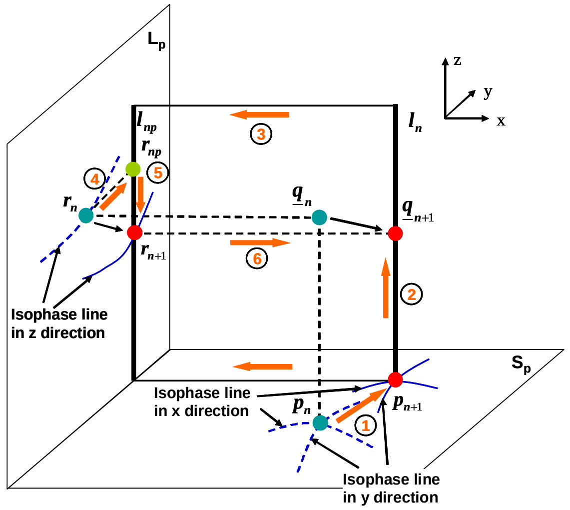

Fig. 1 The 3D SF-HARP material point tracking algorithm.

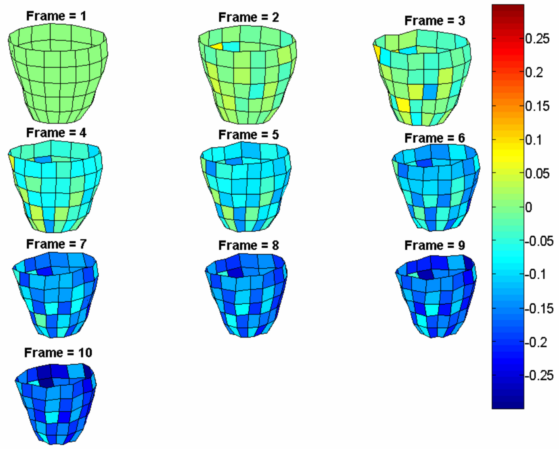

Fig. 2. The 3D E_{cc} strain map in 10 timeframes of the deformed mesh (end-diastole to end-systole). The color of each patch represents the E_{cc} strain of one segment at one SA slice level.