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TRUHARP: SINGLE BREATH-HOLD MRI FOR HIGH RESOLUTION CARDIAC MOTION AND STRAIN QUANTIFICATION

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Abstract

MRI techniques for tissue motion and strain quantifications have limited resolution because of interference from the conjugate echo or spectral peak in Fourier space. Methods have been proposed to remove this interference in order to improve resolution; however, these methods are clinically impractical due to long image acquisition time. In this paper, we propose TruHARP, an MRI motion and strain quantification methodology that involves a novel single breath-hold imaging protocol. In post-processing, TruHARP separates the spectral peaks in the acquired datasets, enabling high resolution motion and strain quantification. The impact of high resolution on circumferential and radial strain is studied using a realistic simulation and the improvement in strain maps is demonstrated in an in-vivo human study.

Keywords

MRI; HARP; tagging; motion and strain estimation

1. INTRODUCTION

Motion and strain profiles of myocardial tissue are important tools for diagnosis and prognosis of cardiac diseases [1], [2]. MR-based techniques to measure these functional profiles include phase contrast (PC) [3], DENSE [4], tagging [5-7], SENC [8], and zHARP [9]. However, these techniques provide limited-resolution motion and strain profiles (*functional resolution*) due to the imaging physics in the case of DENSE and HARP, or have restricted patient screening due to long imaging time in the case of phase contrast (PC) and CANSEL [10]. SENC measures a high-resolution strain profile component only in the slice-selection direction.

In harmonic phase (HARP) analysis of MR tagged images [7], motion and strain profiles are estimated by isolating one of the spectral peaks present in the Fourier spectrum of the tagged data. Therefore, HARP functional resolution is limited by the interference from the neighboring peaks [11]. Interference can be reduced by decreasing the tag spacing thus spreading the harmonic peaks further apart, and also minimizing the number of spectral peaks by using 1-1 SPAMM pulse sequence to generate two harmonic peaks only and one T1-relaxation peak in the center of k-space. Improvement of functional resolution in MR tagging [5,6] has been achieved by the use of decreased tag spacing [12]. Similar to

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decreased tag spacing [13], stronger motion encoding gradient enables DENSE [4] to achieve higher functional resolution by reducing echo interference. The functional resolution of HARP and DENSE can be further improved by removing the effect of DC spectral peak using Complimentary SPAMM (CSPAMM) [9,14] and Slice Following DENSE (SF-DENSE) [15,16], respectively.

Recently, CANCEL [10] was proposed to further improve the resolution of DENSE imaging. CANCEL acquires ten datasets over nine minutes and completely separates all the spectral peaks (referred to as conjugate echoes in the DENSE literature). The duration of image acquisition makes this technique impractical to apply to some patients and also makes it susceptible to mis-registration artifacts arising from bulk patient motion and inconsistent multiple breath-holds.

In this paper, we present a novel single breath-hold two-dimensional (2D) myocardial motion quantification methodology that combines a modified HARP analysis and a novel MR tagging protocol for total removal of unwanted harmonic echoes or peaks (TruHARP). In a single breath-hold, TruHARP acquires five uniquely tagged datasets which are then processed to separate all the spectral peaks. In the absence of spectral interference, resolution of motion and strain profiles are now limited by the noise and resolution of image acquisition and not by the spacing between the spectral peaks. In the following sections, we describe the TruHARP pulse sequence and the post-processing procedures. We then present simulations that demonstrate improved resolution and explore the tradeoffs between resolution and noise. Improvements in strain quantification are then demonstrated in an in-vivo healthy human scan.

2. THEORY

2.1 TruHARP formulation

The image intensity $I_{Ah}(\mathbf{x}, t)$ for a typical image acquired using 1-1 SPAMM pulse sequence shown in Fig. 1 with horizontal tagging is given by

$$\begin{aligned} I_{Ah}(\mathbf{x}, t) &= \rho(\mathbf{P}(\mathbf{x}, t)) e^{j\varphi_e(\mathbf{x}, t)} \left(A_{dc}(\mathbf{x}, t) + A_{hp}(\mathbf{x}, t) \cos(\omega y - \varphi_y(\mathbf{x}, t)) \right) \\ &= \rho(\mathbf{P}) e^{j\varphi_e} \left(A_{dc} + A_{hp} \frac{e^{j(\omega y - \varphi_y)} + e^{-j(\omega y - \varphi_y)}}{2} \right), \end{aligned} \quad (1)$$

where $\rho(\mathbf{x})$ is effective spin density, ω is tag frequency, $\mathbf{P}(\mathbf{x}, t)$ is reference map (position of 3D spatial point $\mathbf{x}$ at the reference time), $\varphi(\mathbf{x}, t)$ is displacement-encoding phase resulting from tagging, $\varphi_e \mathbf{x}, t$ is phase from inhomogeneity and other magnetic field non-idealities, t is time from tag application to image acquisition, and A_{dc} and A_{hp} depend on imaging parameters. A_{dc} increases with time due to T1-relaxation and A_{hp} decreases with time due to tag fading [14]. Similarly, a vertical tagged 1-1 SPAMM dataset has the form,

$$I_{Av}(\mathbf{x}, t) = \rho(\mathbf{P}(\mathbf{x}, t)) e^{j\varphi_e} \left(A_{dc} + A_{hp} \cos(\omega x - \varphi_x) \right) = \rho(\mathbf{P}) e^{j\varphi_e} \left(A_{dc} + A_{hp} \frac{e^{j(\omega x - \varphi_x)} + e^{-j(\omega x - \varphi_x)}}{2} \right). \quad (2)$$

I_{Ah} and I_{Av} in Eqs. (1, 2) can be represented as combination of five separate images I_{dc} , I_h^+ , I_h^- , I_v^+ and I_v^- such that,

$$I_{Ah}(\mathbf{x}, t) = I_{dc}(\mathbf{x}, t) + I_h^+(\mathbf{x}, t) + I_h^-(\mathbf{x}, t) \quad (3)$$

$$I_{A_v}(\mathbf{x}, t) = I_{dc}(\mathbf{x}, t) + I_v^+(\mathbf{x}, t) + I_v^-(\mathbf{x}, t) \quad (4)$$

where

$$I_{dc}(\mathbf{x}, t) = \rho(\mathbf{P}) e^{j \varphi_e(\mathbf{x}, t)} A_{dc}(\mathbf{x}, t) \quad (5)$$

$$I_h^\pm(\mathbf{x}, t) = \rho(\mathbf{P}) e^{j \varphi_e(\mathbf{x}, t)} A_{hp}(\mathbf{x}, t) e^{-j(\omega y - \varphi_y(\mathbf{x}, t))} / 2 \quad (6)$$

$$I_v^\pm(\mathbf{x}, t) = \rho(\mathbf{P}) e^{j \varphi_e(\mathbf{x}, t)} A_{hp}(\mathbf{x}, t) e^{-j(\omega x - \varphi_x(\mathbf{x}, t))} / 2 \quad (7)$$

Eqs. (3, 4) represent a linear system of two equations in five unknown variables. Since this system of equations is under-determined, in conventional HARP analysis the motion encoded images I_h^+ and I_v^+ cannot be extracted directly, and an explicit k-space filtering is necessary. In TruHARP, in addition to I_{A_h} and I_{A_v} , the following datasets are acquired:

$$I_{B_h}(\mathbf{x}, t) = \rho(\mathbf{P}(\mathbf{x}, t)) e^{j \varphi_e} (A_{dc} - A_{hp} \cos(\omega y - \varphi_y)) = I_{dc}(\mathbf{x}, t) - I_h^+(\mathbf{x}, t) - I_h^-(\mathbf{x}, t), \quad (8)$$

$$I_{C_h}(\mathbf{x}, t) = \rho(\mathbf{P}(\mathbf{x}, t)) e^{j \varphi_e} (A_{dc} + A_{hp} \sin(\omega y - \varphi_y)) = I_{dc}(\mathbf{x}, t) + jI_h^+(\mathbf{x}, t) - jI_h^-(\mathbf{x}, t), \quad (9)$$

$$I_{C_v}(\mathbf{x}, t) = \rho(\mathbf{P}(\mathbf{x}, t)) e^{j \varphi_e} (A_{dc} + A_{hp} \sin(\omega x - \varphi_x)) = I_{dc}(\mathbf{x}, t) + jI_v^+(\mathbf{x}, t) - jI_v^-(\mathbf{x}, t). \quad (10)$$

From these five datasets, the x - and y -displacement-encoded peaks and the conjugate peaks are extracted as follows,

$$I_{dc} = (I_{A_h} + I_{B_h}) / 2 \quad (11)$$

$$I_h^\pm = (I_{A_h} - I_{B_h}) / 2 \pm j(I_{C_h} - I_{dc}) / 2 \quad (12)$$

$$I_v^\pm = (I_{A_h} - I_{dc}) / 2 \pm j(I_{C_v} - I_{dc}) / 2 \quad (13)$$

The displacement-encoding harmonic phases (HARP) images Φ_x and Φ_y are now obtained directly without bandpass filtering from the phase component of the complex results

$$\Phi_y = \mathbf{W} (2\omega y - 2\varphi_y) = \angle (I_h^+ (I_h^-)^*) \quad (14)$$

$$\Phi_x = \mathbf{W} (2\omega x - 2\varphi_x) = \angle (I_v^+ (I_v^-)^*) \quad (15)$$

where the symbol $*$ is the complex conjugate operator.

2.2 Single Breath-hold TruHARP pulse sequence

The five tagged datasets in Eqs. (1, 2, 8-10), are acquired by repeating the pulse sequence shown in Fig. 1 five times. Each repetition has unique tagging parameters ($\theta_{\phi_1}^1$, $\theta_{\phi_2}^2$, G_h , and G_v , as shown in Table 1).

In order to acquire the datasets in a single breath-hold, three interleaved spiral k-space data acquisitions are used to acquire each of the five datasets, thus requiring a single 15-heartbeat breath-hold.

2.3 TruHARP motion and strain resolution

Even though there is no interference present after separation of the harmonic peaks, a k-space filtering is still required to reduce the impact of noise. The k-space data acquired for image acquisition is centered at DC while the separated spectral peak is centered at $1/r$ mm^{-1} . The k-space acquired around the spectral peak is asymmetric and the distance between the nearest edge of acquired k-space and the spectral peak is $r_s = 1/2 \Delta - 1/\omega$ mm^{-1} , where Δ is the in-plane resolution of the tagged image slice. Therefore, to avoid artifacts from the asymmetrically sampled spectral peak and noise, a Kaiser-Bessel filter centered at the spectral peak with FWHM of at most $2r_s$ should be applied, thereby restricting the resolution of the image associated with the acquired spectral peak to $1/(2r_s) = \omega\Delta/(\omega + 2\Delta)$ mm. Smaller bandpass filters can be applied to reduce the impact of noise in the higher frequency regions at the expense of resolution.

HARP processing [7] is applied on the separated spectral peaks to track points and estimate the Eulerian strain profile over the imaged slice.

3. METHODS

3.1 Simulation

Simulations were performed to study the effect of noise relative to improvements in strain quantification accuracy. CSPAMM and TruHARP datasets were simulated for a tagged contracting annular region in the presence of a stationary background, mimicking the contraction of left ventricle during systole tagged at end diastole. The simulated images were of size 256×256 pixels with FOV of 280 mm and tag spacing of 7 mm. The annular region was contracted to produce strain of -15%, which is the typical contraction of myocardium at systole. Harp analysis was applied to the CSPAMM and TruHARP datasets by varying the amount of additive white Gaussian noise to achieve CNR = 5 and 15 during data acquisition, and varying the FWHM of the filter from 16 to 80.

3.2 In-vivo Single Breath-Hold Experiments

One healthy male subject, age 24, was scanned using a Philips 3.0T Achieva MRI scanner (Philips Medical Systems, Best, NL) equipped with a six-channel cardiac phased array

surface coil. Channels were distributed equally between the anterior and posterior sides of the chest. MR images were acquired using VECG triggered spiral imaging with a 14 ms acquisition window, 3 spiral readouts/image, 112 samples/spiral, FOV = 280 mm, resolution = 2.5mm×2.5mm, slice thickness= 8 mm, TR = 30 ms, and tag period = 7 mm. The scan was completed in a single breath-hold comprising 15 heart beats. All the data were acquired using segmented k-space spiral acquisition.

4. RESULTS AND DISCUSSION

4.1 Simulation

True and estimated Eulerian circumferential and radial strains over the annular region are shown in Fig. 2. This also shows a scatter plot of estimated strain values over the circumference of radius r inside the myocardium. True strain values (shown as dark points) are uniform over the circumference of myocardium and vary transmurally from epi- to endocardium (solid arrows). TruHARP and CSPAMM have similar distribution of strain profile at typical HARP filter with FWHM=32, corresponding to a Fourier resolution of 8.75 mm. However, when the filter size is increased to FWHM=64 (equivalent to a Fourier resolution of 4.37 mm) both circumferential and radial strain maps obtained using CSPAMM are negatively affected by the interference from the conjugate spectral peak. The effect of interference is shown in Fig. 2 as large variations in strain values at certain radii across the myocardium. In TruHARP, there is no significant change in the circumferential strain with increase in filter size, which could be due to the presence of a constant strain profile in the circumferential direction. The radial strain at mid- and epi-cardium approach their true values (hollow arrows) with an increase in filter size, while the radial strain at endocardium is underestimated, due to low/noisy strain present in the blood pool and air. Effect of noise is more pronounced at larger filter sizes, seen as increase in deviation of estimated radial and circumferential strain at a given myocardial radius.

The RMS error over whole myocardium is plotted in Fig. 3 for CSPAMM and TruHARP as a function of FWHM of the bandpass filter. At a small filter size, the RMS error is primarily due to the partial volume effect (PVE). As the filter size is increased, RMS error decreases due to decrease in PVE (dotted arrows). However, beyond a certain filter size, the error increases due to noise (for both CSPAMM and TruHARP) and interference (for CSPAMM). As shown in Fig. 3, the increase in error due to interference is more significant than that due to noise (solid arrows). The FWHM corresponding to the minimum RMS error in circumferential and radial strain is different for CSPAMM and TruHARP and also, for different noise levels. The minimum strain error is achieved at approximately the FWHM of 32 for CSPAMM compared to 50 at CNR 5, indicating improvement in resolution achieved by using TruHARP versus CSPAMM. Furthermore, the range for filter size for which the error in strain is minimal is wider for TruHARP, indicating a greater robustness to errors.

4.2 In-vivo Single Breath-Hold Experiments

Fig. 4(a) and (b) show the magnitude and Fourier transform, respectively, of the five datasets acquired at end-diastole using TruHARP. The Fourier transforms of these datasets have one DC and two harmonic peaks due to 1-1 SPAMM generated sinusoidal tagging. The four harmonic peaks and DC peak were separated from these datasets using the TruHARP formulation. The magnitude, phase, and Fourier transform of the separated harmonic peaks and DC peak are shown in Fig. 4(c), (d), and (e), respectively.

Fig. 5(a) shows the estimated circumferential and radial strain for the volunteer at end systole using Kaiser-Bessel filter of FWHM 64. The myocardium is divided into 6 sectors and each sector is divided into 9 layers from endocardium to epicardium, as shown in Fig. 5(a). Fig. 5(b) shows the variation of estimated circumferential and radial strain by varying

the FWHM of filter to 32, 48, and 64. Increasing the filter size significantly improves the radial strain but not the circumferential strain. With the increase in filter size, radial strain first increases at all the layers and then converges at the midcardium and endocardium. With further increase in filter size, radial strain increases at the epicardium. These experimental results are consistent with those of simulation.

5. CONCLUSION

TruHARP, an MR imaging protocol and post processing framework in which spectral peaks are isolated, has been described. These spectral peaks have been used to obtain high spatial 2D motion and strain resolution. 2D strain resolution of 4.37 mm has been achieved in an in-vivo human study using the data acquired in a clinically feasible single 15-second long breath-hold. Furthermore, motion and strain resolution is limited by the resolution of acquired image instead of imaging physics. Simulations showed that removal of interference from other spectral peaks leads to higher resolution and more accurate strain maps. This finding has been experimentally demonstrated in an in-vivo human study.

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Fig. 1.

1-1 SPAMM pulse sequence. The values of $\theta_{\phi_1}^{(1)}, \theta_{\phi_2}^{(2)}, G_x$ and G_y to generate TruHARP dataset are shown in Table 1

Fig. 2.

Eulerian circumferential and radial strain for CSPAMM and TruHARP at FWHM of filter given by 32 and 64. Inset picture shows the estimated strain. The plot shows the scatter diagram of estimated (light dots) and true (dark dots) strain over the circumference of myocardium at a given radius.

Fig. 3.
Root mean square error in radial and circumferential strain estimated using TruHARP and CSPAMM by varying the HARP filter size at the acquisition CNR of 5 and 15.

Fig. 4. a) 5 dynamics and their b) Fourier transform. c) Magnitude, d) Phase and e) spectrum of the DC and 4 x- and y- displacement encoded spectral peaks separated using TruHARP.

Fig. 5.
a) Estimated circumferential and radial strain for the volunteer at end systole. b) Spatial profile of strain averaged over AS sector of myocardium at end diastole for filter FWHM of 32, 48 and 64. Mean $\pm$ standard deviation is shown as dotted lines.

Table 1

Slice-selective tagging parameters for the TruHARP pulse sequence in Fig. 1.

	$\theta_{\phi_1}^{(1)}$	$\theta_{\phi_2}^{(2)}$	G_h	G_v
I_{Ah}	$90_x^\circ(\phi_1 = 0)$	$90^\circ(\phi_2 = 0)$	G	0
I_{Bh}	$90_x^\circ(\phi_1 = \pi)$	$90^\circ(\phi_2 = 0)$	G	0
I_{Ch}	$90_y^\circ(\phi_1 = \pi / 2)$	$90^\circ(\phi_2 = 0)$	G	0
I_{Av}	$90_x^\circ(\phi_1 = 0)$	$90^\circ(\phi_2 = 0)$	0	G
I_{Cv}	$90_y^\circ(\phi_1 = \pi / 2)$	$90^\circ(\phi_2 = 0)$	0	G