Increasing Strain accuracy in Strain-Encoded (SENC) imaging using Center-of-mass method

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Purpose: An effective post-processing method used to compute a strain distribution or strain map from acquired Strain Encoded (SENC) imaging is the center-of-mass method. This article presents a novel approach to improving this method in order to produce a more accurate strain map used for detection of stiff masses in soft tissues.

Introduction: MRI is considered one of the best modalities to measure the motion of moving tissues and stiff mass tissue deformations; such as in the detection of breast cancer. A technique known as strain encoding (SENC) with MRI had been developed to measure local strain distribution of deforming tissues [1,3].

Theory: When an image is acquired using SENC with respect to a specific spatial or tuning frequency, this can be mathematically described by: $I(y;t;\omega_o) = \rho(y,t)S(\omega_o - \omega(y,t))$...(1), where $I(y;t;\omega_o)$ refers to the signal intensity of a pixel located at a location y, at time t, $\rho(y,t)$ the proton density at that location, and S(.) the Fourier transform of the slice profile [1]. From equation (1), the shift in S (.) is due to change in the tagging frequency, which is dependent on tissue deformation, and the estimation of tissue strain can be obtained if this frequency is measured. The shift of the function S(.) can be estimated from the intensity of two images, $I_1(p)$, $I_2(p)$ acquired with two different tuning frequencies ω_{T1}, ω_{T2}. and the shifted tagging frequency at each pixel can be estimated by the center-of-mass of the two image intensities using: $\varpi(p) = \dfrac{\omega_{T1} I_1(p) + \omega_{T2} I_2(p)}{I_1(p) + I_2(p)}$.

Writing $\varpi(p)$ in more general terms for any number of tuning frequencies we obtain, $\varpi(p) = \dfrac{\sum_{k=1}^{N} \omega_d(k) I_k(p)}{\sum_{k=1}^{N} I_k(p)}$,...(2)

where $\omega_d(k)$ is the demodulation or tuning frequencies of the kth acquired image, $I_k(p)$.

The local strain at this pixel location can be estimated from this frequency shift using: $\varepsilon(p) = \dfrac{\omega_o(p)}{\varpi(p)} - 1$,...(3)

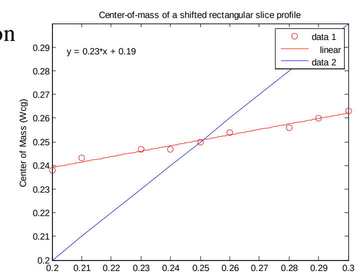
The center-of-mass technique is used to locate the shift of harmonic peak due to changes in the local spatial frequency of tags caused by tissue deformation (1). However, computation of the center-of-mass only provides an approximation of the movement of the harmonic peak. In order to locate the harmonic peak more accurately, an approximate relationship between the center-of-mass and the actual harmonic peak location is necessary. From this relation, the actual harmonic peak can be accurately located. In general, given $I_k(p)$, strain is computed according to eq. (3) as the center of mass $\varpi(p)$ is calculated from eq. (2) and substituted into eq. (3). However, $\varpi(p)$ is only an estimate of the actual peak, $\omega(p)$. The discrepancy between $\varpi(p)$ and $\omega(p)$ can be improved by assuming that the relationship between $\varpi(p)$ and $\omega(p)$ is approximately linear. Therefore the relationship can be described as $\omega(p) = a\varpi(p) + b$, ...(4) A computer simulation was employed to determine the value of *a* and *b* according to the steps below:

Step 1. Calculate image intensity, $I_k(p)$ from eq. (1).

Step 2. Find all $I_k(p)$ for k=1…N

Step 3. Compute $\varpi(p)$ as the center of mass of $I_k(p)$

Step 4. Use linear regression between $\varpi(p)$ and $\omega(p)$ to find a, b.



Figure(1) shows the plot of tuning frequencies (Wo) vs. center-of-mass (Wcg) rectangular slice profile spanning a low tune of .2 mm^-1 and a high tune of .3 mm^-1 and seven equally spaced tunes between low tune and high tune. In the simulation, a rectangular slice profile is shifted by .0125 mm^-1 resolution nine times and for each shift center-of-mass is calculated. The nine points shown as a red circle in Figure (1) represents the center-of-mass corresponding to a shift in the harmonic peak. The blue line indicates the ideal case. Using a basic curve-fitting tool with linear regression the best fitting curve is represented in red line in Figure (1) and the equivalent linear expression is shown as y=.21*x + .2

Normally, the center-of-mass method is implemented with look-up-table based approach dependent on number of tunes used and shifted rectangular slice profile with center-of-mass calculated based on the shift. However, the limitation of this method is discrete nature of the look-up-table introducing inaccuracy and the memory required to store a large look-up-table.

Conclusion: The improved center-of-mass method provides an effective way to locate the harmonic peak shift due to tissue deformation by eliminating the need to use a look-up-table based approach. The new method only requires computing coefficients of a linear relationship between $\omega(p)$ and $\varpi(p)$.

References

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