DIAGNOSIS OF ACUTE MYOCARDIAL INFARCTION USING TISSUE DEFORMATION IN ECHOCARDIOGRAPHIC IMAGING

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ABSTRACT

Detecting abnormalities in the heart motion using ultrasound can be a major diagnostic tool, since reduced wall motion has correlation with ischemic muscle action. Having analyzed such ultrasound scans, it can be shown that the relevant tissue pattern is varying and its motion consists of expansion and contraction in addition to tissue deformations. Accordingly, we introduce a new approach and algorithm to detect and track tissue deformation using multiple hypotheses logic, based on block motion estimation that accounts for tissue expansion and contraction. Our proposed algorithm has been applied to in-vivo 2D scans of the left ventricle, providing useful results for the characterization of heart functionality.

1. INTRODUCTION

For patients presenting with chest pain, rapid diagnosis of Acute Myocardial Infarction (AMI) is important for further management and possible salvage of the myocardial tissue. Ultrasound is an important adjunct to the well-accepted diagnostic tools such as ECG and serum enzymes, especially when the other predominant signs are missing or ambiguous. Wall motion abnormality is the earliest symptom of a nearing AMI, however, specific pattern analysis is needed to classify the situation correctly.

Ultrasound scans of the heart at high frame rates are widely available today and used to diagnose various heart diseases. Detecting abnormalities in the wall motion has become of major importance since reduced motion has correlation with an ischemic muscle action. Automatic movement tracking of the heart walls and calculating their local velocities [8] can make the diagnoses more accurate and useful.

Estimating local velocities in ultrasound scans presents several challenges [3], [10]. The major difficulty is that ultrasound images have high Rayleigh governed speckle noise and Gaussian distributed electronic noise, resulting in a low signal to noise ratio (SNR). In addition, the tissue pattern is fast changing and its motion includes expansion and contraction in addition to rotation and translation. There is also a problem of 'out of plane motion' found in 2D scans causing inconsistency in object motion. The resolution of the images depends on the ultrasound equipment and it usually has high axial resolution and low angular resolution.

The approach introduced in this work significantly improves the algorithm presented in [3]. The new features of the new algorithm are detection and tracking of tissue expansion and contraction. It also has the advantageous features of multiple scan correlation and recursion that allows usage of later measurements for decision on previous measurement associations. This way we are able to detect and track tissue deformation based on complete information and not on scan-to- scan basis, providing far more accurate results.

2. THE PROPOSED ALGORITHM

We start with a general description of the new approach. The flowchart of the derived algorithm is shown in Fig. 1.

2.1. Data Acquisition

In this work we use B-mode scans of the left ventricle to test the proposed algorithm. We show two scans from two different patients. The first set (Fig. 2a) was sampled at 51 frames per second with depth increment of 0.33mm and angular increment of 0.0041º. The second set (Fig. 2b) was sampled at 76 frames per second with depth increment of 0.34mm and angular increment of 0.01º. The algorithm is applied directly to the data without any modifications or transformations.

Tissue pattern of the heart varies fast and its motion contains contraction and expansion, as can be seen in ultrasound scans shown in Fig.2. Thus any assumption that the objects undergo only small changes from frame to frame is usually incorrect in ultrasound scans of the heart, despite the high frame rate and must be of concern.

2.2. Maximum likelihood Criteria

We represent two consecutive scanned volumes by *X* and *Y*. Let $I(x_i)$ be the intensity of a macro block at coordinates $x_i = \{x_{ij}\} \in X$ and $I(y_i)$ be the intensity of a macro block at coordinates $y_i = \{y_{ij}\} \in Y$, where *i* represents all possible macro blocks and *j* is the second coordinate within the macro block. Let $v_i = \{x_i - y_i\}$ be

the displacement vector between the two macro blocks x_i and y_i. Based on the above notations, the maximum likelihood (ML) estimation based on [2] and [4] is:

$$v_i^{ML} = \arg\max_{v_i} \left(I\left(x_i\right) | I\left(y_i\right), v_i \right). \quad (1)$$

There are several models describing ultrasound images with either multiplicative or additive noise. A common model that was used in this work assumes multiplicative Rayleigh distributed noise with distribution function given in [4]:

$$f_x\left(x\right) = \frac{x}{\sigma^2} \exp\left(-\frac{x^2}{2\sigma^2} \right) \quad x > 0. \quad (2)$$

We denote the noiseless value of pixels in macro block *i* by s_{ij}. Assuming statistically independent noise, the model for pixels in the macro blocks is

$$\begin{aligned} x_{ij} &= \eta_{ij}^x s_{ij} \\ y_{ij} &= \eta_{ij}^y s_{ij}, \end{aligned} \quad (3)$$

where η_{ij}^x and η_{ij}^y are two independent noise elements with Rayleigh distribution. Using (3), we obtain:

$$x_{ij} = \eta_{ij} y_{ij}, \quad \eta_{ij} = \frac{\eta_{ij}^x}{\eta_{ij}^y}. \quad (4)$$

η_{ij} is a division of two independent noise elements with Rayleigh distribution given in (2), having the following distribution [6]:

$$f_\eta\left(\eta\right) = \frac{2\eta}{\left(\eta^2+1\right)^2}, \quad \eta > 0. \quad (5)$$

The probability function for this distribution is [4]:

$$\begin{aligned} \mathrm{p}\left(\mathrm{x_i} \mid y_i, v_i\right) &= \prod_j \left[\frac{f_\eta\left(\frac{x_{ij}}{y_{ij}}\right)}{y_{ij}} \right] = \\ &= \prod_j \left\{ \frac{2x_{ij}}{y_{ij}^2 \left[\left(\frac{x_{ij}}{y_{ij}} \right)^2 + 1 \right]^2} \right\}, \end{aligned} \quad (6)$$

and its maximization is equivalent to the maximization of (1).

Taking the natural logarithm of both sides of (4), we obtain the following model:

$$\begin{aligned} &\tilde{x}_{ij} = \tilde{y}_{ij} + \tilde{\eta}_{ij} \ \textit{where}\ \tilde{x}_{ij} = \ln\left(x_{ij}\right), \\ &\tilde{y}_{ij} = \ln\left(y_{ij}\right), \tilde{\eta}_{ij} = \ln\left(\eta_{ij}\right). \end{aligned} \quad (7)$$

Accordingly, the probability function as in Equation (6) is given by [6]:

$$\begin{aligned} \mathrm{p}\left(\mathrm{x_i} \mid y_i, v_i\right) &= \prod_j \left[\frac{x_{ij} f_\eta\left(\frac{x_{ij}}{y_{ij}}\right)}{y_{ij}} \right] = \\ &= \prod_j \left\{ \frac{2\left(\frac{x_{ij}}{y_{ij}}\right)^2}{\left[\left(\frac{x_{ij}}{y_{ij}} \right)^2 + 1 \right]^2} \right\}. \end{aligned} \quad (8)$$

This probability function is used in this work for motion estimation, as described next.

2.3. Motion Estimation (ME)

The motivation for using ME is to trace the movement of objects from one ultrasound frame to the next. Each block in the current frame *X* is compared with the corresponding block at the same coordinates and its neighbors in the following frame *Y*.

We use an *Exhaustive Search* (ES) algorithm or *Full Search* for finding the best match [9]. The algorithm searches in all possible locations within the search window. In this work the search window consists of only non overlapping macro blocks in the neighborhood of the corresponding macro block:

$$\begin{aligned} X &= \bigcup_i x_i \quad x_i \bigcap x_j = \varnothing \ \textit{for}\ i \neq j \\ Y &= \bigcup_i y_i \quad y_i \bigcap y_j = \varnothing \ \textit{for}\ i \neq j. \end{aligned} \quad (9)$$

This approach reduces drastically the search options thus increasing the speed of the ES, but more importantly, allows implementation of the *Multiple Hypotheses Tracking* (MHT) method by limiting the number of possible hypotheses.

This limited search window may increase the errors in the best match search, but on the other hand it eliminates the need for searching for the nearest displacement vectors and the associated errors when building hypotheses. The cost function used to define the best match is the maximum likelihood criterion defined in (8). All displacement vectors in the search window are kept with their maximum likelihood value representing the probability of displacement to the particular location the current macro block can move to.

The output of ME function is a display of all the displacements in terms of pixels of each macro block of the current frame in each of the dimensions along with their respective probabilities.

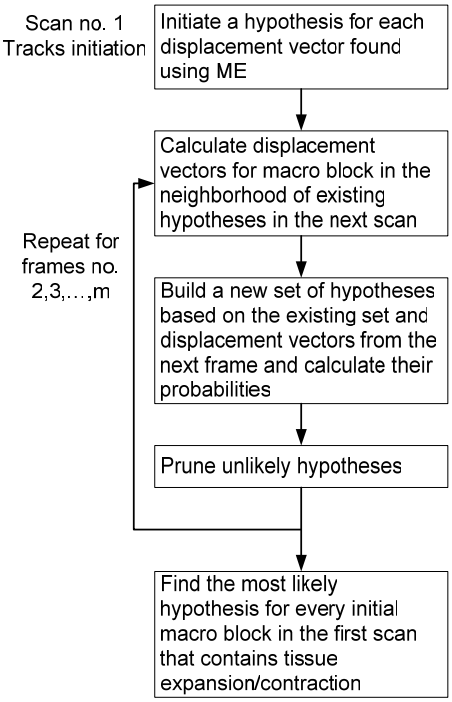

Figure 1 – Flowchart of the proposed algorithm.

This is different from the traditional usage of ME, where only the best match (highest probability) displacement is used because in this application we wish to detect tissue expansion and contraction. Tissue expansion is characterizes by several matches in the same search window having the highest probability. When tissue contraction occurs, several displacement vectors with highest probability from neighboring macro blocks have their ending at the same macro block. Therefore, we consider all possible displacement and make the decision at a later stage when the complete (or large enough) motion history is available.

The ME is calculated only for macro blocks that are above the mean noise level. This level is calculated here as an average value of 1000 samples taken randomly from the scanned volume [7]. We based this value on an assumption that the scanned tissue occupies only a small part of the volume and the rest of it is noise, as can be seen in Fig. 2. By doing so we reduced the number of calculations as well as the number of false hypotheses caused by apparent movements of macro blocks that do not contain tissue information.

The process is repeated for all the scans. The displacement vectors are used to build hypotheses of the tissue movement as described next.

2.4. Multiple Hypothesis Method

Estimation of displacement vectors of different macro blocks is not sufficient when the purpose is detecting tissue deformation. If we wish to diagnose tissue condition, we have to examine the movement for a prolonged period of time, or literally track its behavior.

To achieve this goal, we use Multiple Hypotheses Method (MHT). MHT is a deferred decision logic in which alternative data association hypotheses are formed whenever there are observation to track conflict situations [1]. The hypotheses are propagated through the scans assuming that subsequent data will resolve the uncertainty. In this work hypotheses oriented approach that continuously updates the hypotheses by expanding and pruning was used [11].

The hypotheses were created by connecting sequential displacements of each macro block. With every consecutive frame, as new data is received, the number of hypotheses grows and pruning is required. Pruning removes the most unlikely hypotheses and is required to limit the number of hypotheses and reduce the computation and memory requirements. It is performed periodically.

We applied the hypothesis generating technique presented in [8] to the ultrasound data. Let $V(m)=\{V_n(m), n=1,2,\ldots,N\}$ denote the set of displacement vectors in scan *m*, $V^m=\{V(1),V(2),\ldots,V(N)\}$ denote the cumulative set of displacement vectors up through the scan *m* and $\Phi^m=\{\Phi_j^m, j=1,2,\ldots,J_m\}$ denote the set of all hypotheses at frame *m* that associate the displacement vectors to the hypotheses. After a new set of displacement vectors $V(m+1)$ is calculated using ME, a new set of hypotheses Φ^{m+1} is repetitively built for each prior hypothesis Φ_j^m and each of the new displacement vectors $V_n(m+1)$.

The probability of hypothesis Φ_j^m given the displacement vectors up through scan *m* is denoted P_j^m and is given by:

$$P_j^m = P\left(\Phi_j^m \mid V^m\right). \tag{10}$$

Let $p_i^m\left(x_i^m \mid y_i^m, v_i^m\right)$ denote the probability of a displacement vector v_i^m in the hypothesis Φ_j^m. P_j^m is defined as a cumulative probability of all displacement vectors v_i^m in the hypothesis Φ_j^m and can be written as [6]:

$$P_j^m = 1-\prod_m\left(1-p_i^m(x_i^m \mid y_i^m, v_i^m\right). \tag{11}$$

The hypotheses are evaluated at the final frame by computing hypothesis scores that is defined as a cumulative probability. For each starting block in the initial frame, a hypothesis (track) having the highest cumulative probability P_j^m is chosen. This way tissue movement is examined through all the scans based on the best hypotheses that are chosen after all the information is available, instead of best match on a frame-to-frame basis that does not necessarily provide the best results.

2.5. Tracking Tissue deformation

Tissue contraction is detected when two or more hypotheses with the highest value of the cumulative probability P_j^m have a common displacement vector $V_n(m)$. In our algorithm a single displacement vector can be associated with more than one hypothesis. This way, by merging common displacement vectors V^m of different hypotheses we can account for tissue contractions that occur in the fast varying tissue pattern. This assignment logic causes hypothesis merging through the scans and continuous reduction in the number of hypotheses with common displacement vectors. The hypotheses may have a number of common displacement vectors through a number of scans.

Tissue expansion naturally creates multiple hypotheses from a single one, all of them having the highest value of the cumulative probability P_j^m. These hypotheses have a common source $V_n(m)$ at any frame and can split more than once through the scans.

Although it is possible to detect and track tissue expansion and contraction on a single scan to single scan basis, MHT dismisses by pruning incorrect expansions and contractions that can be produced by ME, as described in Section 2.3, thus making the process more accurate.

The maximum likelihood value of displacement vectors that belong to the same expansion or contraction instance may not be precisely equal due to presence of noise and additional tissue deformations. Hence, some flexibility is needed the selection of most likely hypotheses. By setting a threshold for the cumulative probability and selecting splitting or merging hypotheses according to this threshold, we allow detection and tracking of tissue expansions in the presence of noise and additional tissue deformation.

3. RESULTS

The new algorithm has been tested on in-vivo scans of the left ventricle of the human heart to detect and track tissue expansion and contraction during the scans. Here we use 2D scans for easier presentation, but this new algorithm can be easily generalized to 3D. The scans were divided into macro blocks of 9×9 pixels. Hypotheses pruning was performed every second scan, leaving the 2% of the most likely hypotheses for each initial macro block in the first scan that passed the noise threshold. The threshold for tissue expansion and contraction was set empirically. In Fig. 2 we show movements from frame to frame that belong to hypotheses where tissue expansion or contraction was detected at least once during the scans. These hypotheses have the highest cumulative probability P_j^m as described in Section 2.4. The calculated movements from frame to frame are represented by a single arrow.

The average time to processes a single frame on AMD Athlon™ 3000+ computer with 1GB of RAM was 11 seconds.

4. CONCLUSIONS

Tissue deformation detection and tracking using a Multiple Hypotheses approach with motion estimation and maximum likelihood criteria has been proposed. Our test results using in-vivo data show that this method can be used for ultrasound scans in order to analyze tissue characteristics with emphasis on contraction and expansion for prolonged period. This universal approach is suitable for practical use in ultrasound scans of various types of tissues, including the myocardium, as in this case. The complexity of the proposed algorithm is low and is very suitable for parallel computing, making it instrumental for real-time classification of AMIs.

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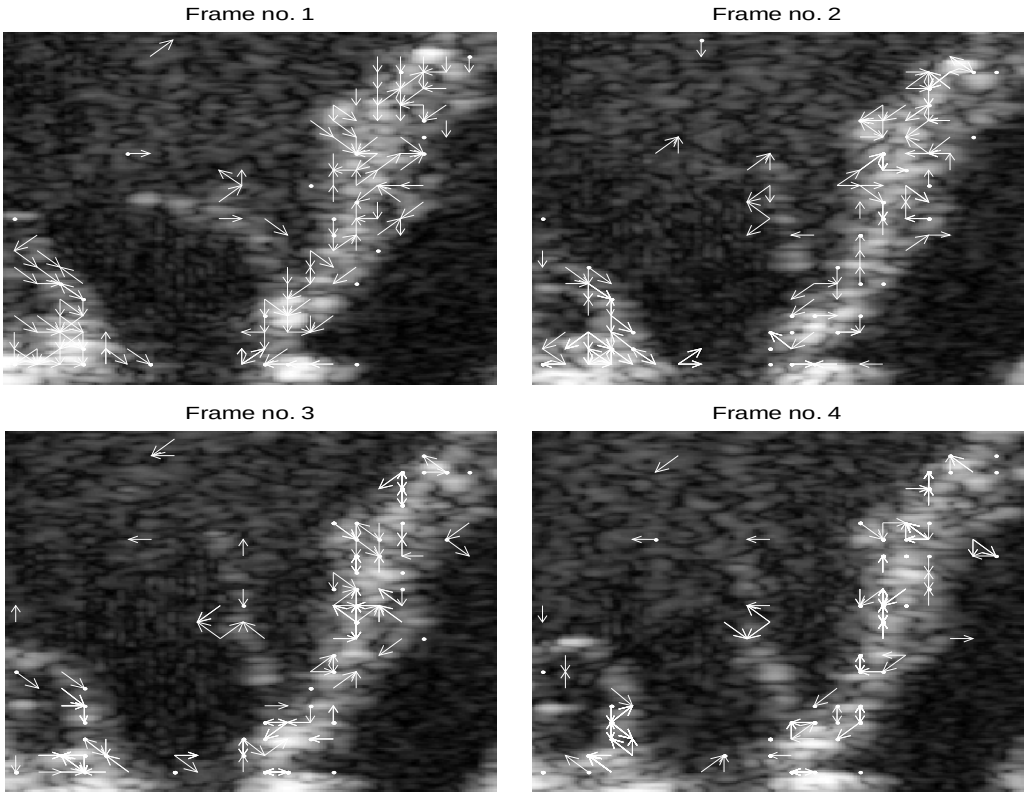
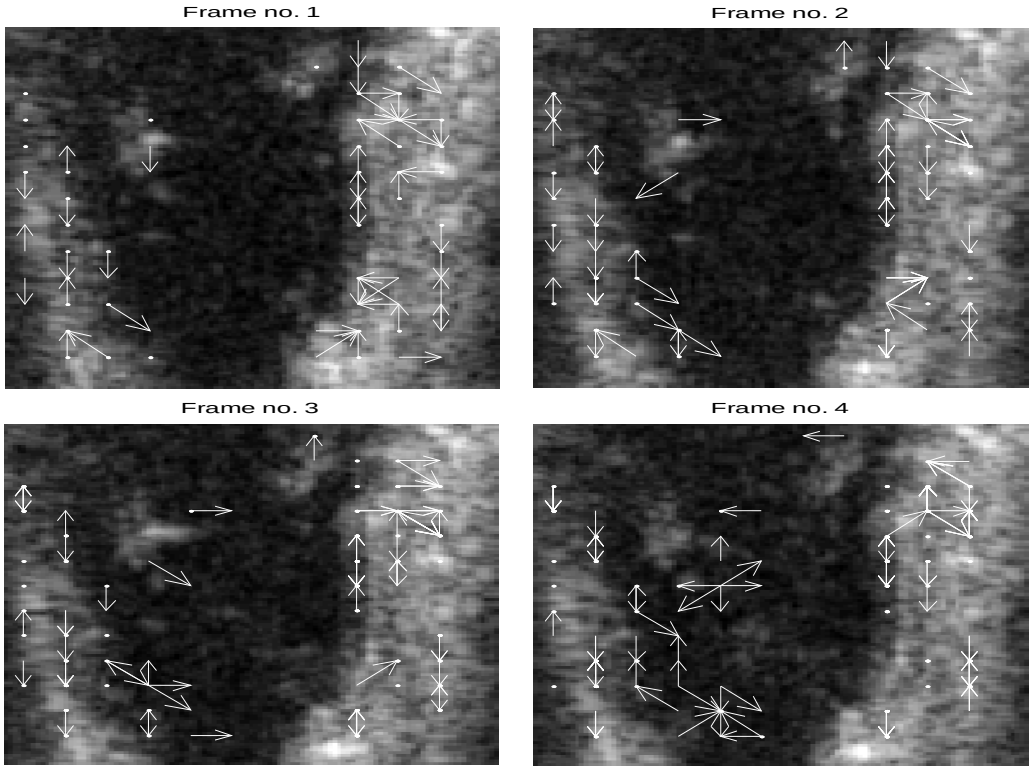


(a)



(b)

Figure 2 – Four consecutive in-vivo scans with displacement vectors from two patients. Each image presents a single scan with displacement vectors to the following scan. Only displacement vectors that belong to hypotheses that include expansion contraction are displayed.