Cardiac Motion Analysis from Magnetic Resonance Imaging: Cine Magnetic Resonance versus Tagged Magnetic Resonance

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Abstract

The objective of this work is to compare the results obtained from the motion analysis of tagged vs. CINE MR sequences when using spatio-temporal non-rigid registration techniques based on pixel intensity. Those techniques have been previously validated on tagged MR images. Moreover, registration algorithms have been applied to MR CINE sequences to obtain radial displacement and strain parameters demonstrating its usefulness to quantify regional myocardial function.

Tagged and CINE MR short axis sequences from 10 subjects were examined. Four segments were manually selected in both the tagged MR and CINE sequences. Automatic estimation of the myocardial motion field was performed using a consecutive non-rigid registration algorithm based on a semilocal Bspline parametric model. Finally, a statistical analysis was applied to compare the systolic displacement and strain estimations from both types of sequences. An important discrepancy between results obtained from tagged MR based strain analysis and CINE MR has been found.

1. Introduction

The usefulness of MR imaging to assess regional myocardial deformation has been widely demonstrated [1-3]. Different techniques have been proposed to compute motion fields on tagged MR data, either using deformable models or registration algorithms. However, the accuracy and feasibility of measuring 2D myocardial motion fields using conventional CINE MR has not been deeply studied.

CINE MR imaging is of great importance to assess quantitative cardiac function for clinical practice. However not many studies have compared the results on these sequences with respect to those obtained from tagged MR sequences. The parameter 'displacement' has been previously studied using a 3D scheme showing important discrepancies when the circumpherential motion is assessed [8].

In this work our aim is to compare the movement estimation of the myocardium obtained using CINE and tagged sequences in a 2D framework. The same non-rigid registration techniques are used to estimate de myocardial motion fields form conventional CINE MR short axis sequences and tagged MR short axis ones.

The algorithms used to estimate the myocardial motion are based on non-rigid registration techniques. They have been validated for tagged sequences, achieving subpixel accuracy (sumbmilimetric) [4]. The same algorithms have been applied to CINE MR sequences acquired from healthy volunteers and patients, proving the feasibility of using these techniques to estimate myocardial motion from CINE-MR without user interaction [5].

In this work the motion fields obtained from CINE and tagged MR sequences are compared, specifically the systolic radial displacement and strain. Regression and Bland-Altman analysis were used to compare both methodologies.

2. Methods

2.1. Algorithms

The non-rigid registration techniques used to perform the automatic estimation of myocardial motion are described in detail in [6]. The estimated displacement field is represented as a linear combination of Bspline functions, placed on a uniform rectangular grid.

$$\mathbf{g}'(\mathbf{x}) = \sum_{j \in Z^N} \mathbf{c}_j \beta_r \left(\frac{\mathbf{x}}{h - \mathbf{j}} \right)$$

The parameter h determines the knot spacing, while coefficients $\mathbf{c_j}$ control the solution smoothness.

After obtaining the dense motion field, the lagrangian strain function (E) is calculated. The deformation

gradient F is calculated from the analytical expression of the dense displacement field. A function $\mathbf{g'_t}$ is obtained for each pair of consecutive images in the sequence and the motion field is obtained following the expressions:

$$\mathbf{g}_t(\mathbf{X}) = \mathbf{g'}_t(\mathbf{x}_{t-1}) + \mathbf{g}_{t-1}(\mathbf{X}) \quad \text{where} \quad \mathbf{x}_{t-1} = \mathbf{g}_{t-1}(\mathbf{X}) \quad \text{for}$$

$$t=2,\ldots T \quad \text{and} \quad \mathbf{g}_1(\mathbf{X}) = \mathbf{X} \quad \text{for} \quad t=1$$

Then we obtain a deformation gradient for each time step:

$$\mathbf{F'}_t = \frac{\partial \mathbf{x}_{t+1}}{\partial \mathbf{x}_t}$$

Then, the deformation gradient $\mathbf{F^t}$ is calculated using $\mathbf{F'}_t$ obtained from each pair of images as:

$$\mathbf{F}^t = \mathbf{F'}_t \cdot \mathbf{F'}_{t-1} \ldots \mathbf{F'}_2 \cdot \mathbf{F'}_1 = \frac{\partial \mathbf{x}_t}{\partial \mathbf{X}}$$

This function is then used to calculate the Green-Lagrange strain tensor $\mathbf{E}^t$ for each time point using the following equation:

$$\mathbf{E}^t = \frac{1}{2}\left(\mathbf{C}^t - \mathbf{I}\right) = \frac{1}{2}\left(\mathbf{F}^{tT}\mathbf{F}^t - \mathbf{I}\right)$$

2.2. Imaging

The sequences used in this study were acquired with a Philips Intera 1.5 T (Philips Medical Systems, The Netherlands) using a five element phased-array coil dedicated to cardiac imaging.

CINE MR scans were performed using a breath hold Balance Fast Field Echo (B-FEE) sequence, obtaining images with a pixel size between 1mm and 1.3 mm.

The tagging sequence used consists of an enhanced version of the free breathing SPAMM sequence provided by the manufacturer for our Phillips Intera scanner [7]. The main advantage of this sequence is that the tag contrast is well sustained through the whole sequence.

2.3. Data Analysis

Six healthy volunteers and four patients were examined acquiring short axis images. For each subject two sequences with the same geometry were acquired in the same session, a CINE MR sequence and a tagged MR sequence.

Four segments localized in the septal, anterior, lateral and inferior myocardial walls were manually selected on the first frame on both the tagged and CINE MR sequences, as shown in Figure 1.

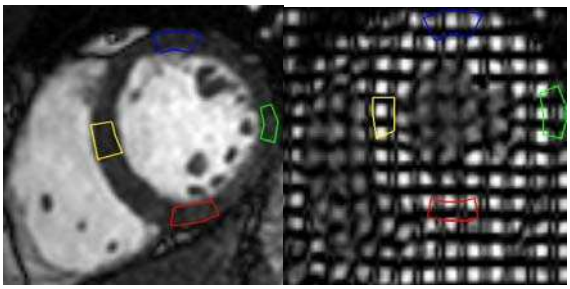

Figure 1: ROIs selected, in a CINE MR sequence (*left*) and in a tagged MR sequence (*right*).

The delimitated segments were propagated through time using the resultant myocardial motion field.

Using the dense displacement field estimated by applying the non-rigid registration scheme, mean radial displacement is calculated for each segment, performing the radial projection for each point within the ROI.

Radial strain is also calculated following the methodology described in section 2.1 for each myocardial segment.

Radial displacement and strain temporal evolution curves were obtained and the maximum systolic value was selected.

Maximum systolic strain and displacement were compared using a Bland-Altman plot. A regression analysis through the origin was also performed to find the best linear fit between both measurements. Regression through origin has been chosen, because it is assumed that both techniques should provide a displacement or strain zero when there is no movement.

3. Results

Bland-Altman representation for the maximum systolic radial strain is shown in Figure 2. On this graphic, the difference between the estimation of maximum systolic radial strain using the CINE MR sequence and the tagged sequence is represented using the tagged estimation as reference value. All the subjects and all the segments are considered in this analysis. Mean and standard deviation of the difference were 21,84 ±22,34 %.

Bland-Altman representation for the maximum systolic radial displacement difference (-0,25±1,91 mm) is shown in Figure 3. Mean difference is smaller than in the former case for the strain. One possible reason is that the parameter is of smaller magnitude.

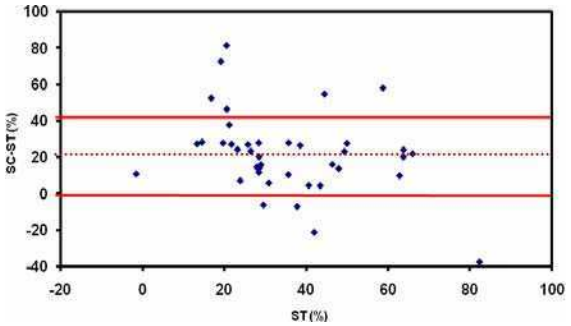

Figure 2: Bland-Altman representation for the difference between maximum systolic radial strain (%) calculated with both techniques

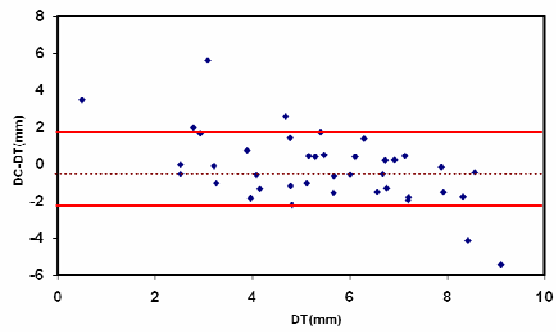

Figure 3: Bland-Altman representation for the difference between maximum systolic radial displacement (mm) calculated with both techniques

Further analysis steps addressed the study of the maximum systolic mean radial strain, as it is considered to be a good representative parameter of the systolic myocardial function. SC stands for the estimation of this parameter from CINE MR sequences and ST from tagged sequences.

Table 1 shows the results of the linear regression analysis. The lowest standard error of the estimation corresponds to the septal segment.

Table 1: Regression analysis through the origin. $y=bx$

Segment	b ± std error	Model Std Error
Anterior	1,648±0,167	17,23379
Lateral	1,601±0,198	26,58407
Inferior	1,093±,206	33,17526
Septal	1,875±,221	18,08249
All	**1,421±0,108**	**26,66177**

In Figure 4 the regression line of best fit through the origin for all the segments is represented on the scatter plot of the data (Table 1).The ordinate axe represents the CINE MR estimation (SC %), and abscissa represents the tagged MR estimation (ST %).

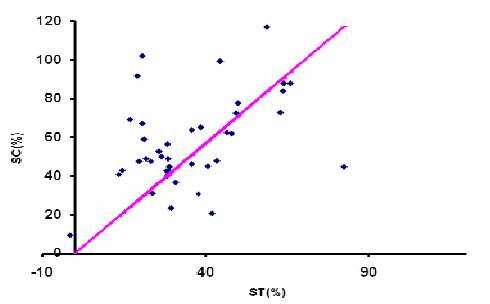

Figure 4: Regression through origin: line of best fit for all the selected segments

Table 2: Range of the differences between strain estimations with CINE and tagged sequences.

Segment	Strain Difference Range CI 95%
Anterior	[-14,245 55,959]
Lateral	[-18,373 75,853]
Inferior	[-50,892 74,088]
Septal	[3,116 49,254]
All	**[-22,845 66,535]**

In Table 2 the ranges of the strain differences are shown with a confidence interval of 95%. The smallest range corresponds to the septal segments, and the highest one to the segments placed in the lateral wall.

4. Discussion and conclusions

In this work we have concentrated on the estimation of the radial compknent of myocardial parameters, mainly because circumpherential components estimated from CINE sequences have been demonstrated not to be accurate in previous studies [8]. This fact is due to several factors, the most important ones being the lack of texture information inside the myocardial wall in this type of sequences [8, 9] and the possible influence of trabeculae and papillary muscles of the heart in the measurement [10].

The results described in the previous section comparing the myocardial motion estimation using CINE and tagged MR sequences show the existence of an important discrepancy.

Attending to the Bland-Altman representation we conclude that strain estimations using the CINE MR sequence are overestimated (mean difference of 20) but it is necessary to consider that the value of the standard deviation of the approximation is near 20 %. This fact demonstrates that the variance of the difference is very noticeable and we cannot assume a systematic

overestimation error between the two measurement techniques.

Main possible causes of the large difference between the two estimates are on the one hand the effect of trabecular tissue and papillary muscles attached to the endocardial border at the end of the systolic phase (Figure 5). On the other hand, the out of plane motion may also appear as a fictitious thickening actually not present. These two effects have a much more important influence in the CINE MR than in the tagged MR mainly because the main features tracked in the CINE MR data is the epicardial and endocardial border movement. The intramyocardial information present in the tagged data avoids significantly these effects.

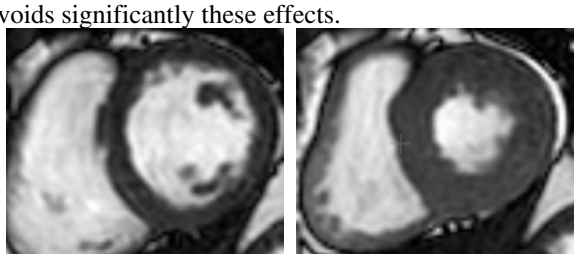

Figure 5: End-diastolic and end-systolic images from a CINE MR sequence. Intraventricular structures have become undistinguishable from endocardial border.

Another interesting result is that the smallest difference between both estimates was found in ROIs placed in the septal region of the myocardium. One explanation for this fact could be that the influence of trabecular tissue and papillary muscles around this area, is much lower. On the other hand, this effect is more serious on the lateral and inferior myocardial walls. These results are consistent with those previously shown in other study that reveals the effect of trabecular tissue using high resolution MR [10]. In figure 5 a cleaner edge in the septum is also observed.

Summing up, this work has shown the existence of a discrepancy between results obtained from tagged MR based strain analysis and CINE MR. Therefore, our results suggests to be cautious when CINE MRI datasets are used to extract quantitative measurements of active contraction. Further research will be conducted in this direction.

Acknowledgements

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