Nonrigid registration of myocardial perfusion MRI

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Abstract

This paper describes a fully automatic registration of 10 multi-slice myocardial perfusion magnetic resonance image sequences. The registration of these sequences is crucial for the clinical interpretation, which currently is subjected to manual labour. The approach used in this study is a nonrigid registration algorithm based on free-form deformations due to Rueckert et al. Inspection of difference images from the wash-out part of the perfusion sequences indicates that a good registration accuracy is obtained.

1 Introduction

Within the last decade magnetic resonance imaging (MRI) has proven able to assess myocardial perfusion in an accurate and safe manner, see e.g. [2, 3]. While scanning times have decreased substantially, the amount of manual post-processing renders the method prohibitive to clinical practice. Marking up points of correspondence on the myocardium constitutes a major part of this manual labour, which is essential to ensure compensation of motion during the perfusion sequence. This paper presents an approach aiming at replacing this resource-demanding, tedious and error prone task with an automated image analysis method.

The data material comprises 3500 myocardial perfusion, short-axis, MRI obtained from ten freely breathing patients with acute myocardial infarction. Five slices were acquired before, during and after the arrival of a contrast agent in a total sequence length of 70 frames. The contrast agent was Gd-DTPA. Registration relative to the heart-cycle was obtained using ECG-triggered acquisition from a whole-body MR unit, Siemens Vision, operating at 1.5 Tesla. Frame time was approximately three seconds. MR pulse sequence: Inversion recovery turbo-FLASH (fast low-angle shot), matrix size=128×128, field of view=300×300 mm, slice thickness=10 mm.

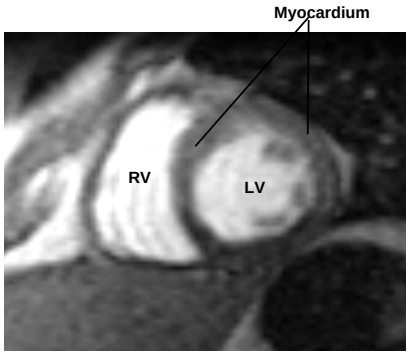

Figure 1: Myocardial MR data: An example image frame from one slice zoomed in at the heart. Right ventricle, left ventricle and myocardium are labelled.

The regions of the heart which are of interest in this study are the *right ventricle* (RV), *left ventricle* (LV) and *myocardium* (heart muscle). These regions are labelled in Figure 1.

To give an example of the appearance of the data, Figure 2 shows four time frames before, during and after the contrast arrival within the same slice.

Due to the MR scanning method used to acquire the myocardial perfusion sequences, slices are displaced with respect to each other and the cardiac cycle. This means that a three-dimensional (3D) registration is not appropriate, hence the registration task at hand is two-dimensional (2D).

A few approaches for registration of myocardial perfusion MRI have been reported in the literature. Breeuwer and Spreeuwers [1] use a translation/rotation based registration with normalised cross-correlation as a similarity measure. Subsequently, detection of the myocardial and RV boundaries are obtained by region growing on feature images and a deformable snake model. Yang et al. [9] use the phase difference of the raw MR data between successive image frames to correct for translational motion. Shape changes are compensated for by using a deformable model. Stegmann et al. [7] use coupled, cluster aware Active Appearance

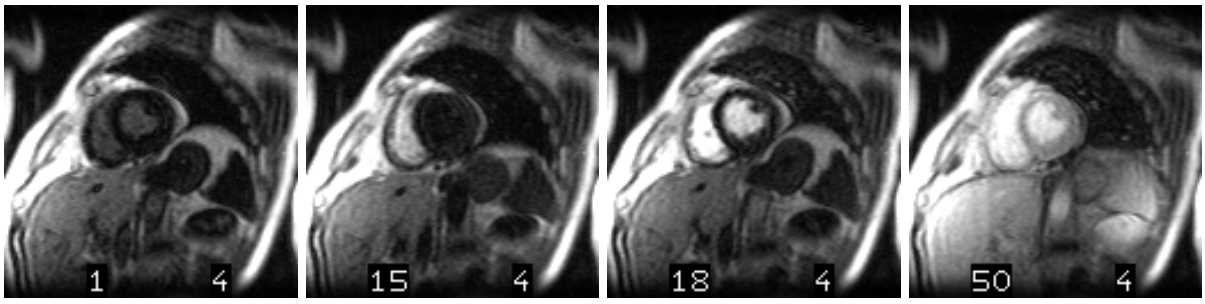

Figure 2: Four time frames from the same slice of a myocardial perfusion MR sequence. From left to right: Before contrast arrival, during contrast arrival to the right ventricle, during contrast arrival to the left ventricle, after contrast arrival.

Models (AAMs) for simultaneous registration of all slice sequences. Minimum Description Length (MDL) Shape Modelling is applied for semi-automatic training set formation. Refer to this paper for a more thorough review of related work.

The registration method applied in this study is a nonrigid registration algorithm by Rueckert et al. [5, 6]. This method will be described in the following section.

2 Method description

The goal of image registration is to warp one image into the coordinate system of another using an optimal transformation $\mathbf{T}(x, y) \mapsto (x', y')$. A basic image registration algorithm requires the following:

- A transformation type
- A measure of image similarity
- An optimisation method to optimise the transformation parameters with respect to the similarity measure.

The nonrigid registration algorithm applied in this study includes both a global and a local transformation model, i.e.

$$\mathbf{T}(x, y) = \mathbf{T}_{\boldsymbol{global}}(x, y) + \mathbf{T}_{\boldsymbol{local}}(x, y). \quad (1)$$

The global transformation model describes the overall motion of the heart in the time sequences. This is achieved by the affine transformation which includes rotation, translation, scaling and shearing. In 2D this leads to a model with six degrees of freedom which can be written as

$$\mathbf{T}_{\boldsymbol{global}}(x, y) = \begin{pmatrix} \theta_{11} & \theta_{12} \\ \theta_{21} & \theta_{22} \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} \theta_{13} \\ \theta_{23} \end{pmatrix} \quad (2)$$

where the θ coefficients are the parameters of the affine transformation.

The fact that the heart muscle deforms in a nonrigid manner requires a local transformation model. The Free-Form Deformation (FFD) model based on B-splines has proven to be a powerful tool when modelling such deformations. In 2D, the FFD is defined by an $n_x \times n_y$ mesh of control points $\mathbf{\Phi}$ with spacing (δ_x, δ_y). The underlying image is then deformed by manipulating the mesh of control points. The FFD can be written as the tensor product of the one-dimensional (1D) cubic B-splines

$$\mathbf{T}_{\boldsymbol{local}}(x, y) = \sum_{l=0}^{3} \sum_{m=0}^{3} B_l(u) B_m(v) \phi_{i+l, j+m} \quad (3)$$

where $i = \lfloor x/n_x \rfloor - 1, j = \lfloor y/n_y \rfloor - 1$,
$u = x/n_x - \lfloor x/n_x \rfloor, v = y/n_y - \lfloor y/n_y \rfloor$ and B_l represents the lth basis function of the B-spline

$$\begin{aligned} B_0(u) &= (1-u)^3/6 \\ B_1(u) &= (3u^3 - 6u^2 + 4)/6 \\ B_2(u) &= (-3u^3 + 3u^3 + 3u + 1)/6 \\ B_3(u) &= u^3/6. \end{aligned}$$

The main advantage of applying B-splines instead of e.g. thin-plate splines or elastic-body splines is that they are computationally more efficient. Changing a control point $\phi_{i,j}$ affects the transformation only in a local neighborhood of that particular control point.

Various similarity measures have been used for image registration depending on the different applications. The nature of the myocardial perfusion sequences is that the intensities vary markedly across time due to the injection of the contrast agent. This prevents the use of similarity measures that assume linear or identity relationships

between the images. Consequently, the similarity measure used in this study is an information theoretic measure, the normalised mutual information [8]. For optimisation of the similarity, a local gradient descent based method is used.

3 Results

An implementation of the nonrigid registration algorithm described above has been made freely available by Daniel Rueckert[1]. This implementation was used for the registration of the myocardial perfusion sequences.

For each patient, each frame in a slice sequence was registered to a reference frame within the same sequence. The reference frame was chosen to be the last frame of the sequence in all cases. This is due to the fact that in this frame the intensities have stabilised after arrival of the contrast. No manual interaction was needed in the registration process. Registration of each slice sequence of 70 frames took approximately 13 minutes on a 1.7 GHz Pentium M processor.

To give a qualitative impression of the registration accuracy, difference images between the reference frame and frames from the sequence can be inspected. Due to the contrast agent, such images are not reliable until the intensities have stabilised. Therefore, difference images from the wash-out part of the sequences (last 40 frames in this case) were inspected. Examples of these are given in Figures 3 and 4.

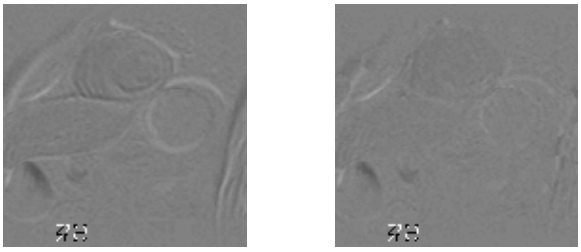

Figure 3: Patient 7: Difference images between the reference frame and frame 45 before (left) and after (right) registration.

To give a more quantitative impression of the registration the sum-of-squared differences was calculated for each frame of the wash-out part of the sequence (frame 30-70) with respect to the reference frame. Table 1 shows the mean sum-of-squared differences and the standard deviations for slice 2 from all patients along with the percentage improvement.

[1]See http://www.doc.ic.ac.uk/∼dr/software/

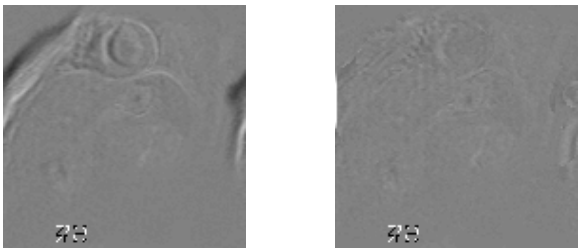

Figure 4: Patient 9: Difference images between the reference frame and frame 45 before (left) and after (right) registration.

Table 1: Mean sum-of-squared differences (MSD) and their standard deviation (Std.) from the stable part of the sequences from slice 2 for all patients before and after registration. Improvement in % is also provided.

	Before reg.		After reg.		
#	MSD	Std.	MSD	Std.	Improvement
1	2208	216	2189	176	0.9%
2	2316	348	2202	277	4.9%
3	2010	203	1964	183	2.3%
4	2546	524	2157	237	15.3%
5	2185	301	2148	259	1.7%
6	2057	235	1968	202	4.3%
7	2013	182	1933	175	3.9%
8	2218	411	2167	427	2.4%
9	2435	744	2234	445	8.3%
10	1948	175	1902	132	2.3%

The table reveals an improvement from 0.9 to 15.3% in terms of sum-of-squared differences.

4 Discussion and Conclusion

It is evident from Figure 3 that the motion of the patient's chest-wall between the two different frames has been reduced by the nonrigid registration. In the registered case, fewer structures are visible than in the unregistered case. The fat layer to the right has been eliminated as well as deformations in the right ventricle and the myocardium. Figure 4 also indicates that an improvement has been made by the nonrigid registration. In the registered case, the fat layers to the right and left are no longer visible and the myocardium has been deformed to match the reference frame.

In this study, a region of interest has not been extracted from the images prior to registration. Consequently, features in the images such as the digits in the bottom put bounds on the transforma-

tion. This means that the affine part of the transformation does not improve the similarity. On the contrary, the FFDs are able to deform small structures in the images to match the reference frame. Since these deformations are needed in a relatively small part of the image, the percentage improvement in Table 1 is small in some cases. These numbers would be improved by introducing a region of interest around the heart. It has been shown that a suitable region of interest can be extracted automatically prior to registration [1]. In addition, registration of cropped images will be computationally more effective. It is therefore clearly desirable to add this step to the method introduced here.

Further evaluation of this study will include transforming landmarks marked on the reference frame on the remaining frames of the sequence using the optimal transformation already obtained. This allows for a quantitative comparison of ground-truth labelling versus labelling generated by the automatic registration. Additionally this will also enable a comparison to our previous study [7].

The major drawback of the nonrigid registration algorithm is its high computational complexity. Hence, a future goal of this study is to integrate the nonrigid registration algorithm into the more computationally efficient AAM framework. The nonrigid registration algorithm would then be applied to automatically generate a labelled training set. From this set appearance models would be built and any unseen multi-slice sequence could then be rapidly registered by AAMs.

A preliminary clinical validation of the perfusion sequences can be obtained by a semi-quantitative perfusion assessment. This includes signal-intensity (SI) curves and perfusion maps of the myocardium [3]. A comparison between the registered and unregistered sequences in terms of these factors will give a good impression of the registration accuracy. We have carried out such experiments in [4] and one of the future steps is to include these in this study as well.

In conclusion, we have applied the FFD nonrigid registration algorithm to the registration of myocardial perfusion MRI. Preliminary registration results are promising and the next steps will primarily involve the inclusion of a region of interest along with a further evaluation of the method.

5 Acknowledgments

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