Automated Affine Registration of First-Pass Magnetic Resonance Images

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Abstract – Quantitative first-pass magnetic resonance (MR) imaging studies assist in characterizing the severity of ischemic heart disease. Cardiac motion due to a patient's difficulty in maintaining the required breath hold is often severe, making registration necessary. In this paper we present a novel automatic affine registration algorithm. The algorithm utilizes an affine active contour to determine affine registration errors in first-pass MR studies. We compare our results to the original unregistered studies and a normalized crosscorrelation registration method.

I. INTRODUCTION

Quantitative first-pass magnetic resonance (MR) imaging studies assist in characterizing the severity of ischemic heart disease. In first-pass MR perfusion imaging, a contrast agent is injected into the bloodstream and imaged during its first pass through the body. It has been shown that blood flow to a region of tissue can be calculated using this technique [1].

To calculate myocardial perfusion, signal intensity vs. time curves must be created for regions of interest (ROIs) in both the ventricular cavity and the myocardium. To generate these curves, scientists must delineate the endocardial and epicardial borders of the left ventricle (LV). Manually segmenting these borders throughout an entire study is both tedious and time consuming.

Cardiac motion within an MR study is often severe. This is primarily due to a patient's difficulty in maintaining the required breath hold of 30 seconds to 1 minute. Thus, scientists must segment each image in a study to assure that the myocardial borders are well localized. Registration of an MR study would allow scientists to segment only one frame.

Image registration is an active and important area in MR research. Previous work includes registration via crosscorrelation [2] and affine transformations [3]. Since the motion of the heart is non-rigid, the affine registration produces superior results. Traditional affine registration techniques require manual selection of anatomical landmarks within each image [3].

In this paper, we will present a novel automated affine registration algorithm. We will then compare the results to the original unregistered MR studies, as well as studies registered via normalized cross correlation. Success will be measured by the RMSE of anatomical features.

II. METHODS

We propose a novel automated affine registration process. After image preprocessing, we track several manually defined contours, and then apply inverse affine transformations from the active contour to the image, thereby registering the study.

A. Preprocessing

An area open-close filter is applied to the images to remove impulse noise. Area open removes small bright connected components. Area close removes small dark connected components. An unprocessed image and a filtered image are shown in Fig. 1.

B. Affine Active Contours

Active contours, or snakes, are used to segment a ROI from an image [4]. Snakes have been used extensively for segmenting the myocardium in MR images [5], [6], [7]. These algorithms, however, do not limit contour point movement to affine transformations. To track the heart, we propose the use of an affine snake [8].

An affine transformation consists of translation, rotation, shear, and scaling. Parallel lines in the original image remain parallel in the transformed imaged. This can be represented by the general affine transformation matrix T as follows:

$$T = \begin{bmatrix} a & b & c \\ d & e & f \\ 0 & 0 & 1 \end{bmatrix}.$$
 (1)

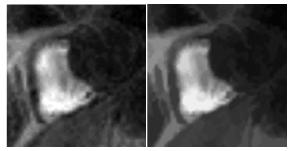


Fig. 1: Image before (left) and after (right) preprocessing.

Let $[x_0,y_0]$ represent a point in our initial set of 2D contours X_0 . We can define the affine transformation of this point, [x,y], in homogeneous coordinates as follows:

$$\begin{bmatrix} x \\ y \\ 1 \end{bmatrix} = T \begin{bmatrix} x_0 \\ y_0 \\ 1 \end{bmatrix}.$$
 (2)

Thus, we have constrained all points according to a single affine transformation. Note that the initial set of contours is not necessarily smooth, closed, or continuous.

We wish to find the set of contours which minimize the following energy functional:

$$E_{aff} = -\int_{\mathcal{C}} M(x, y) ds + \lambda \cdot \sum_{A_{ij}} \frac{\partial |\mathbf{A}|^2}{\partial A_{ij}}, \qquad (3)$$

$$\mathbf{A} = \begin{bmatrix} a & b \\ d & e \end{bmatrix}$$
 (4)

 λ is a weighting parameter that controls the smoothness of the movements of the affine snake and *M* is a function of the image, e.g. the negative image gradient [8].

We minimize this functional with respect to each affine parameter (a-f) via a steepest descent method. For example, the update equation for the parameter *a* is as follows:

$$a_{t+1} = a_t + \tau_a \left[\sum \left(M(x_t, y_t) \cdot x_0 \right) + \lambda \left(2e_t^2 - 2d_t e_t - 2b_t e_t + 4a_t e_t - 2b_t d_t \right) \right].$$
 (5)

where τ_a is the time step. Update equations for *b*-*f* are developed in a similar manner [8].

To ensure a large capture range, we define M as the function that maximizes the generalized gradient vector flow (GGVF) given by [9]:

$$M(x, y) = \begin{bmatrix} u(x, y) & v(x, y) \end{bmatrix},$$
 (6)

$$E_{GGVF} = \iint g(|\nabla f|) \cdot (u_x^2 + u_y^2 + v_x^2 + v_y^2),$$

+ $h(|\nabla f|) \cdot |M - \nabla I|^2 dx dy$, (7)

where g and h are weighting functions, and f is an edge map of the image I(x,y). In this case, f is the gradient magnitude of the image.

C. Affine Registration

Let X_k represent the set of contours in frame k, where $k \in [0, N-1]$. Let T_k represent the transformation from X_{k-1} to X_k . Taking note that a combination of affine transformations is itself an affine transformation, we can find the transformation between any frame and frame 1:

$$\begin{aligned} X_{1} &= T_{1} \cdot X_{0} \\ X_{2} &= T_{2} \cdot X_{1} = T_{2} \cdot T_{1} \cdot X_{0} \\ \vdots \\ X_{k} &= T_{k} \cdot X_{k-1} = T_{k} \cdot T_{k-1} \cdot \ldots \cdot T_{1} \cdot X_{0} \end{aligned} \tag{8}$$

Given the affine parameters from the active contour we register the study. Registered pixel locations in any frame with respect to the original frame can be found applying the inverse of consecutive affine transformations.

To demonstrate this procedure we create a set of two synthetic images where the second image is an affine transformation of the first image. We then use our algorithm to register the two frames. Fig. 2 displays the average of these images before and after affine registration, as well as the affine active contour segmentation results.

III. RESULTS

We tested our method on six first-pass MR imaging sequences. We utilized 31 frames per sequence, after the myocardium showed significant contrast. Each sequence was 128x96 pixels at a resolution of ~3mm/pixel. Thus the heart was ~40 pixels across.

Our contour set included the endocardial border of the right ventricle (RV), the endocardial border of the left ventrical (LV), and the entire pericardium. For our test set, we utilize all three contours. In different stages of a sequence we can utilize other combinations of these three contours, e.g. when the contrast agent is passing though the LV only, we could utilize the LV contour only.

Fig. 3 displays the average of two frames from a sample MR study before and after affine registration, as well as the affine active contour segmentation results. After registration, the myocardial walls are more defined in the average frame.

A trained technician ground-truthed anatomical landmarks on each frame of each sequence. For each landmark, we measured the distance between the landmark's location in frame k and its location in frame 1 before and after registration. Clearly, small distances imply successful registration.

We measured success by calculating the maximum, standard deviation, and RMSE of these anatomical landmark distances. We compared our registration technique to registration via normalized cross-correlation, and the original unregistered sequence. Table I summarizes the results. All numbers are reported in pixels. Under all three measures, automatic affine registration was superior.

TABLE I. SUMMARY OF RESULTS, ERRORS REPORTED IN PIXELS

Method	RMSE	Max Dist	StdDev Dist
Unregistered	1.76	4.70	0.96
Normalized Cross-Correlation	1.77	4.36	0.94
Automatic Affine Registration	1.62	3.89	0.85

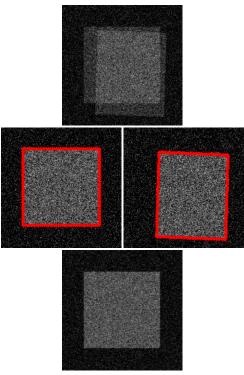


Fig. 2: Synthetic data set. Average before registration (top); segmentation (middle); average after segmentation (bottom).

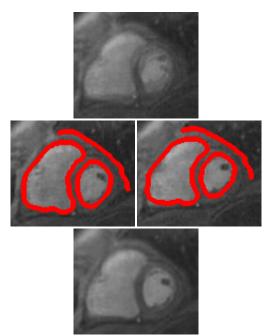


Fig. 3: Two sequential frames of an MR study. Average before registration (top); segmentation (middle); average after segmentation (bottom).

IV. CONCLUSIONS AND FUTURE WORK

In this paper we presented a novel automatic affine registration algorithm. The algorithm utilized an affine active contour to determine the affine registration errors in first-pass MR studies. We compared our results to unregistered studies and a normalized cross-correlation method. We found our algorithm to be superior with respect to RMSE, maximum error, and standard deviation of anatomical landmark distance.

Future work can extend the registration algorithm to three dimensions. Changes to the algorithm would be dependent on data point resolution in the third dimension.

If intraplane resolution is significantly worse than within plane resolution, as with the data used in this paper, contour point movement should be constrained to be within plane. In this case, the contour point's third dimension, z, is held constant through time and only the function M is changed in implementation.

If the data is isometric, and therefore truly threedimensional, contour points should be permitted to move freely in the third dimension. Update of the energy functional and transformation matrix is relatively straightforward.

REFERENCES

- Wilke, "Myocardial perfusion reserve: assessment with multisection, quantitative, first-pass MR imaging.," Radiology, vol. 204, pp. 373-84, 1997.
- [2] Eisner, "Use of cross-correlation function to detect patient motion during SPECT imaging.," Journal of Nuclear Medicine, vol. 28, pp. 97-101, 1987.
- [3] Dromigny-Badin, "Fusion of cine magnetic resonance and contrastenhanced first-pass magnetic resonance data in patients with coronary artery disease: a feasibility study.," Investigative Radiology, vol. 33, pp. 12-21, 1998.
- [4] M. Kass, A. WItkin, and D. Terzopoulous, "Snakes: Active Contour Models," International Journal of Computer Vision, pp. 321-331, 1987.
- [5] M. A. Guttman, J. L. Prince, and E. R. McVeigh, "Tag and contour detection in tagged MR images of the left ventricle," Medical Imaging, IEEE Transactions on, vol. 13, pp. 74-88, 1994.
- [6] R. L. Janiczek, N. Ray, S. T. Acton, R. J. Roy, B. A. French, and F. H. Epstein, "Markov chain Monte Carlo method for tracking myocardial borders," presented at Computation Imaging III, San Jose, CA, 2005.
- [7] D. L. Kraitchman, A. A. Young, C.-N. Chang, and L. Axel, "Semiautomatic tracking of myocardial motion in MR tagged images," Medical Imaging, IEEE Transactions on, vol. 14, pp. 422-433, 1995.
- [8] M. E. Welser and S. T. Acton, "Projection model snakes for tracking using a Monte Carlo approach," Journal of Electronic Imaging, vol. 13, 2004.
- [9] C. Xu and J. L. Prince, "Generalized gradient vector flow external forces for active contours," Signal Processing, vol. 71, pp. 131-139, 1998.