

Mediated Spatiotemporal Fusion of Multiple Cardiac Magnetic Resonance Datasets for Patient-specific Perfusion Analysis

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Abstract

Patient-specific correlation of perfusion defects and coronary arteries responsible for blood supply in the affected territories has the potential to improve accuracy of diagnosis and intervention planning, but cardiac cycle phase difference between perfusion and angiography datasets precludes the use of standard methods of 2D/3D registration. This paper presents a work-flow for mediated spatiotemporal registration of perfusion series and angiography volumes; the solution of the registration problem relies on the use of the 4D wall motion series as a mediator for non-rigid registration of perfusion and angiography datasets. The work-flow assumes the availability of the localised/segmented main coronary arteries in the angiography dataset. Results of evaluation on clinical data show the utility of the method in perfusion analysis while highlighting its potential applicability to other areas of cardiac image analysis.

1. Introduction

Cardiovascular Magnetic Resonance (CMR) imaging provides diagnostic information for the assessment of myocardial anatomy, contractile function, perfusion, myocardial tissue viability, coronary artery anatomy and coronary blood-flow with accuracy similar or superior to that provided by other established tests. In particular, non-invasive assessment of myocardial perfusion by Dynamic Contrast-Enhanced Magnetic Resonance Imaging (DCE-MRI) in patients with known or suspected Coronary Heart Disease (CHD) could more accurately and more cost effectively identify those patients who require coronary revascularization than the 'battery of tests' currently used in clinical practice [1]. Fusion of the various CMR components into a single CMR examination improves the sensitivity for the diagnosis of significant CHD over and above that of any individual component [2]. However, imaging of myocardial perfusion by DCE-MRI is an evolving technique which has yet to become part of routine clinical practice. One of the reasons for this is the inherent incompatibility between X-

ray angiography (the currently accepted gold standard) and information provided by DCE-MRI: micro-vascular perfusion assessment does not necessarily correlate to anatomical morphology of coronary arteries as assessed by X-ray angiography. The results of the X-ray angiography are currently interpreted and correlated with DCE-MRI using a general model of coronary artery blood supply [3].

We are developing a framework for establishing direct correspondence between DCE-MRI findings and a patient-specific model of coronary artery supply obtained from Magnetic Resonance Angiography (MRA). This paper describes the crucial component of this framework designed to establish a reliable correlation between perfusion defects and coronary arteries responsible for these defects.

Registration of 2D DCE-MRI and coronary 3D MRA datasets has the potential to provide the solution for patient-specific mapping of perfusion defects to coronary supply territories. However the standard methods of rigid and non-rigid registration are not applicable in this context because of the potential cardiac phase mismatch between DCE-MRI and MRA datasets. Myocardium shape variation across the heart cycle precludes the use of rigid slice-to-volume registration, while the difficulties associated with weak perspective in nonrigid slice-to-volume registration impede the use of the standard non-rigid techniques. Research published to date does not provide a reliable method of registering DCE-MRI and MRA datasets.

We present an approach for mediated spatiotemporal registration designed to overcome the difficulties associated with perfusion and angiography registration. Our method is based on the use of a non-rigid transform obtained from the analysis of temporal series (4D MR cine datasets). A non-rigid transform spanning the phases from angiography to perfusion is derived from the 4D cine; this transform is used as the spatiotemporal registration mediator in the process of correlating perfusion defects with the coronary arteries. Contrary to previous assertions [4], the approach described here shows that 3D alignment of slices is possible through the use of a 4D reference dataset to guide non-rigid registration of images acquired at distinct phases of the cardiac cycle. The evaluation results con-

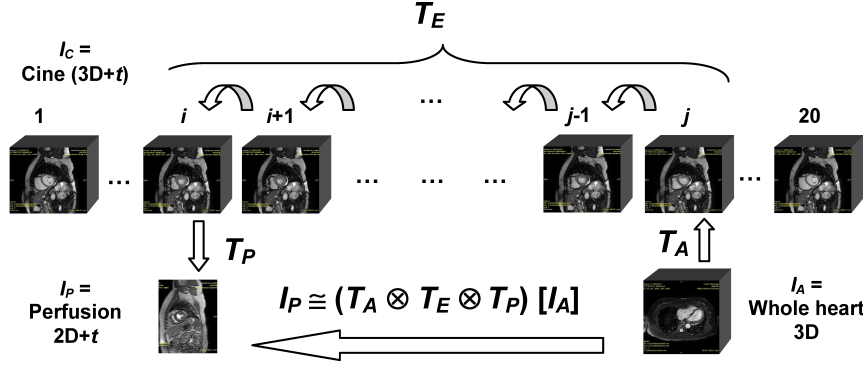


Figure 1. Stages of mediated spatiotemporal registration. Registration of a perfusion slice to the corresponding phase t_i in the cine dataset produces a rigid transform T_P ; registration of the whole heart angiography volume to the corresponding phase t_j in the cine dataset produces a rigid transform T_A ; non-rigid transform T_E is obtained through sequential registration of cine phases from t_i to t_j ; the total transform is composed of the transforms T_P , T_E and T_A . The direction of the arrows indicates the direction of the derived transforms.

firm that 3D alignment of perfusion slices provides better outcomes in comparison to results reported in [4].

2. Methods

The registration method proposed here is designed to fuse 2D perfusion short-axis images of myocardium acquired at either systolic or diastolic phases of the cardiac cycle with 3D angiography volumes acquired during the phase of maximum myocardial relaxation. The method is centered around the computation of a non-rigid 3D transform to be used as a mediator for the non-rigid registration in the multi-step process attempting to link two arbitrary phases of a cardiac cycle. Prior to registration the cine series were preprocessed to correct for slice misalignment which results from the variation in breath-hold positions during series acquisition. The misalignment was corrected using the slice-to-volume registration as described in [5].

In general, image registration is described by the equation: $T = R(I_F, I_M)$, where fixed image I_F is registered with moving image I_M to produce transform T that can be used directly to resample the moving image into the coordinate space of the fixed image. Fig. 1 shows the stages of mediated spatiotemporal registration.

The temporal phase t_P within the cine series is determined through the normalization of cardiac cycle trigger offsets which are recorded in DICOM headers; the closest value of a normalized cine trigger offset to the normalized perfusion trigger offset determines the matching cine phase t_P . Rigid slice-to-volume registration with the Mutual Information (MI) metric [6] of perfusion slice I_P to the corresponding phase t_P of the cine series I_C results in a rigid transform $T_P = R(I_P, I_C)$. Similarly, the phase match between angiography volume and cine series is found through the normalization of the cardiac cy-

cle trigger offsets; the closest trigger value determines cine phase t_A . Rigid 3D-to-3D MI-based registration of the angiography volume I_A to the corresponding cine I_C image at phase t_A results in a rigid transform $T_A = R(I_C, I_A)$.

Given the phases of the perfusion image t_P and the angiography volume t_A , the non-rigid 3D transform T_E between the t_P and t_A phases of the cine series is obtained with the composition of the 3D transforms derived from non-rigid pair-wise registration of all adjacent phases. In the experiments described here 3D transformations were obtained with Demons registration method [7]. The composition of sequential transforms draws on the Eulerian registration framework where the deformation is viewed as flow in time, as opposed to the deformation of an elastic material in the Lagrangian framework where the deformation is always calculated as the transform between the first and last stages of the process [8]. Note that only direct transforms are used in the final composite transform $T_M = T_A \otimes T_E \otimes T_P$: therefore we avoid the need for transform inversion. The application of the transform T_M to the angiography volume I_A results in its non-rigid warping into the perfusion frame of reference: $I_P \cong T_M(I_A)$. Thus if coronary arteries are segmented in I_A then transform T_M will place the arteries into the perfusion coordinate space. Further details on our method of mediated spatiotemporal registration are provided in [9].

The evaluation was carried out with ten anonymized clinical datasets chosen with prior consent from the pool of data acquired for the CE-MARC study [10]; the datasets included five female and five male patients with an average age of 62 years. The registration experiments were performed with basal and medial perfusion slices with maximal ventricular contrast; the slices were chosen as described in [4]. The performance of our method was compared against 2D affine registration of DCE-MRI and the

corresponding reformatted 2D slices from MRA without 3D alignment as described in [4].

Quantitative evaluation was carried out against ground truth with two types of manually annotated data: (1) left-ventricular (LV) endocardial, LV epicardial and right-ventricular (RV) endocardial contours for medial and basal slices with maximal myocardial contrast in both ventricles in rest perfusion data; the contours were manually drawn on QMass MR 6.2.1 from Medis Medical Imaging Systems and examined by a cardiologist, and (2) manual segmentation of LV endocardial and epicardial and RV endocardial surfaces in whole heart angiography volumes carried out in ITK-SNAP from Penn Image Computing and Science Laboratory. The accuracy of registration was evaluated as the physical distance for each voxel from LV endocardial and epicardial and RV endocardial contours defined in perfusion slices to the segmented LV endocardial and epicardial and RV endocardial surfaces defined in angiography volumes and warped with the transform derived through mediated spatiotemporal registration. This in-plane error calculation represents the lower bound approximation of the 3D error; true 3D error is inaccessible since the true position of the contours on the segmented LV and RV surfaces at phase t_A is not known.

3. Results

A quantitative comparison between spatiotemporal and 2D affine registration [4] is shown in Fig. 2; average Hausdorff distance [11] measures how closely perfusion contours match the transformed myocardium segmentations. These results suggest that spatiotemporal registration is more suitable for perfusion-to-angiography registration than 2D affine registration. In the case of the medial LV endocardial and epicardial slices the t-Test indicates a statistically-significant difference of average Hausdorff distances ($P = 0.001$ and $P = 0.011$ respectively) between our approach and 2D affine registration.

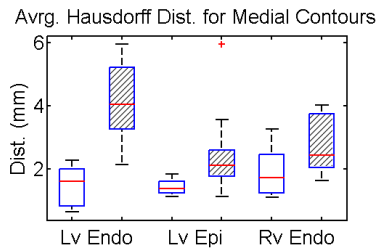


Figure 2. Comparison between mediated spatiotemporal registration and 2D affine registration (textured plots) of medial perfusion and angiography images on the basis of average Hausdorff distance for LV endocardial contours.

A comparison of the contour-to-segmentation error distance distribution for LV endocardial contours is given in

Fig. 3; the weaker results for 2D affine registration without 3D motion are explained by the insufficiency in degrees of freedom in 2D affine registration. The histograms show that the 2D affine registration has a much stronger bias in the LV endocardial contours, which is explained by the larger mass of the myocardium guiding the 2D affine transform optimization, while the LV endocardial contour including the LV blood pool bears less influence on the optimization process.

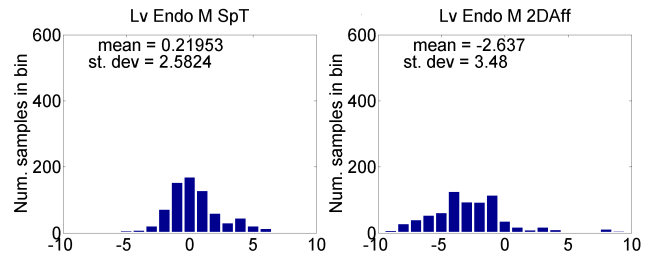


Figure 3. Comparison between mediated spatiotemporal registration (left) and 2D affine registration (right) of medial perfusion and angiography images on the basis of error distance distribution for LV endocardial contours.

4. Discussion and Conclusions

The presented approach to spatiotemporal registration has been developed as a component in a project focusing on the analysis of DCE-MRI. Evaluation results indicate that angiography and perfusion datasets can be fused through the perfusion-to-angiography phase difference transform. Although at this stage the performance of our approach presents an incremental improvement on 2D affine registration, overall spatiotemporal registration has more potential for all short-axis slice locations and phase differences; while both methods demonstrate equivalent performance on “easy” data, spatiotemporal registration produces reliable results with “difficult” data. An example of registration outcome for medial slice from rest perfusion sequence and angiography volume is given in Fig. 4. The phase difference between perfusion and angiography is more striking in the case of medial perfusion slices, because in our data medial perfusion slices are acquired during systole, while angiography is acquired at diastole. Although our approach does not explicitly account for tissue twist that occurs during myocardial motion, experimental results suggest the approach provides suitable accuracy for correlating angiography with perfusion defects.

We intend to use mediated spatiotemporal registration in conjunction with coronary tree segmentation, perfusion analysis and myocardium viability data to produce patient-specific maps of coronary supply territories as described in [12]. More generally, our method combined with auto-

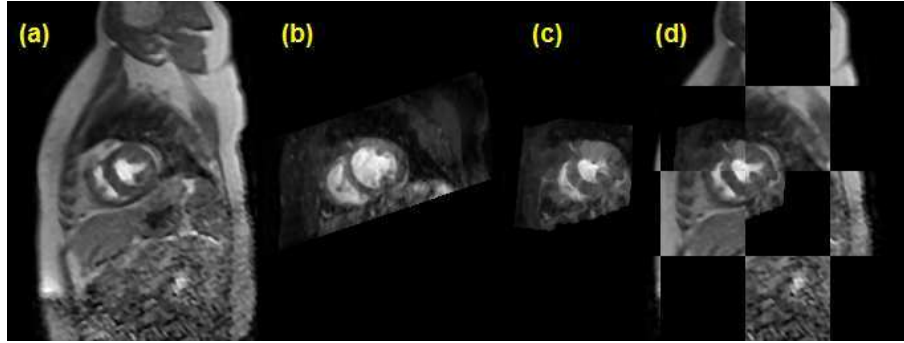


Figure 4. Example output for registration of a medial perfusion slice and angiography: (a) medial perfusion slice, (b) reformatted angiography slice extracted at the location and orientation of the perfusion slice, (c) reformatted angiography slice after the application of the transform T_M , (d) checkerboard overlay of perfusion and transformed angiography slices.

matic myocardium segmentation in high-resolution whole-heart angiography volumes can be applied to the problematic task of myocardium segmentation in low-resolution perfusion data; application of the transform spanning the phase difference between angiography and perfusion phases to automatically segmented myocardium can produce myocardium labelling in the whole perfusion series if they were initially corrected for breathing motion. To our knowledge this approach for perfusion segmentation has not been explored in research literature.

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