Stack Alignment Transform for Misalignment Correction in Cardiac MR Cine Series

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Abstract

Stack misalignment in cardiac MR cine series distorts the correct appearance of anatomical features and reduces the reproducibility of volumetric measurements computed for diagnostic purposes. This paper describes a method for correction of stack misalignment in cardiac MR series. Our method involves registration against a reference volume and features a prominent enhancement designed to circumvent the weaknesses associated with slice-to-volume registration. The core of the presented method is a custom stack alignment transform which parametrises the in-plane movement for all slices independently of each other; at the same time the image similarity metric for every optimisation iteration is calculated on the whole stack with all slice correction parameters contributing to the result. The method was evaluated on 50 clinical datasets with a 100 simulated optimisation runs for every dataset. The results show that on average the method is able to recover alignment parameters with sub-voxel accuracy.

1 Introduction

Excellent tissue contrast along with high spatial and temporal resolution in Cardiovascular Magnetic resonance (CMR) imaging cast it as one of the most accurate and reproducible modalities for Coronary Heart Disease (CHD) diagnosis. Comprehensive CMR exams consist of a number of scans which provide in a single test the greatest volume of diagnostic data, including detailed ventricular and coronary anatomical information, myocardial function, perfusion, tissue viability and coronary blood flow. Wall motion and volumetric measurements for the assessment of myocardial function are derived from cine stacks spanning the cardiac cycle. Breath-holding is used as the means to exclude respiratory motion in cine series; a patient holds their breath multiple times and one to three slices over all phases are acquired during each breath-hold. Stack misalignment in cine series is caused by the inconsistencies in breath-hold positions between slice acquisitions. This paper presents a novel solution for cine correction which is motivated by the role of registration mediator that cine series play in spatiotemporal registration of MR perfusion and angiography.

1.1 Misalignment Correction Background

As with most registration applications, the solutions to the problem of slice misalignment in cine stacks rely on a reference image, which provides the bias for motion recovery during registration. A solution describing long-axis (LA) cine series as the reference image for short-axis (SA) slice-by-slice 2D translation misalignment correction in [7] provides reliable results; the use of 4D (3D + time) images in the registration enhances the appeal of the method, but it is only feasible if the LA series are multi-slice series; this is not the case in every study. Another solution relies on the slice-to-volume registration of SA slices to a high-resolution reference volume [2]; the multi-resolution registration optimises a 3D rigid transform for each SA slice from end-diastolic phase as it is registered to the whole heart volume. The results of stack correction with slice-to-volume registration experiments show the improvement in the accuracy for ventricular function analysis, although the study was performed on a relatively small number of healthy volunteers. Furthermore, as the authors in [1] observe, slice-to-volume registration can become an under-constrained problem due to the method's weakness which lies in out-of-plane rotations. A method with the potential to avoid the pitfalls of slice-to-volume registration in [6] was used for correction of multi-slice foetal brain MR images; the solution does not rely on slice-to-volume registration, however it requires at least three orthogonal stacks of slices.

Research publications on cardiac motion provide the evidence of through-plane respiration-induced motion of up to 23 mm translation along with some rotation (which varies considerably for each patient) due to patients' inconsistency in breath-hold positions [9]. Such displacements in the context of the method in [2] with its unconstrained 3D motion of the individual slices indicate that there is a high likelihood that some slices would be moved past their initial positions in the stack. While in the general context it is desirable for the individual slices to be registered to their precise 3D locations in the context of the reference volume, one side-effect of such correction is likely to manifest as some overlaps and "holes" in the reconstructed volumes, which in turn may require the use of some interpolation technique. However, the quality of reconstructions with linear interpolation based on non-adjacent stack slices degrades the features in the image.

1.2 Stack Alignment Transform Overview

Stack alignment transform has been developed as a component in an over-arching project aimed at establishing the co-location of perfusion defects (observable in perfusion series) with the coronary vessels (identifiable in angiography volumes) that might be responsible for these defects [11]. The project proposes a method of spatiotemporal registration of perfusion and angiography data; in this method the cine series are used for deriving the non-rigid transforms spanning an arbitrary difference between cardiac phases. The phase-to-phase transforms can be used to map the coronary anatomy derived from angiography volumes into an arbitrary phase of the cardiac cycle, *e.g.* the perfusion coordinate space. Hence the method for spatiotemporal registration is primarily concerned with recovering the finer components of the contractile motion such as the rotation of the myocardium and coronary vessels around the LA of the heart. In this context the primary concern is to constrain the slice displacements to in-plane motion to avoid the loss of image features due to out-of-plane slice displacements and non-adjacent slice interpolation. The parametrisation of the stack alignment transform deliberately avoids out-of-plane displacements; this approach presents a suitable alternative for cine correction in the context of perfusion and angiography fusion.

More generally, our solution is designed to circumvent the issues associated with slice-to-volume registration. Consider the case of slice-to-volume registration where the Mutual Information (MI) image similarity metric is evaluated from the region of overlap of a single slice and a volume: in this instance the joint probability distribution is likely to be a poor representation of the *true* joint probability distribution. However, a much better representation of the joint probability can be obtained from the overlap of the complete stack and reference volume because in this case the joint histograms computed for the calculation of the MI value contain a larger number of co-occurrences of grey-levels which represent the types of tissue in the images. This method of MI optimisation is made possible with a customised stack alignment transform presented and evaluated in this paper.

2 Materials and Methods

CMR images in this study were acquired on a dedicated cardiac research scanner (1.5 Tesla Intera CV, Philips, Best, The Netherlands) during a comprehensive trial on CMR imaging in CHD, CE-MARC [4]; the experiments involved two types of cardiac data:

Coronary MR angiography: Three dimensional, whole heart coronary MR angiography acquired using a balanced SSFP sequence and a respiratory navigator to compensate for respiratory motion during free breathing. Timing of the diastolic rest period is estimated from the four-chamber free breathing cine scan; matrix 304 304, field of view 320-460 mm, slice thickness 0.9 mm, 100-120 slices as required.

Resting wall-motion: Contiguous cine stack encompassing the entire left ventricle (LV) in 10-12 slices (depending on LV LA length) acquired during multiple breath-holds; matrix 192 192, field of view 320-460 mm, slice thickness 10 mm, at least 20 phases per cardiac cycle, 1 2 slices per breath-hold.

Further information on the pulse sequences is available in [3]. For this study 50 representative datasets from the CE-MARC trial were selected randomly by the clinical trials unit; one dataset was excluded because of severe motion artefacts in the angiography volume.

2.1 Cine Phase Selection and Angiography Pre-registration

Prior to the optimisation of the stack alignment parameters it is necessary to determine the cardiac phase in the cine series to match the end-diastolic reference angiography volume. Although either visual examination of the cine series or ECG-based trigger delay normalisation can be used to calculate the matching phase, this study uses MI-based phase match determined by the best MI value computed for all of cine phases and angiography volume during pre-registration. In practice, the best match usually falls in a window of 4 phases within the normalised trigger delay of the angiography volume. The pre-registration method in this case is a straightforward example of volume-to-volume registration with a translation transform, with a given cine phase and angiography volume used as fixed and moving images respectively. A set of elliptical masks derived from manually-defined rectangular regions of interest (one region for each slice) in the end-diastolic phase of the cine was used to exclude irrelevant anatomical features. Multi-resolution registration (two levels) with a Regular Step Gradient Descent optimiser and Matte's implementation of MI [8] available in ITK [5] provided fast and reliable results.

It should be noted that although it would be just as easy to optimise a rigid 3D transform with rotation instead of a translation-only transform, it was deliberately avoided. The

rationale for this decision was that the high-resolution angiography volumes carry the most amount of anatomical information in comparison to the sparse and likely misaligned cine series; theoretically there can be multiple cases of stack misalignment favouring 3D rotations. Hence it is preferable to use the simplest possible transform to avoid rotational errors.

2.2 Stack Alignment Transform and Misalignment Correction

Our stack alignment transform is a custom spatial transform which parametrises the in-plane movement along the X and Y dimensions for the individual stack slices independent of each other. In addition, the transform also includes a parameter for global translation along the Z direction. Fixed transform parameters include image origin, spacing and size, all obtained from the corresponding cine phase. For example, if the cine series consist of 12 slices, the transform will be parametrised as $T \quad S_1 \quad S_{12} \; z_g$, where $S_n \quad x_n \; y_n$ and n is the slice number calculated from the fixed parameters based on a given point in 3D space. For a point $P \quad x \; y \; z$ in 3D space, the transformed point $P \quad x \quad y \quad z$ is calculated as follows:

$$\begin{array}{lll} x & x & x_n \\ y & y & y_n \\ z & z & z_g \end{array} \tag{1}$$

Apart from the transform, the rest of the registration components for this stage are the same as for pre-registration: multi-resolution pyramids (two levels), Regular Step Gradient Descent optimiser, Matte's MI and fixed image masks. During the registration the cine stack is used as the fixed image, because the image MI similarity metric collects samples from the moving image on the fixed image grid. After the registration the inverted transform can be applied to correct all phases in the cine series.

2.3 Evaluation Protocol

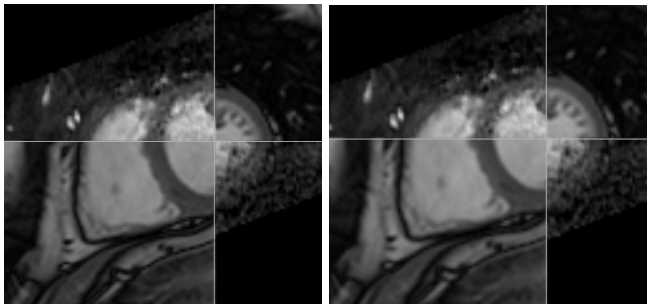
The performance of alignment parameter recovery was evaluated with a protocol of registration uncertainty measurement described in [10]; in this evaluation method the mean transform is used as a pseudo-gold standard based on the assumption of a zero mean distribution of errors. The core of the protocol is in the assessement of the accuracy of registration in a large number of runs each with a known introduced misalignment. In our study a 100 random simulated misalignments for all slices in a given dataset were generated; the in-plane offsets $X_M \quad x_{M1} \quad x_{M100}$ and $Y_M \quad y_{M1} \quad y_{M100}$ were restricted to 4 mm. This type of simulated error is significantly more severe than the misalignment common for clinical datasets, because typically only a small portion of slices in a stack contains observable movement, while the simulated transforms displace every slice. During the evaluation, a clinical dataset with its unknown error repeatedly was further misaligned with one of the 100 simulated offsets. If after registration with a 100 simulated offsets the recovered in-plane displacement for each slice are to be represented as $X_R \quad x_{R1} \quad x_{R100}$ and $Y_R \quad y_{R1} \quad y_{R100}$ respectively, then the estimated correction parameters for the slice are represented as $X \quad X_M \quad X_R$ and $Y \quad Y_M \quad Y_R$ with their arithmetic means $\bar{X}$ and $\bar{Y}$ representing the mean transform over 100 simulated runs. The magnitude of registration error distance $D_{err} \; n$ for slice n shifted with a simulated offset n can be calculated as follows:

$$D_{err} \; n \quad \sqrt{x_n \quad \bar{X}^{\,2} \quad y_n \quad \bar{Y}^{\,2}} \tag{2}$$

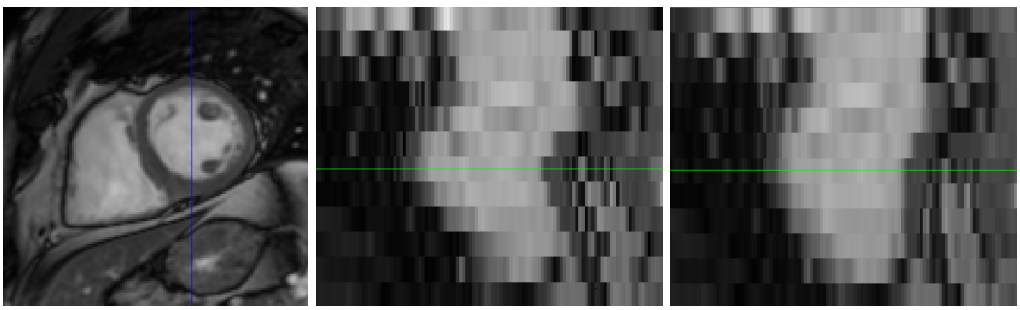
3 Results

Visual inspection of the registration results for the 49 datasets (without simulated errors) showed that alignment was recovered successfully in all cases; Checkerdoards showing cine and double-oblique reformatted reference volumes were used for visual validation. Figure 1 presents a pair of examples of misalignment and its correction (typical for this study); most datasets needed correction for a small subset of slices (usually one to three) while a few datasets required correction for all slices. Although no obvious registration failures were detected it should be noted that correction of apical slices may not always be viable due to the absence of clearly visible myocardium and blood-pool. A small number of apparent phase mismatch cases possibly could be explained by the unaccounted out-of-plane rotations.

Parameter recovery using the stack alignment transform with simulated offsets described in the previous section was compared against the slice-by-slice registration (restricted to in-plane movement) with the same parameters. Figure 2 shows the comparison of the distributions of the error distance (as defined in equation (2)) for the 49 datasets; the higher error ranges for the extreme apical and basal slices are explained by three factors: (a) insufficient image features (*e.g.* no clearly visible ventricular/myocardial walls); (b) insufficient overlap region between apical or basal slices in cine and angiography; (c) presence of a rotational component of displacement which is not considered in this study. For the slices with clearly visible myocardium, the error mean is around one voxel (1.3 mm approx.) and is bounded by the 2.5 mm in 95% of cases for both slice-by-slice alignment and stack alignment experiments. However the difference between the overall shape of the error distributions shows that stack alignment transform is more consistent in all slices and has a greater capture range.



(a) SA before (b) SA after



(c) Slicing plane indication (d) LV before (e) LV after

Figure 1: Misalignment correction examples: checkerboards in (a) and (b) show the alignment of a single SA slice from a cine stack and double-oblique reformatted angiography volume before and after correction; images in (d) and (e) show one phase from a cine stack before and after correction; orientation and location of the slicing plane is indicated in (c).

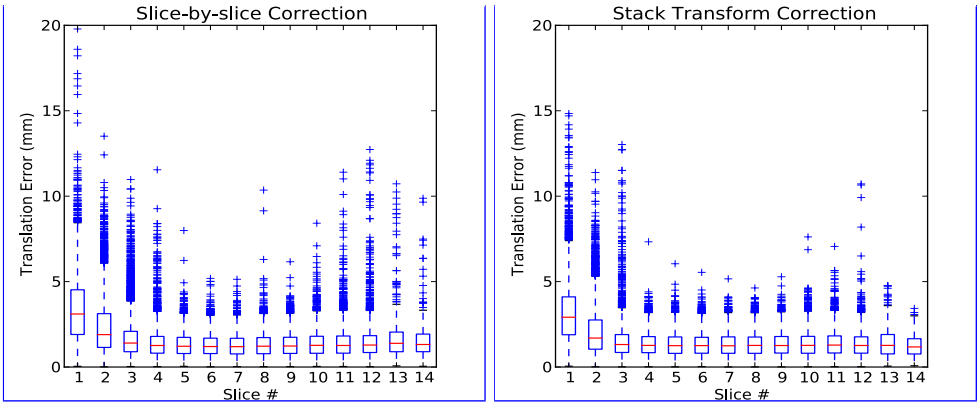


Figure 2: Distribution of error distance D_{err} as defined in equation (2); left: slice-by-slice correction; right: stack alignment transform correction. The boxplots summarise the errors for a 100 simulated runs for all datasets, one bar per single slice index in a stack.

4 Discussion and Conclusions

In this paper we presented an alternative solution for stack misalignment correction in MR cine series. The solution relies on a novel spatial transform, the stack alignment transform; it has been developed in the context of spatiotemporal registration of perfusion and angiography data, where it is preferable to avoid the degradation of the image features in the stack in order to recover the finer components of the contractile motion reflecting the radial rotation around the LA of the heart. The key feature of the stack alignment transform is its ability to harness the power of the MI image similarity metric by enabling the computation of the joint probability distributions based on the overlap of the whole stack and reference volume, rather than an overlap of one slice with the reference volume. The evaluation of the stack alignment transform on a large clinical dataset proves that the proposed method for cine correction offers a robust solution which restricts the single slice motion to in-plane translation and favours the integrity of the cine series. In future work we anticipate extending the stack alignment transform to recover the rotational component of the myocardial motion. In addition, a more extensive evaluation with manually drawn myocardial contours to be used as the gold-standard could provide a further insight into the benefits of the stack alignment transform; in our experience, visual correction validation with checkerboards is not specific enough for assessing the finer components of recovered motion.

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