Segmentation-Free MRI to CT 3D Registration for Cardiac Resynchronization Therapy Optimization

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Abstract

The purpose of this work is to include tissue and dynamic information from cardiac magnetic resonance (CMR) sequences in a previously proposed fusion framework aiming to optimize Cardiac Resynchronization Therapy (CRT). To do so, the 3D iconic registration between 3D+t cardiac MR and 3D+t cardiac computed tomography (CT) sequences is explored. Two rigid registration approaches have been evaluated: end-diastole (ED) images registration and dynamical time warping (DTW) based registration. DTW is used to align both sequences in time. They are tested on five patients that underwent for CRT. Quantitative evaluation has been performed using the dice score between ED delineations of left ventricle (LV). An average error of 4.71% (std 4.58%) is obtained for ED registration. For DTW registration, an average error of 2.68% (std 2.76%) is obtained using the normalized correlation curves of MR and CT sequences. These results demonstrate the feasibility to perform a 3D registration of MR and CT sequences without the need of temporal interpolation.

1. Introduction

Cardiac Resynchronization Therapy is a well established routine aiming to treat patients with New York Heart Association NYHA class III or IV heart failure level, biventricular dissynchrony (QRS $>$ 120 ms) and severe left ventricular (LV) systolic dysfunction (LV ejection fraction $<$ 35%) [1]. One third of the patients are non responders and the reasons of rejection are not well established. To optimize the response to CRT, either at patient selection or at pre-operative planning, the anatomical, functional, mechanical and electrical information of the heart should be described in a common reference to extract new markers.

CRT outcome can be improved by the optimization of LV lead placement. For this purpose, the site of latest activation has to be localized (e.g. using Speckle Tracking Imaging (STI) and Electro-Anatomical Mappings (EAM)) and characterized in terms of postero-lateral (transmurality) scar. Moreover, the anatomy of the veins, which are used to place the lead, has to be determined. In this context, we have previously proposed a surface-based registration framework including EAM, STI and, as an anatomical reference, CT image [2, 3].

CMR sequences and CT images contain valuable information to perform the aforementioned characterization. Cine and late gadolinium enhanced (LGE) CMR sequences allow the analysis and assessment of global/regional function and myocardial scared region, respectively [4]. On the other hand, cardiac CT allows to characterize the anatomy (cavities, myocardium, coronary tree) of the heart with high spatial resolution. CT is specially suitable to extract the access path trough coronary veins in LV lead placement [5]. In both modalities, the ECG signal is used to gate the acquisition. This work focuses on the registration of 3D+t CT and 3D+t cine-CMR sequences in order to place these data in the same coordinate system.

In this context, two main difficulties arise. First, the selection of an appropriate metric to handle the intermodality nature of the images to be registered. Second, the temporal synchronization of both dynamic data must be handled. Indeed, although ECG signals would allow the temporal alignment of CMR and CT acquisitions for a given patient, this is not always possible. One reason is that ECG signals are not always stored and, sometimes, just the time stamps are available. In such a case, since a change in R-R interval may mean a non-linear variation of the ECG, a linear equivalence of time stamps from different acquisitions should not match the same cardiac phases.

To overcome this difficulty, temporal landmarks extracted from a cross-correlation curve can be used in an interpatient 3D+t free-form deformation registration of cine-

CMR short axis view (MR-SA) sequences in [6]. These sequences are also registered in [7] using the concept of "bridging points" to include information from neighboring phases. The latter is extended in [8] where the formulation of "trajectory constraints" (to consistently map the same physical points over time) allows to register CT images of different patients.

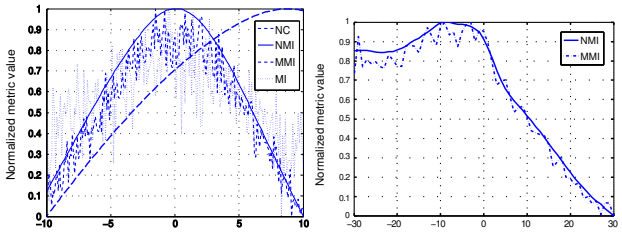
In this work, a segmentation-free registration between cine/LGE CMR sequences and CT images is presented, aiming to include tissue and dynamic information to the framework. Different CMR to CT iconic registration approaches were analyzed in two steps: (i) metrics study and, (ii) rigid registration process. Rigid registration was selected because input images came from the same patient before the implantation of the CRT device. In (i), four classical similarity metrics were evaluated and the best was incorporated to the registration process. In (ii), two rigid registration approaches were developed and evaluated: one static and one dynamic relying on a temporal matching based on the DTW method. The remainder of this paper presents the methods and results for the metrics study and registration process steps.

2. Metrics study

The goal of this study is the selection of the most appropriate metric to perform the rigid registration between MR-SA and CT sequences. Then mutual information (MI), Mattes mutual information (MMI), normalized mutual information (NMI) and normalized correlation (NC) similarity metrics were studied in terms of smoothness and location of the optimum. A reference transformation obtained from segmentations of the LV on both modalities was applied to the MR-SA image before the study.

The end-diastole MR-SA (MR_{ED}) and the R-peak volume of the CT sequence (CT_0) were used in the study. The reference transform was obtained by aligning the centroids of LV in both images. For MR-SA, the delineation of the inner contour of LV for the end-diastole phase was used. For CT, an automatic segmentation process was used to extract the LV [2, 9]. The orientations of MR-SA and CT sequences were considered to be consistent. So, the alignment corresponds to an estimation of the optimal registration between MR_{ED} and CT_0; therefore, the optimum value for the appropriate metric must be close. CT_0 and the translated MR_{ED} were used to compute the metrics curves and perform their evaluation.

In order to evaluate metrics smoothness and optimum localization, the curves were first studied according to translation (along X, Y and Z axes with a step of 0.5 mm) and then to rotation around the great axis (from $\pm 30°$ with a step of $0.5°$).



(a) Translation along X (in mm). (b) Rotation around GA (in °).

Figure 1. Normalized metrics profiles: 1(a) NC, NMI, MMI and MI curves using a translation along X axis (Y=0, Z=0); 1(b) NMI and MMI curves for the rotation test.

2.1. Results

The evolution of each metric for a translation along the X axis is shown in Figure 1(a). It can be noted that MI metrics perform better in terms of location of the optimum. Among them, NMI and MMI are the two smoother. Figure 1(b) shows the evolution of these two metrics for different rotations around the great axis computed from the translated MR_{ED} image. From Figures 1(a) and 1(b) it can be noted that NMI is the best metric in terms of location of the optimum and smoothness. Then, NMI metric was selected in the metrics study to be incorporated in the rigid registration process.

3. Rigid registration process

After metrics analysis, NMI was included in the intensity-based registration process. In the registration process no segmentation was used. Though the end-diastole phase is known for MR-SA sequences, two approaches were evaluated given the dynamic nature of MR and CT acquisitions: a 3D registration approach where MR_{ED} is registered to CT_0 and a 3D+t registration approach where the 3D registration of MR-SA to CT sequences is performed after their temporal alignment using the DTW method [10].

3.1. End-diastole registration

The rigid registration between MR_{ED} and CT_0 was performed by computing the parameters $\boldsymbol{\omega}_{op} \in \mathbb{R}^6$ of a rigid transform $T_{op}(\bullet)$, such that a cost function $\mathcal{C}$ is minimized:

$$\boldsymbol{\omega}_{op} = \underset{\boldsymbol{\omega} \in \mathbb{R}^6}{\arg\min}\ \mathcal{C}\left(T(MR_{ED}), CT_0\right) \qquad (1)$$

with $\boldsymbol{\omega}_{op} = [\mathbf{t}_{op}, \boldsymbol{\theta}_{op}]^\top$ composed by a translation and a rotation vector (3D Euler transform), $\boldsymbol{\omega}$ the parameters of $T(\bullet)$ and $\mathcal{C}(\bullet, \bullet) = -NMI(\bullet, \bullet)$ the NMI metric.

A multi-resolution registration approach was used to obtain the optimal transformation between MR_{ED} and CT_0.

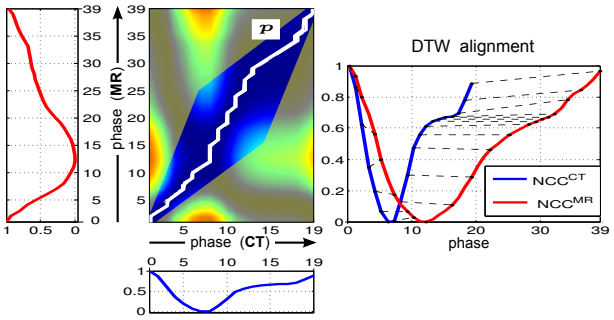


Figure 2. DTW using NCC curves for patient 01 (masked region appears shadowed). p is the warping time function between **MR** and **CT** images. At right the correspondences between $NCC^{\mathbf{MR}}$ and $NCC^{\mathbf{CT}}$ are shown.

$\mathcal{C}(\bullet,\bullet)$ in (1) was optimized using the regular gradient descent method (0.001 and 0.5 the minimum and maximum step lengths, respectively). Also, a 3D Euler transform (initialized in such a way that the geometrical centers of MR_{ED} and CT_0 bounding boxes match) and a B-spline interpolator (order=1 during iterations, order=3 at final iteration) were used. The library elastix was used to implement the registration process [11]. The evaluation of the MR_{ED} to CT_0 registration is presented in Section 3.3.1.

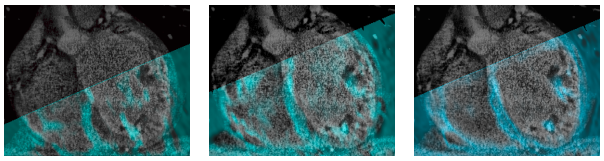
3.2. Registration after DTW alignment

We propose the use of DTW method to perform the temporal alignment of CT and MR acquisitions. DTW allows the measurement of similarity between two sequences varying in time and was depicted in [10]. It is advantageous because temporal interpolation is not needed. The only requirement to use DTW is that both image acquisitions must share the same gating considerations. For cine-CMR and CT sequences this means that their first and last phases are equivalent.

To perform the temporal alignment using the DTW method, the normalized correlation curve (NCC) was computed for each sequence. It has been demonstrated that correlation curves allows to obtain temporal landmarks (phases) for MR-SA sequences [6]. Let $\mathbf{MR} = \{MR_0, MR_1, .., MR_{N-1}\}$ be the set of images in the MR-SA sequence acquired at times $\mathbf{t^{MR}} = \{t_0^{\mathbf{MR}}, ..., t_{N-1}^{\mathbf{MR}}\}$ (the subindex n indicates the phase being $n = 0$ the index at the peak of the R-wave). Similarly, let $\mathbf{CT} = \{CT_0, CT_1, .., CT_{M-1}\}$ be the set of images in the CT sequence acquired at times $\mathbf{t^{CT}} = \{t_0^{\mathbf{CT}}, ..., t_{M-1}^{\mathbf{CT}}\}$. The NCC curve for a sequence $\mathbf{A}$ is given by:

$$NCC^{\mathbf{A}}\left(t_i^{\mathbf{A}}\right) = NC\left(A_0, A_i\right) \tag{2}$$

with $NC(A_0, A_i)$ the normalized correlation between A_0 and A_i. For the MR-SA sequence $\mathbf{A} = \mathbf{MR}$, $t_i^{\mathbf{A}} = t_i^{\mathbf{MR}} \in \mathbf{t^{MR}}$. The same stands for CT if $\mathbf{A}$ is substituted by $\mathbf{CT}$.



(a) MR_{ED} to CT_0. (b) DTW registration. (c) LGE-MRI by DTW.

Figure 3. Superposition of CT (gray) and inverse MR (cyan) images after registration (same patient, coronal view). 3(a) MR_{ED} to CT_0 registration, 3(b) MR_{ED} and $CT_{p(ED)}$ after DTW registration and, 3(c) LGE-CMRI after applying the output transform from DTW registration.

$\mathrm{NCC}^{\mathbf{MR}}$ and $\mathrm{NCC}^{\mathbf{CT}}$ (Figure 2) were used as the query and template sequences in the DTW method, respectively. The output of the DTW is a warping time function denoted by p, which provides the temporal correspondences between the template and the query sequences [10]. We denote the computation of p by the DTW procedure, as:

$$p = DTW(\mathrm{NCC}^{\mathbf{CT}}, \mathrm{NCC}^{\mathbf{MR}}) \tag{3}$$

The warping path function allows to obtain a one-to-one temporal correspondence between the MR-SA and CT sequences. Its computation was constrained using a mask like the one in Figure 2. Therefore, a rigid transform $T(\bullet)$ can be computed after the temporal alignment using a 3D multi-image registration procedure [11]. To do so, the cost function in (1) is replaced by:

$$\mathcal{C}(\mathbf{MR}, \mathbf{CT}) = \frac{1}{M}\sum_{m=0}^{M-1}\mathcal{C}(T(MR_{p(m)}), CT_m) \tag{4}$$

with $p(m)$ the corresponding phase in **MR** for the phase m in **CT**. The best multi-resolution test from the end-diastole registration (Section 3.3.1) was used and, except for the computation of $\mathcal{C}(\bullet,\bullet)$, the same registration framework was employed (Section 3.1). The evaluation of the DTW registration is presented in Section 3.3.2.

3.3. Results for the registration process

Real data of five patients were used to test the two approaches. MR-SA sequences have 30 phases for two patients and 40 phases for the others. CT acquisitions have 10 phases for two patients and 20 phases for the others. The resulting registrations were visually validated by comparing the position of mitral valve (when included in the field of view) and of papillary muscles. To perform a quantitative evaluation, the alignment obtained after the centroid matching in the metrics study (Section 2) was used as a

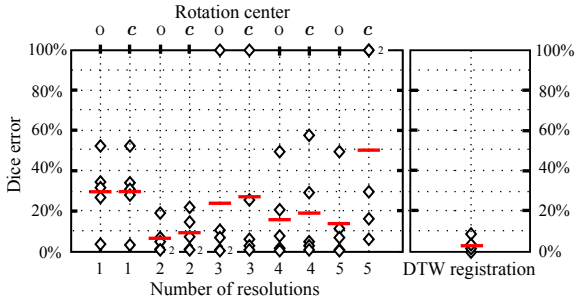


Figure 4. Dice evaluation (◇: patients, —: mean values). An error of 100% means a complete misalignment. Left, dice error for ED registration (o: CT_0 origin, c: centroid of the LV for CT_0). Right, dice error for DTW registration.

reference registration. The considered quantitative indicator is the percentage error between the dice score obtained after LV centroid matching (reference dice) and the dice score obtained after the rigid registration.

3.3.1. 3D registration of MR_{ED} and CT_0

One to five levels of resolution were evaluated in the multi-resolution approach, using a recursive half-size subsampling and linear interpolation. Besides, two centers of rotation were assessed: the origin of CT_0 (o) and the centroid of the LV segmentation on CT_0 (c). A total of 10 tests were performed for each patient. The dice evaluation is shown at Figure 4 (left). The best result was obtained for two resolutions and the origin of CT_0 as center of rotation (mean=4.71%, std=4.58%). The result for the worst case is shown at Figure 3(a). It can be noted that there is a bad alignment of papillary muscles and inter-ventricular septum.

3.3.2. Registration after DTW alignment

Figure 4 shows the evaluation for the DTW approach. It can be noted that it performs better than ED registration (mean=2.68%, std = 2.76%). This is in agreement with Figure 3(b) where it could be noted an improvement in the alignment of both the papillary muscles and the inter-ventricular septum. These mean that the DTW method has the ability to perform the temporal alignment of CT and MR-SA sequences.

Finally, Figure 3(c) shows an example of registration of the LGE sequence using the output transform from MR-SA to CT registration after DTW. It can be noted a good alignment between CT and LGE-CMR images.

4. Conclusion and perspectives

It was demonstrated that an iconic 3D rigid registration can be used to align cardiac 3D+t MR and 3D+t CT sequences in order to add tissue information coming from LGE-CMRI. Besides, quantitative performance suggests that DTW is an appropriate method to align the sequences in time without the need of temporal interpolation.

Future work should focus on the definition of a quantitative evaluation approach of the spatio-temporal registration. Also, the scar quantified from LGE sequences should be incorporated to the framework in order to optimize CRT.

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