4D Cardiac Volume Reconstruction from Free-Breathing 2D Real-Time Image Acquisitions using Iterative Motion Correction

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Abstract

For diagnosis, treatment and study of various cardiac diseases directly affecting the functionality and morphology of the heart, physicians rely more and more on MR imaging techniques. MRI has good tissue contrast and can achieve high spatial and temporal resolutions. However it requires a relatively long time to obtain enough data to reconstruct useful images. Additionally, when imaging the heart, the occurring motions - breathing and heart beat - have to be taken into account. While the cardiac motion still has to be correctly seen to asses functionality, the respiratory motion has to be removed to avoid serious motion artefacts.

We present initial results for a reconstruction pipeline that takes multiple stacks of 2D slices, calculates the occurring deformations for both cardiac and respiratory motions and reconstructs a coherent 4D volume of the beating heart. The 2D slices are acquired during free-breathing over the whole respiratory cycle, using a fast real-time technique. For motion estimation two different transformation models were used. A cyclic 4D B-spline free-form deformation model for the cardiac motion and a 1D B-spline affine model for the respiratory motion. Both transformations and the common reference frame needed for the registration are optimized in an interleaved, iterative scheme.

1998 ACM Subject Classification I.4.5 Transform methods

Keywords and phrases MRI, Cardiac, Registration

Digital Object Identifier 10.4230/OASIcs.ICCSW.2012.69

1 Introduction

Physicians are relying more and more on non-invasive imaging techniques to assess the functionality and morphology of the heart. In present practice echocardiography is still the standard, due to higher availability, lower costs and shorter acquisition and analysis times. But with increasing technical advances, both in acquisition hardware and image reconstruction and processing algorithms, MR imaging is becoming the favoured modality. MRI takes advantage of the magnetic properties of tissue, explicitly the signal response of hydrogen, which can be found in abundance in the whole human body, as it is mainly made out of water. During examination, the patient is placed inside a strong magnetic field, which aligns the otherwise unoriented nuclear spins of the nuclei. Gradient coils then spatially encode the signal produced by a radiofrequency exitation pulse, allowing the system

2012 Imperial College Computing Student Workshop (ICCSW'12).
Editor: Andrew V. Jones; pp. 69–74

OpenAccess Series in Informatics
Schloss Dagstuhl – Leibniz-Zentrum für Informatik, Dagstuhl Publishing, Germany

to gradually fill the so called K-space [6], which is a representation of the image in the Fourier domain. This raw signal can be Fourier transformed into an image, showing for example one slice of the human body or even a whole volume, depending on the setting. But the system has to wait for the tissue to reach a steady state again before continuing with the acquisition of the next spatial position. This can make MR imaging rather slow and prone to inconsistencies in the data, due to motion between acquisition steps, either in between different parts of K-space (results in blurring artifacts) or between slices (results in an inconsistent image volume). Especially imaging the beating heart, also moving due to respiration, poses a challenging problem, both from the acquisitional and reconstructional point of view.

Common methods as described in the literature to deal with this problem can be divided into two categories. The straight forward method requires the subject to hold its breath for about 20s. This produces very good results, but is not always feasible, as patients with heart problems are often not able to hold their breath long enough. Other ways to deal with respiratory motion rely on so called gating techniques [2]. They use some kind of surrogate signal (e.g. chest bellows or 1D pencil beam monitoring the diaphragm motion) to divide the respiratory cycle into small segments and only use data acquired at specific times (usually end-expiration). The problem with this approach is that it assumes that the breathing pattern is always the same, which of course is not the case (chest vs. abdominal breathing), resulting in minor motion artifacts. And the data from all other time points is either thrown away or not acquired at all, resulting in a much prolonged scanning time. In both cases the cardiac motion is usually dealt with by using the ECG signal to divide the cardiac cycle into small, near motion-free intervals and gradually filling the K-space of those time frames over a couple of heart beats [1].

We propose to use fast real-time imaging techniques to acquire individually motion-free slices [7], covering the heart volume in dense spatial and temporal positions. Those slices will be corrected for respiratory motion, with respect to a chosen reference breathing position and combined afterwards to form a complete 4D cardiac volume. To be able to register all images, we also have to estimate the cardiac motion towards a reference time point in the cardiac cycle. We model the cardiac motion by cyclic 4D B-Splines and choose an affine model for the respiratory motion.

2 Methods

The acquisition train is as follows: The scanner acquires 2D slices of the heart at a fixed spatial position using real-time techniques. To avoid gaps in the volume, due to translational motion, the respective slice is scanned over multiple heart beats (approximately one breathing cycle). After scanning one spatial position, we move to the next adjacent one. This scheme is necessary, as real-time techniques take some time to build up (to reach steady state). Thus the first couple of images are of inferior image quality and essentially useless for reconstruction. For further accelerate the individual slice acquisitions, we apply multiple receiver coils (SENSE) [8] and half-Fourier reconstruction.

We want to find a 3-dimensional reference volume $I_{0,0}$ and a time-dependent transformation $T_{k_i,l}$ that warps the 2-dimensional observed real-time images $I_{k_i,l}$ to locally fit this reference image. In the setting of free-breathing, cardiac cine MRI, we differentiate between two occurring motions, which we assume to be independent.

The first is the approximately periodic, non-rigid deformation of the heart T_{Φ^c} due to its self-induced contraction and following relaxation. We use a multi-level 4D cubic B-Spline

model [5] defined on a mesh of control points, where Φ^c is the vector of deformations in (x, y, z)-direction for all control points:

$$FFD(x, y, z, t) = \sum_{o=0}^{3}\sum_{l=0}^{3}\sum_{m=0}^{3}\sum_{n=0}^{3} B_o(\tau)B_l(u)B_m(v)B_n(w)\Phi^c_{i+l,j+m,k+n,h+o} \tag{1}$$

Note that actually Φ^c also contains a fourth component for the time, which is also modeled by B-splines. But since we assume the time points of the slices, denoted by the index $k_i \in [0, 1]$ with the corresponding cardiac cycle given by $i \in \{0, ..., N_k\}$ to be known (as taken from the ECG), an optimization for these parameters is not necessary. Since we continuously acquire one slice for every time point during one cardiac cycle and then jump to the next slice position, we have to assume that the cardiac movement of the heart is identical over all heart beats, aside from differences in their duration. To enforce periodicity we simply change the neighborhood definition for the B-Splines, effectively forcing the last to be equal to the first temporal control point.

The second transformation is the temporally smooth and approximately affine motion $T^l_{\Phi^r}$ induced by breathing. Φ^r is the vector of the 12 degrees of freedom, namely translation, rotation, scale and screw for all coordinates (x, y, z) respectively, and the index l denotes the real time points in the acquisition starting with $l = 0$ for the first slice. With the use of a navigator l can also be mapped into a smaller 1D or 2D space according to the momentary breathing state. Although the respiratory motion includes some small, local, free-form deformation, an affine model defined in a bounding box around the heart is a close enough approximation to start with [4]. We will try to incorporate a non-rigid motion model for the breathing motion at a later stage, using the periodicity of the cardiac motion to separate both simultaneously occurring motions.

To solve for the different degrees of freedom given by $I_{0,0}$, T_{Φ^c} and $T_{\Phi^r_l}$ we use an iterative scheme that minimizes the following cost function:

$$(I_{0,0}, \{\Phi^c\}, \{\Phi^r\}) = \underset{I_{0,0},\{\Phi^c\},\{\Phi^r\}}{\operatorname{argmin}} C(\{I_{k_i,l}\}, I_{0,0}, \{\Phi^c\}, \{\Phi^r\}) \tag{2}$$

where

$$\begin{aligned} &C(I_{k_i,l}, I_{0,0}, \{\Phi^c\}, \{\Phi^r\}) = \\ &C_{data}(\{I_{k_i,l}\}, I_{0,0}, \{\Phi^c\}, \{\Phi^r\}) + \lambda_0 C_{img}(I_{0,0}) + \lambda_1 C_{card}(\{\Phi^c\}) + \lambda_2 C_{resp}(\{\Phi^r\}) \end{aligned} \tag{3}$$

The first term is a similarity criterion between the transformed reference volume and the observed, 2D slices. We chose the sum of squared differences (SSD) measure, since we are dealing with monomodal data and we can assume that the image intensities stay constant during motion:

$$C_{data}(\{I_{k_i,l}\}, I_{0,0}, \{\Phi^c\}, \{\Phi^r\}) = \frac{1}{|\mathcal{L}||\Omega|}\sum_{\{l\}}\sum_{\mathbf{x}\in\Omega_l}(I_{k_i,l}(T_{\Phi^c}(T_{\Phi^r}(\mathbf{x}, l), k_i)) - I_{0,0}(\mathbf{x}))^2 \tag{4}$$

where Ω_l is the 2D domain of the current slice in the 3-dimensional volume Ω and $|\mathcal{L}|$ and $|\Omega|$ are the amounts of temporal and spatial voxel coordinates respectively.

The second term in (3) is an optional regularization term for the reference image, that can be used in a super-resolution framework. For example an image gradient magnitude operator in an l_2-norm would be appropriate if the number of acquired slices is small, thus resulting in an underdetermined super-resolution volume reconstruction problem. It penalizes the high-frequency components in the estimated image.

The last two cost terms regularize the two occurring motions. The periodic B-spline description of the cardiac motion directly enforces spatial and temporal smoothness. Whether it is necessary to apply some regularization, for example enforcing diffeomorphic transformations or an incompressability constraint of the myocardium has yet too be determined.
For the respiratory motion we introduce a temporal smoothness penalty that ensures a slow and smooth evolution of the motion parameters, starting from an identity transformation for $l = 0$:

$$C_{resp}(\{\Phi^r\}) = \sum_{\{i\}} d\Phi^r_{l_i,l_{i+1}} ||\Phi^c_l - \Phi^r_{l+1}||^2_2 \tag{5}$$

where $d\Phi^r_{l_i,l_{i+1}} = \frac{1}{l_{i+1}-l_i}$ is a temporal normalization and i the set of indices of all ls. This is necessary as the temporal offsets between the acquisition of two slices are not always uniform, because in real-time imaging changing the slice position costs some time for the excitation to reach steady-state again. So if the temporal distance is big, the confidence in the solution is small and $d\Phi^r_{l_i,l_{i+1}}$ reduces the weight of the corresponding term.
In the above cost terms λ_0, λ_1 and λ_2 are regularization parameters, weighting the relative contributions of the corresponding terms. The parameters are chosen experimentally.

The iterative scheme to solve the least square problem (2) starts with an initial estimate of $I_{0,0}$ and Φ^r and alternates between optimizing the 3 different sets of parameters:

Step 1: $(\{\hat{\Phi}^c_{(n+1)}\}, \{\hat{\Phi}^r_{(n+1)}\}) = \underset{\{\Phi^c\},\{\Phi^r\}}{\operatorname{argmin}} C(\{I_{k_i,r}\}, I^{(n)}_{0,0}, \{\Phi^c\}, \{\Phi^r\})$

Step 2: Calculate new $I^{(n+1)}_{0,0}$ using Scattered Data Interpolation

Step 3: Check for stop criterion and if not full-filled increment n and go to Step 1

where the stop criterion is $||C^{(n+1)} - C^{(n)}|| < \epsilon$ with an empirically chosen ϵ (usually $\epsilon = 0.0001$).

To be able to capture larger deformations, the data is first divided into spatially and with regard to the cardiac phase temporally continuous blocks/volumes. In subsequent iterations, these blocks are partitioned into ever smaller blocks. This makes the algorithm much more robust and we are also able to blur the images in the through-plane direction, which is necessary to calculate large deformations in that direction. Additionally the image resolution starts with a larger one and is gradually decreased to its original setting, while the images are at the same time blurred with a Gaussian in all possible directions.

3 Results

So far we evaluated the performance of the algorithm without respiratory motion. Two data sets were used. Both are cardiac and respiratory gated. The first one is a 3D cine of the heart with resolution 1.25x1.25x2mm (fig. 1) and the second was acquired with real-time techniques depicting the volume by 14 adjacent slices with a resolution of 1.25x1.25x8mm (fig. 2). Fig. 2 shows the heart in end-systole from different orthogonal views. Due to the large slice thickness in Fig. 1 we have chosen here only one view (short-axis) at different positions in the volume also in end-systole. The end-systole time point was chosen because it has the largest deformations with regard to the reference time point. Although both volumes have a lot of tissue moving in and out of the field of view, the proposed registration method manages to capture the deformations of important structures like the myocardium which will be important for estimating the respiratory motion. This can be seen when comparing the yellow isolines (taken from the ground truth image) with the edges of e.g. the

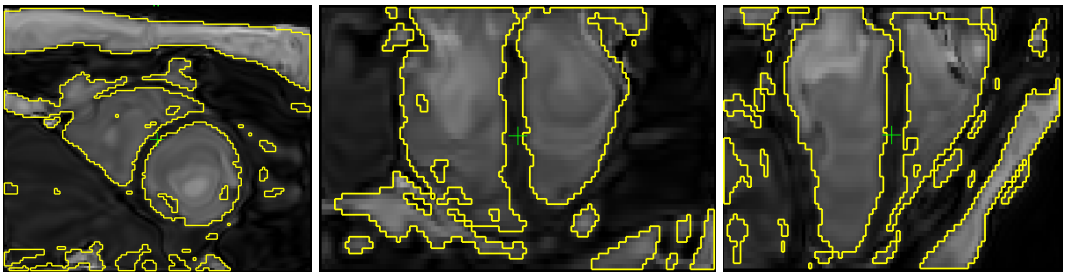

Figure 1 Registration result as tested on a 3D cine of the heart with resolution 1.25x1.25x2mm. From left to right: short-axis and 2 orthogonal long-axis views, all at end-systole. The yellow lines show the isolines of the ground truth.

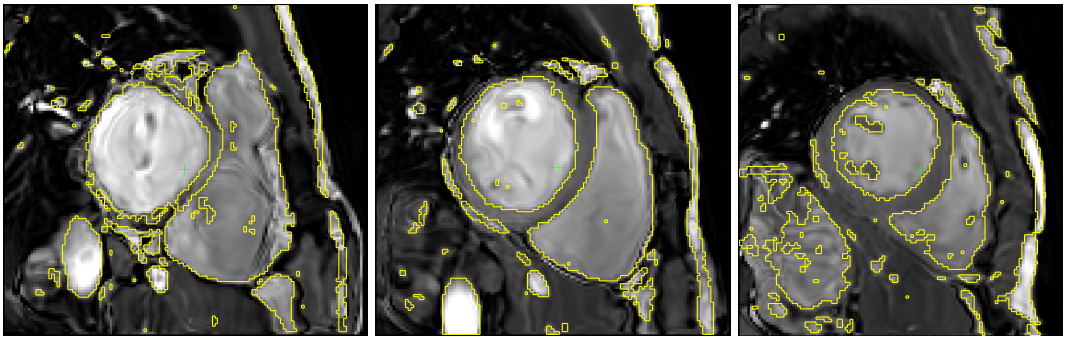

Figure 2 Registration result as tested on a stack of real-time images of the heart with resolution 1.25x1.25x8mm. Images were taken at different spatial positions of the volume, all at end-systole. The yellow lines show the isolines of the ground truth.

blood pool (lighter regions). When acquiring slices in the proposed way the sampling in the through-plane direction will be much denser, which will make it easier to accurately capture also the through-plane deformations.

4 Conclusion

The results show that the proposed method is able to accurately estimate the cardiac motion induced deformations. And it is robust towards through-plane motion and tissue moving in and out of the field of view, which is important for 2D to 3D registration. Jiang et al. [3] showed, for a similar problem the successful registration of 2D slices towards a successively updated reference frame using a linear transformation model. Based on those results, we are confident that we will be able to use the proposed iterative motion estimation scheme to estimate and correct for the respiratory motion.

Future work includes the successful computation of the affine transformation, tested with an example respiratory motion model applied on a common cardiac cine sequence and with real free-breathing data. And we want to incorporate super-resolution techniques into the framework to improve spatial and temporal resolution.

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