Automated Breathing Motion Correction in First-Pass Myocardial Perfusion MRI

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Introduction

First-pass myocardial perfusion MRI offers a validated non-invasive alternative to emission tomography techniques (SPECT/PET) for the assessment of myocardial perfusion. However, many imaging protocols consist of a breath hold followed by a series of shallow breathing phases. This can lead to the acquisition of images with a varying diaphragm position and thus a varying heart position within the image, hampering the extraction of regional perfusion curves. The goal of this work was to develop 1) an unsupervised method to identify and locate perfusion events in the image sequence and 2) a fully automatic algorithm for registration of perfusion data that is robust against the large contrast variations during bolus passage, and does not require manual interaction or ROI definition.

Methods

Our approach aims at separating the different sources of contrast variations to automatically distinguish breathing-induced variabilities from perfusion events by applying Independent Component Analysis (ICA) with a small number (3) of components to the perfusion sequence. This yields 1)a set of feature images that denote the main events separated in time and space, and 2)feature weighting functions that show a similar shape to the one expected for time-intensity curves for corresponding regions of interest (see Figure 1).

The characteristic form of these components and weighting functions enables the automatic identification of the RV, LV and myocardial bolus arrival and the LV ROI. Based on the feature images and the weighting curves, registration is performed as follows (Figure 2). For each frame, a reference image is computed, which is a linear combination of ICA feature images weighted by the corresponding weighting coefficients. Its features present similar intensity values as the original image to be matched against. It is computed over the ROI, which is displaced over a displacement range in both x and y directions to obtain a cost matrix M(x,y). The maximum value of this cost matrix provides the optimal displacement that is used to correct the input dataset for that frame.

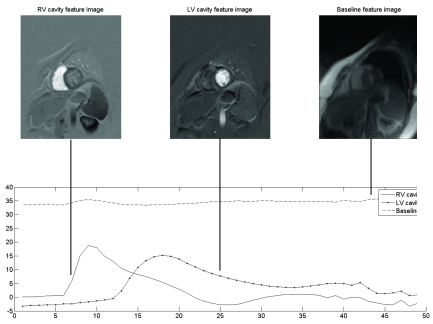

Figure 1

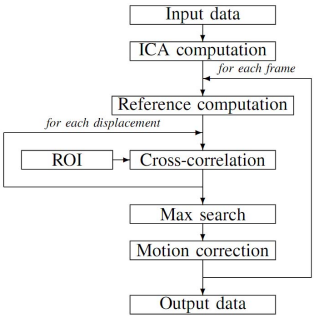

Figure 2

The registration approach in Figure 2 is traversed in a multi-resolution scheme where two successive 5×5 search spaces are explored, one after sub-sampling by a factor 2 in each spatial dimension and the other at full resolution. Computing time to register a 50 frame sequence amounts to 1 min.

Experimental setup

The unsupervised registration was tested on 46 datasets from 35 subjects in the MESA study [1]. Three slices were acquired in a short-axis orientation (in-plane resolution: 1.37×1.37 mm2, slice thickness: 8 mm, slice gap: 8 mm, breath-hold between 12 to 18 seconds). A Gadolinium-DTPA bolus (0.04 mmol per kg of body weight) was injected, starting at the third or fourth heartbeat, followed by a saline flush of 10 ml. For comparison, endocardial and epicardial contours were traced on a reference frame and adjusted to each frame constituting the sequence. Registration results were evaluated on: 1) LV center motion before and after registration and 2) perfusion curves before and after registration compared to perfusion curves derived from the manual contours

Results and discussion

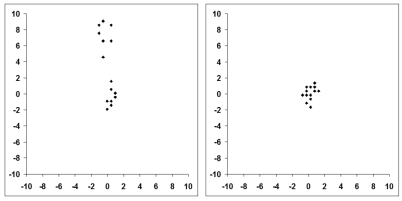

Figure 3

	Mean	SD	Median	Min	Max
Original	1.26	0.87	1.15	0	5.36
Registered	0.64	0.46	0.49	0	2.36

Table 1

		Mean	SD	Median	Min	Max
R^2	Original	0.88	0.16	0.97	0.19	1
	Registered	0.92	0.10	0.98	0.50	1
Average NMSE	Original	2.65	7.89	0.05	0	48.58
	Registered	0.87	3.88	0.03	0	34.05
$\sigma_{x,t}$	Original	2.33	2.30	1.52	0.28	12.42
	Registered	1.31	1.14	1.04	0.30	7.80

Table 2

Figure 3 gives a typical example of LV center motion before (left pane) and after registration (right pane) w.r.t. the average LV center position throughout the whole perfusion sequence in pixels. This clearly demonstrates the reduction in motion amplitude. Table 1 shows an approximate 50 % decrease of all LV center motion indicators due to the registration. Compared to uncorrected data, Table 2 shows a markedly improved correlation for the perfusion curves from the registered datasets with the manual contours, along with a strongly reduced NMSE. Obtained results demonstrate: 1) a high robustness of the method, 2) a substantial reduction in LV center motion after registration, with an average motion of 0.64 ± 0.46 pixel, 3) an increase in the percentage of studies with a motion below 1 pixel from 32% before to 88% after registration and 4) a substantial improvement due to registration of the correlation and NMSE of perfusion curves compared to manually derived perfusion curves. We conclude that this fully automatic ICA-based registration shows an excellent accuracy, robustness and computation speed, adequate for use in a clinical environment.

References [1] D. E. Bild, e.a., "American Journal of Epidemiology, vol. 156, no. 9, pp. 871–881, 2002.