Model Based Automated 4D Analysis for Real-Time Free-Breathing Cardiac MRI

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Background. Cardiac Magnetic Resonance Imaging (CMR) has advanced to provide morphological and functional information even in the presence of variations in cardiac cycle length or for patients having difficulty to hold their breath [5]. Fast and accurate assessment of cardiac function requires precise localization of the structure of interest while taking into account any potential source of error from the image acquisition. Simultaneously, increasing availability of medical imaging databases and advances in machine learning techniques make possible to automatically estimate the cardiac models parameters from the imaging data using discriminative learning methods. We propose to exploit recent advances in automatically fitting a parameterized 4D cardiac model to volumetric imaging data to simultaneously correct for spatial slice misalignment and quantify the morphological and dynamical information for both left (LV) Fig. 1 Left and right ventricles model and right (RV) ventricles from CMR. We show that our method can be applied to both



standard breath-hold short axis SSFP stacks as well as to a recent real-time free-breathing protocol (RTFB) [5].

Methods. For both SSFP and RTFB images (see [5] for detailed protocol), a pseudo 3D volume sequence is initially reconstructed according to the MR physical coordinates. Next, given a database of aligned stacks with expert delineations of the chambers we train a series of detectors that are able to estimate the model parameters relative to imaging data. The standard model parameters are heart pose (translation, rotation and scale) and boundary location to which we add the global position of each slice. We estimate heart pose and boundary including dynamics as described in [1, 2, 3]. Intuitively, during the training phase, we learn prior knowledge of the cardiac anatomy from the database and embed it into a detailed parametric 4D models of the LV and RV where key physiological landmarks are specifically encoded (Fig. 1) [2]. For the position of each slice we estimate the translation using global image information under a heart shape constraint given by the 4D model to preserve the curvature of the heart. Therefore we simultaneously solve for inter-slice mis-alignment and estimate an accurate, patient-specific 4D heart model. The outline of the algorithm is as follows: 1. Automatic estimation of 3D model from cine MRI stack [3] (method relies on shape priors robust to misalignment); 2. Determine the myocardium region from 2D model intersection and perform inter-slice registration using a diffeomorphic symmetry-consistent image registration algorithm [4]. 3. Update slice translation only using the myocardium region and re-construct the pseudo-volume. Recursively iterate the process.

Results and discussion. We have applied the automated 4D MR analysis to an initial set of 10 patients with data acquired using the improved radial GRAPPA method for real-time free-breathing acquisitions [5]. The model was trained off-line on a regular breath-hold set of 100 volumes (from 70 patients) with a cross-validated error of 2.9±4.8mm for the endocardium. An example of the slice re-aligning result is illustrated in Fig. 2 along with a

typical result of fitting the 4D model. Automated analysis was possible on all cases and for 5 patients we compared the results with acquisitions under regular breath-hold protocol (Table 1). Average error for ejection-fraction (EF) is $3.44\pm4.1\%$, ED volume is -0.4 ± 2.2 ml and ES volume is 5.3±5ml which are well within the accepted clinical variability.



Fig. 2 Pseudo 3D volume based on physical coordinates (a) and aligned based on model (b). Typical 4D model fit (c).

	Breath-hold			Free-breathing		
	EF(%)	EDV(ml)	ESV(ml)	EF(%)	EDV(ml)	ESV(ml)
P1	58.33	168.08	70.03	54.42	168.15	76.64
P2	48.36	131.09	67.69	52.05	133.92	64.22
P3	59.57	129.69	52.43	53.63	128.21	59.45
P4	58.54	147.85	61.3	53.3	150.39	70.24
P5	57.56	144.71	61.42	51.75	142.84	68.93

Conclusion. We have shown that using a model based approach it is feasible to reduce the slice alignment artifacts while providing a quantitative assessment of both LV and RV. Next step will consist to extend the proposed approach to account for inter-slice temporal shifts. Furthermore, it is feasible to perform the automated analysis based on real-time free-breathing sparse acquisition protocol while training our model on standard CMR acquisitions. This suggests a good generalization potential to be adapted to specific acquisition protocols.

References. [1] Georgescu et al. IEEE CVPR, 2:429, 2005. [2] Zheng et al. IEEE TMI, 27:1668, 2008. [3] Lu et al. FIMH, 250-258, 2011. [4] Guetter et al. ISBI, 590-59, 2011. [5] Seiberlich et al. MRM, 65:492-505, 2011.