A variational approach to image registration in DCE-MRI of human kidney

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Introduction

Dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) is an emerging technique for a more accurate assessment of local renal function [1]. However, the measured time intensity curves used for quantification of renal blood flow or glomerlar filtration rate are hampered by motion artefacts, mainly from respiration of the patient [2]. To correct for such motion, image registration is needed. Here, we analysed the feasibility of a variational approach to image registration in DCE-MRI of the human kidney.

Materials and Methods

5 patients were examined on a 1.5T Siemens Symphony Vision scanner using a 3D VIBE sequence with TR/TE/FA= 3.3 ms/1.76ms/9°. Matrix size was 256x256x22 with spatial resolution of 1.5x1.5x4.0 mm³. A dose of 2ml (0.5 mmol/ml Gadodiamide) of contrast agent was injected after recording the fifth 3D volume. In total 100 volumes were acquired at temporal resolution of 2.8s. Patients were instructed to hold breath as long as possible and then take another breath and repeat the breatholding.

The data sets were registered with an algorithm based on a variational framework proposed by Chefd'Hotel et al. [3]. To align a source image with a reference image, the source image is warped with a displacement field, e.g. a 3 dimensional displacement vector for each voxel. This displacement field maximizes the cross correlation between the two images. For optimization, a gradient descent strategy is used. The displacement field, resulting from each iteration, is multiplied by an exponentially decreasing step factor, smoothed by convolution with an isotropic Gaussian kernel and added to the sum of displacement fields computed in all prior iterations. The algorithm stops when mean values of cross correlation for 10 subsequent iterations cease to increase. For image interpolation, cubic B-splines are used for the final iterations, otherwise linear functions are used.

Evaluation of the registration was performed by compiling checkerboards for visual inspection, measuring the vertical displacement of an anatomical reference point as in [4], and fitting a 2 compartment model [5] to a carefully selected region of interest (ROI) in the renal cortex.

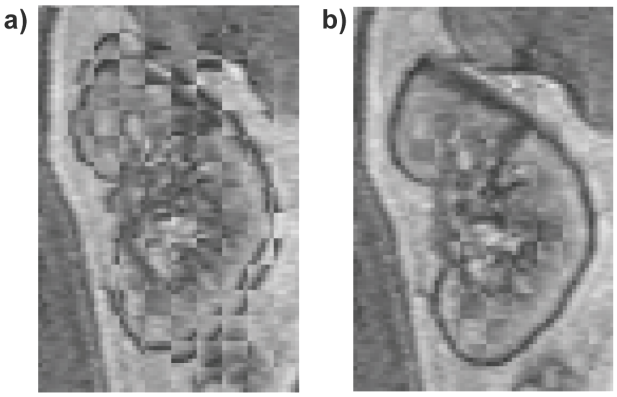

Fig. 1: Checker board images of (a) unregistered and (b) registered kidney.

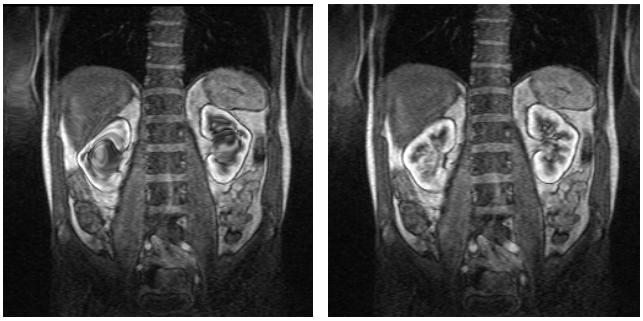

Fig. 2: Influence of the width of the smoothing kernel. Left, σ=14mm, the inner structure of the kidney is distorted. Right, σ=26mm, inner kidney structure not distorted.

Results

Registration was successful for 4 out of the 5 data sets. In one data set, no acceptable alignment could be obtained. Thereby, a smoothing kernel with σ = 14mm to 22mm could reduce the motion to below the in-plane resolution of 1.5mm while maintaining the structure of the kidney (cf. Fig. 2). Measured coronal motion for unregistered data was on average 2.5mm. Figure 1 depicts registration result from one kidney; similar results are achieved for the other 3 patients. The checkerboards clearly show good continuity of the borders of the kidney. Figure 3 depicts results of fitting a 2 compartment model to time intensity curves of a ROI from the kidney. The Akaike fit error is reduced by registration up to 24 % in our data.

Discussion

Registration of kidney perfusion data using our variational approach seems feasible. The cross correlation criteria can suppress breathing motion while not influencing the tracer flow in the images. The width of the smoothing kernel thereby plays and important role: it balances the suppression of motion on the one hand and distortion of the images on the other hand. However, the stability of the estimated optimal values need further testing in a larger set of data.

Fitting a 2 compartment model to the registered data demonstrated that the fit improves, i.e. the Akaike fit error decreases. This suggests that also parameters like renal blood flow or glomerular filtration rate should become more stable; however, this has to be evaluated in a further study. Besides the quality of the tissue signal intensity curves, a good choice of the arterial input function also influences these parameters.

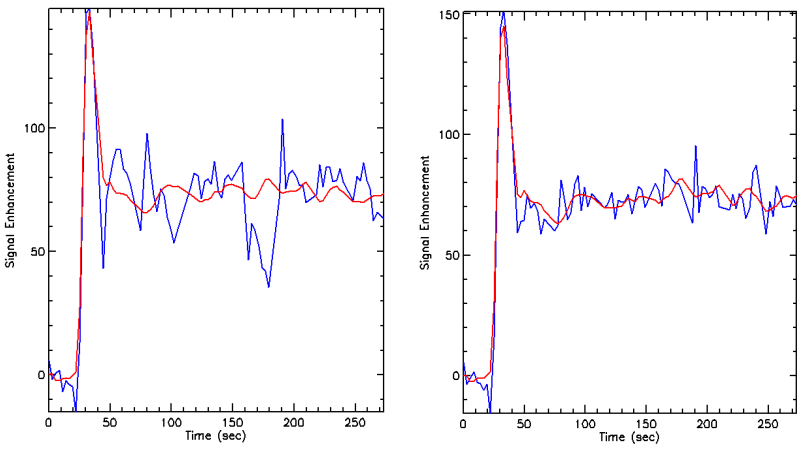

Fig. 3: Fits of a 2 compartment model to ROI of the kidney. Left, data from the unregistered kidney, right after applying our variational approach. Blue lines, mean time intensity curve of ROI, red lines, fit of compartment model.

References

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