Alignment of 3D DCE-MRI Abdominal Series for Optimal Quantification of Kidney Function

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Abstract

The importance of the reliable assessment of the renal perfusion and filtration lies in its impact on the evaluation of the kidney function. However, these dynamic measures are challenging as they have to overcome the movement of the organ of interest due to the respiration and the pulsations of the patient throughout the acquisition.

In this paper we propose an efficient registration algorithm for the motion and deformation compensation in Magnetic Resonance Renography (MRR) studies with 3D Dynamic Contrast Enhanced Magnetic Resonance Imaging (DCE-MRI).

1. Introduction

Renal function traditional indicators such as creatinine or inulin are not sufficiently sensitive, and require multiple blood and urine samples. Among non-invasive alternatives, Magnetic Resonance Renography (MRR) has the potential to identify and locate diseases that affect different regions of the vascular-nephron system, and is a quite promising technique.

Nevertheless, before MRR becomes a clinically viable tool, several challenges must be overcome, as pointed out by Huang et al [1]. On the one hand, since these dynamic studies require the previous administration of the contrast agent substance, it is important to determine the optimum dose to be injected to the patient. On the other hand, quantification of contrast concentration from the measured MRI signal intensity values involves the determination of a complex relationship due to its dependency with the acquisition parameters and the relaxivity of tissues.

Finally, in order to assure that every time-intensity course represents the tracer passage in a fixed anatomical location, supporting the subsequent pharmacokinetic interpretation, spatial alignment of dynamic data is required. We have focused on this last task, developing the registration algorithm described in the following sections.

2. Data and Acquisition

We have worked with Gd-DTPA (gadopentate dimeglumine) enhanced 3D DCE-MRI studies, recorded from healthy volunteers. The use of this Gd quelate is justified since it behaves like inulin and is freely filtered at the glomerulus without tubular secretion or resorption, so that its kinetics can be analyzed to determine physiologic parameters of renal filtration, including the glomerular filtration rate (GFR).

Table 1 summarizes the main acquisition parameters for 4D analyzed data sets, all of them acquired at the Department of Radiology of the University of Bergen (Norway). Two scanners were used: a 1.5 T Siemens Symphony and a 3 T GE Signa Excite.

Table 1: Characterization of the exams subjected to the registration method

Exam	Scanner	Sequence	Spatial Resol. (mm)	Temporal Resolution	Size
1	1.5 T	VIBE	1.48 x 1.48 x 3.0	Non uniform	256x256x20x20
2	1.5 T	VIBE	1.48 x 1.48 x 3.0	2.5 s.	256x256x20x118
3	1.5 T	VIBE	1.48 x 1.48 x 3.0	3.0 s.	256x256x24x80
4	3 T	LAVA	1.37 x 1.37 x 4.0	2.7 s.	256x256x12x64
5	3 T	LAVA	0.86 x 0.86 x 2.4	3.0 s.	512x512x44x60
6	3 T	LAVA	1.72 x 1.72 x 2.4	3.7 s.	256x256x22x60

3. Algorithm description

Numerous registration methods have been attempted to compensate the motion and deformation of the kidneys along DCE-MRI dynamic studies. However, most of them involve manual intervention, temporal and spatial constraints or deal only with 2D images [2, 3]. We have proposed an automated 3D registration algorithm which consists of two steps, as sketched in ***Figure 1***. It has been implemented using the open source software toolkit ***ITK*** (*Insight Segmentation and Registration Toolkit*).

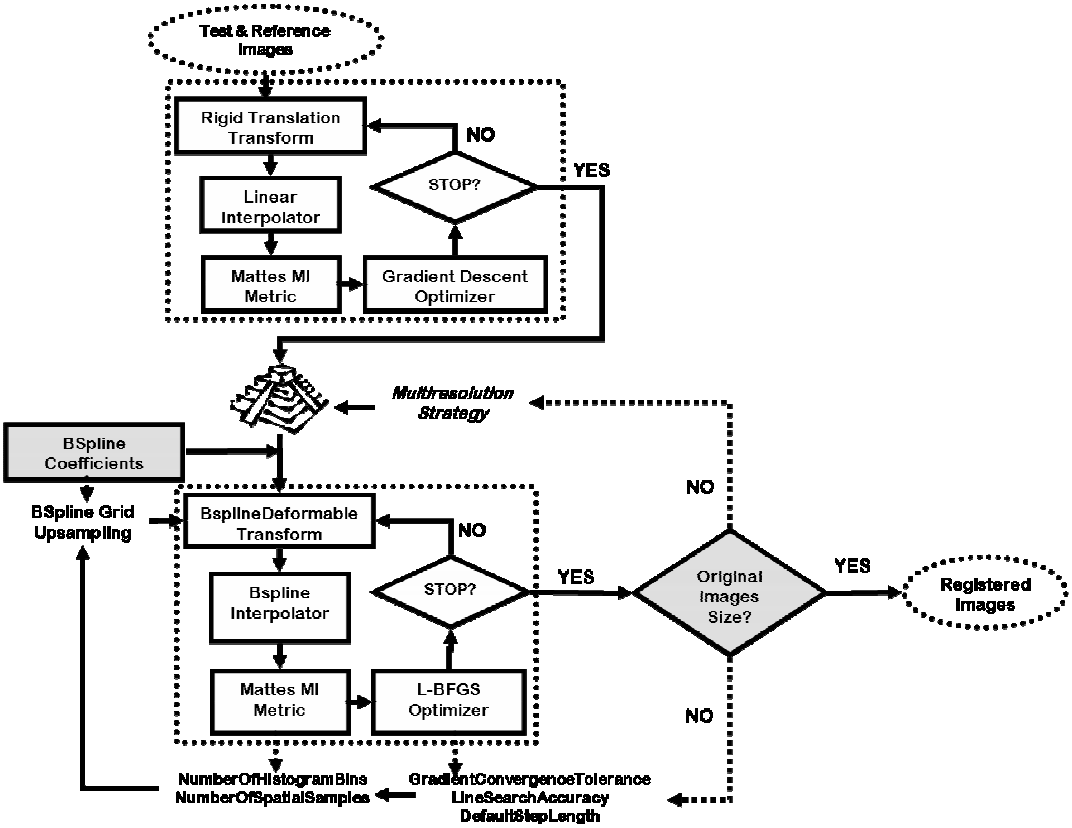

Figure 1: Sketch of the proposed registration algorithm

The large intensity variations caused by the tracer passage lead us to the use of similarity function based on the mutual information (MI), a value based on the statistical information theory which is usually chosen for multi-modality registration. MI measures how much information one random variable (image intensity in one image) tells about another random variable (image intensity in the other image), or how much the knowledge of the first random variable reduces the uncertainty about the second variable, with the advantage that the actual form of the dependency does not need to be specified. Along the whole algorithm, we used the Mattes implementation of this metric, which does not require pre-processing and yields quite a good robustness. The only requirement to determine the MI between two input images is its joint histogram, whose spreading out is clearly reduced along the registration process (***Figure 2***).

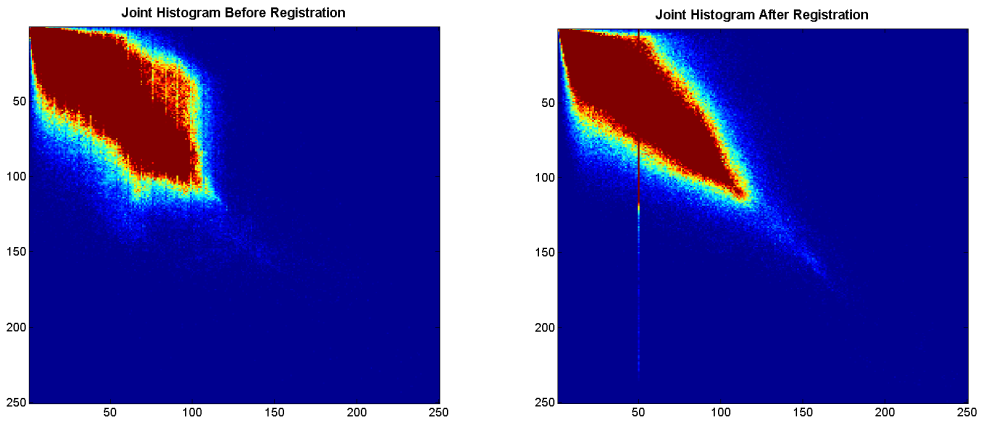

Figure 2: Joint histograms from a pair of images belonging to the exam number 5, before registration (*left*) and after registration (*right*).

As seen in ***Figure 1***, the first step of the global scheme is a simple rigid registration algorithm, where the transformation is defined by a small set of parameters and the optimization is carried out with a regular step implementation of the common gradient descent method. In this way, the main head-to-feet organ displacement tendency (due to the diaphragm movement) is quickly and easily corrected. This intermediate result is later used to initialize the second (non-rigid) step.

The second step is a non-rigid registration algorithm, where the transformation is defined by a deformation model based on a grid of control points described by B-splines basis functions, and the optimization is carried out by a quasi-Newton BFGS optimizer, as described in [4, 5]. In order to reduce the computation time and increase the robustness of this step, we used a multiresolution strategy in which the upsampling is applied simultaneously on the input images (size and resolution) and on the deformation model (density of the warping grid). This is a way of regularization which contributes to create a coarse-to-fine effect and additionally reduces the execution time.

4. Results

The validation of the proposed algorithm is limited by the absence of a gold-standard method to compare with, so that we evaluate the results by means of visual inspection and by assessing the obtained time-intensity courses, although strictly this cannot be considered a quantitative validation method.

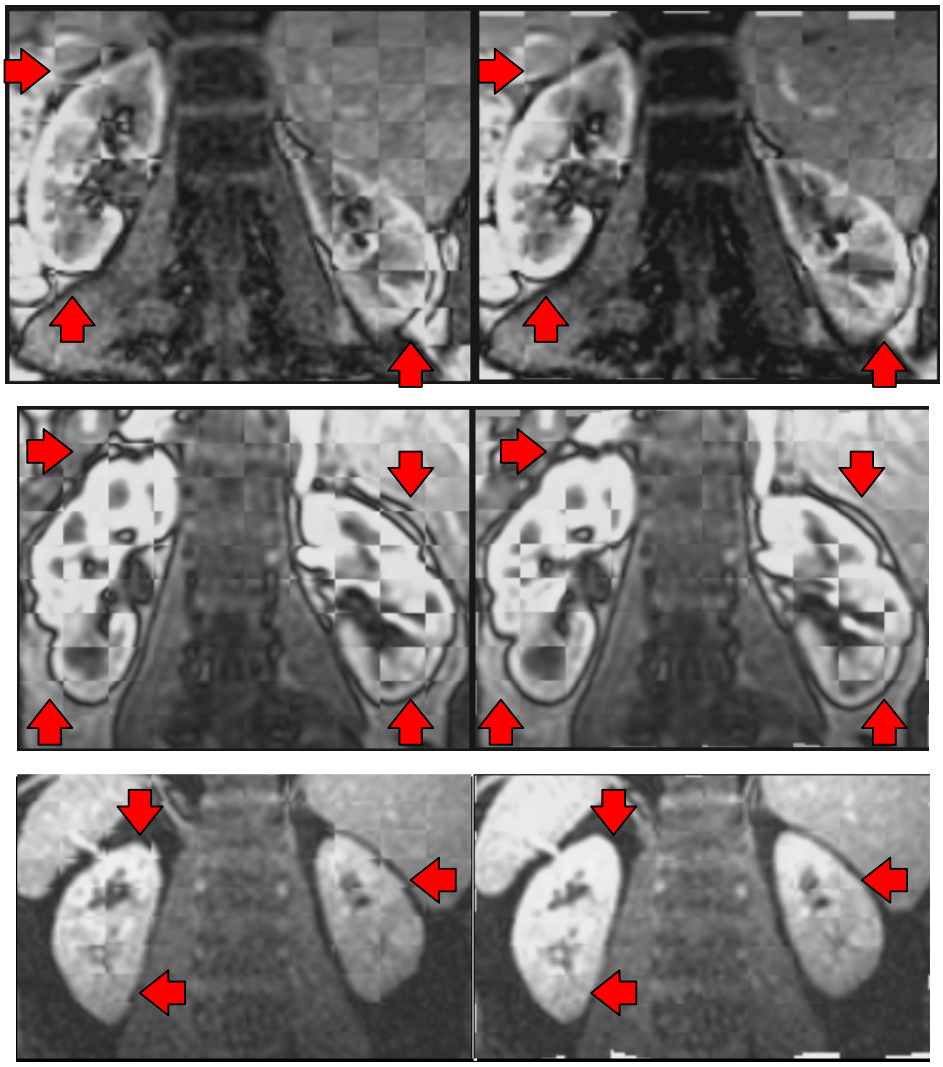

Figure 3: Checker-board composite images made from pairs of images before (*left*) and after registration (*right*). The arrows emphasize the improvement of the alignment.

Figure 3 represents the checker-board images composed of one coronal slice belonging to a couple of frames for three of the series analyzed (exams 4, 5 and 6). The alignment can be assessed by checking the improvement in the continuity of the contours in this checker-board like images.

Figure 4 depicts the time-intensity courses extracted from the exam 4 for small manually selected regions of interest (ROIs) on the main kidney functional regions (cortex, medulla and pelvis), for the original (blue lines) and the registered series (red lines).

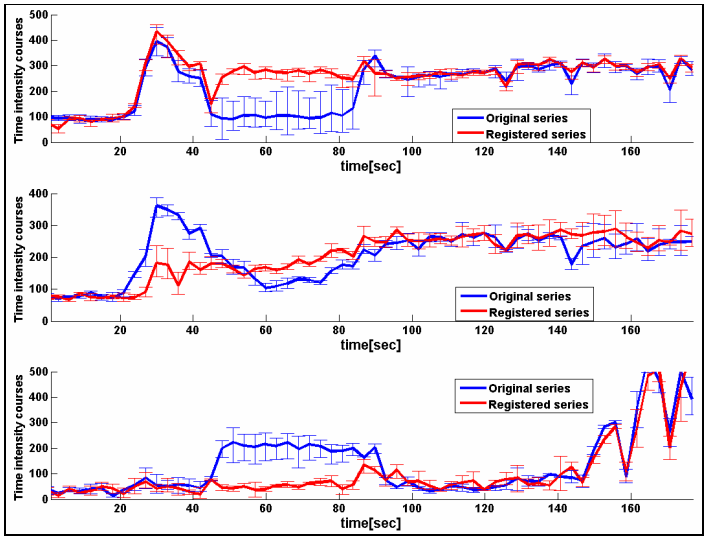

Figure 4: Comparison between the mean intensity time courses within manually selected ROIs in cortex (*top*), medulla (*middle*) and pelvis (*bottom*), before (*blue*) and after (*red*) registration.

The confusing wash-out for the cortex and enhancement for the pelvis about one minute after the tracer injection in the original series is corrected after registration, as well as the peak in the medulla, which could not be explained by any kinetic modeling for a healthy kidney.

In ***Figure 4*** the mean signal intensity value of the voxels included in each ROI is shown together with its standard deviation. It is clearly seen how the registration process reduces this standard deviation values.

5. Conclusions

In this paper we propose an efficient automated registration algorithm for the alignment of tracer enhanced MRR studies. This is an essential step towards the validity of the renal function analysis based on the tracer tracking, among many other interesting applications [6-8].

The validation of the algorithm is unresolved, but from the results here presented we dare to defend the good behaviour of this method.

Acknowledgments

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