

Model-Based Registration for Motion Correction of Inversion Recovery and Multiple-Time Point Renal ASL

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Introduction

There has been increasing interest in applying perfusion measurement techniques, such as Arterial Spin Labelling (ASL), to the kidneys in light of concerns over the link between gadolinium-bearing contrast agents and nephrogenic systemic fibrosis (NSF). Correction or avoidance of breathing-induced motion artefacts in the kidneys is beneficial, and recent publications have addressed this for ASL during free breathing, timed breathing, triggered acquisitions and breathholding [1,2]. Free breathing approaches combined with successful image registration have several advantages: there is no need for a reliable trace from respiratory bellows, patients need not be expected to cooperate with breath holding or other breathing manoeuvres, and the repetition time (TR) is not constrained to the variable respiratory cycle. These benefits make registration-based solutions attractive options in patient populations. Recent work has shown that multiple-time point [3] and multiple phase [4] approaches for ASL can aid renal perfusion quantification by extracting the bolus arrival time (the time for labelled blood to reach the renal tissue), which itself may have clinical relevance.

When combining a multiple-time point approach with presaturation, there are large contrast differences in the raw ASL images at different inversion times (TIs), relative to the ASL signal, which makes registration problematic – e.g. after saturation the label and control signal intensities at the different TIs will recover due to T_1 -relaxation, with the ASL labelling causing a difference of a few percent between them. This range of image contrasts that can be present in ASL signals at different labelling times can confound signal intensity-based image registration methods, leading to a risk of failure of motion correction. This is also a problem for inversion recovery (IR) sequences applied to the kidneys.

A similar problem has recently been addressed for dynamic contrast enhanced (DCE) MR techniques by using a model-based registration (MBR) method based on a model of the underlying contrast mechanism of the technique [5]. In this abstract we demonstrate the feasibility of a similar MBR approach, based on the T_1 -recovery of signal intensities, for registration of multiple-time point ASL and IR sequences applied to the kidneys.

Methods

Coronal-oblique images are taken aligned along the long axis of the kidneys, and it's assumed most of the motion is in this plane. For the MBR we first perform a 3 parameter T_1 fit to the ASL or IR data, averaged over any repetitions. Note that if saturation around the ASL label [6] is used, as is often the case, then label and control ASL images follow a saturation recovery curve (which can be fit to the 3-parameter model). In the ASL examples given below, we take an average of the label and control images to perform the registration. Based on the initial T_1 fit parameters, a set of synthetic T_1 model fit-derived target images are created corresponding to the set of TI times, which therefore have a similar contrast to the raw data. Images at each TI are then registered to their corresponding target image using an ROI-weighted 2D, 3 parameter, rigid body registration [7]. Each kidney is registered independently using a single mask created from the unregistered T_1 -map. A second T_1 fit is then performed on the registered images and the process may be iterated if necessary to improve the quality of the fit [5].

Five healthy volunteers (informed written consent was given) were imaged using a 1.5 T Philips Achieva scanner. ASL (3 volunteers) and IR (two volunteers) sequences were performed. For ASL data the method was evaluated using STAR labelling technique [3] with a single shot turbo spin echo (TSE) readout with SENSE factor 2 or TSE with 0.6 half-Fourier. 8 TIs between 300 and 3500 ms were acquired with at least 20 control-label pairs. The method was evaluated on two different IR sequences, one with 6 TIs between 200 and 5000 ms and 3 repetitions, and the other with 9 TIs between 100 and 6000 ms and 2 repetitions – both taken using a HASTE readout.

To quantify the improvement in the T_1 -fit the residual sum of squared error (RSSE) was calculated, for each pixel, between the pre and post registration images for a manually drawn region over the whole kidney. The mean RSSE was then calculated for each kidney.

Results

For the ASL data (See example in Figure 1) the effect on the T_1 -maps is evident, with the medulla-cortex boundaries becoming sharper post registration. The fitting improvement in T_1 values is highlighted in the mean RSSE (Table 1) which shows a decrease of over 35% in all examples. The flow maps also show improved medulla-cortex differentiation, as expected, due to the increased flow in the cortex – this example was chosen to highlight the improvements that can be made. The MBR showed improved cortex-medulla differentiation between pre and post registered IR T_1 -maps (Figure 2), more than halving the mean RSSE in both examples. For both ASL and IR sequences subsequent iterations of the MBR technique did not provide any visual improvement in image quality.

Conclusions

We have demonstrated that a MBR approach for registration of ASL and IR images is feasible and effective for renal imaging. This approach should overcome difficulties involved in registering IR and ASL data sets, and should easily be extendable to multi-slice acquisitions.

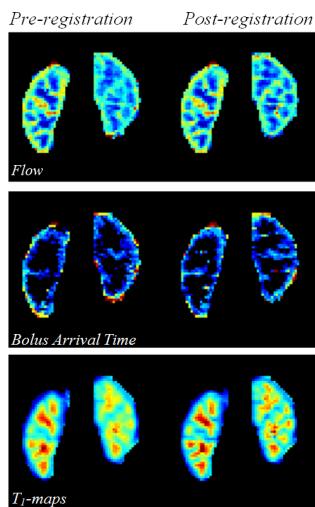


Figure 1. (left) Maps of flow (ml blood min^{-1} 100 ml), bolus arrival time (s), and T_1 -tissue (s) for volunteer 2. Pre-registered images are shown on the left and post registration on the right of the figure. Radiological viewing convention used.

Figure 2. (below) The resulting T_1 -maps from the inversion recovery sequence (volunteer 1). For the IR sequence there is an obvious difference between the pre-registration (top of figure) and the post-registration (bottom of figure). Radiological viewing convention used.

<u>Subject</u>	<u>Left kidney (10^9)</u>		<u>Right Kidney (10^9)</u>	
	<u>Unregistered</u>	<u>Registered</u>	<u>Unregistered</u>	<u>Registered</u>
<u>1 - ASL</u>	5.9	3.4	7.4	4.6
<u>2 - ASL</u>	2.2	0.90	0.84	0.58
<u>3 - ASL</u>	1.7	0.84	2.3	1.7
<u>1 - IR</u>	47	8.1	25	3.0
<u>2 - IR</u>	11	4.0	5.7	2.3

Table 1. Mean residual sum of squared error on T_1 -Fit.

Acknowledgements: AstraZeneca and EPSRC for funding.

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