Improvement of Functional MRI measurement with automatic movement correction in native and transplanted kidneys

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Purpose/Introduction

Non-invasive and accurate measurement of renal perfusion and glomerular filtration rate (GFR) could have a major impact on understanding renal physiopathology and for serial monitoring of the course of many acute and chronic kidney diseases. Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) can now be used for the evaluation of these functional parameters. Because dynamic MR images have to be acquired during spontaneous breathing, a critical problem in the post-processing step is correction of respiratory movements. This study describes a suitable method for 2D correction of kidney motion during the passage of the bolus of contrast with subpixel accuracy. The Patlak-Rutland model [1] was used to calculate GFR in the kidney cortex on a voxel-by-voxel basis. Corrected and uncorrected data were then compared in two different clinical conditions (healthy volunteers and kidney transplant patients) using different technical protocols characterized by different spatial resolutions and different levels of Signal-to-Noise ratio (SNR).

Material and Methods

MRI imaging: Dynamic contrast-enhanced MR renal studies were obtained in 2 different clinical populations:
1) 10 healthy volunteers (1.5T Siemens scanner using an abdominal TIM coil, a gradient-echo 3D-FLASH pulse-sequence, TR=1.63ms, TE=0.53ms, strong fat saturation, matrix: 125×104×18, Voxel: 3.1×3.1×7.5mm^3, Taq/dyn=2.5s, gadolinium injection: 0.05mmol (0.1ml/kg).
2) 10 patients following kidney transplantation (1.5T Philips system using a body phased-array coil, a 3D SR-TFE pulse sequence, TR=4.4ms, TE=2.5ms, no fat saturation, matrix: 128×50×5, Voxel: 3.2×8×10mm^3, Taq/dyn=1.5s, gadolinium injection: 0.03mmol (0.06ml/kg).

2D motion correction framework: The implemented registration model was proposed by Sun et al in 2004 [2]. A region of interest (noted m), encompassing the renal parenchyma, excluding the renal sinus, was manually drawn by a radiologist on an enhanced image (noted I_{ref}). In its original form, the algorithm was based only on the estimate of 2D translation displacements restricted to m, with a pixel resolution which may be insufficient for low amplitude movements (as in transplants). Our implementation allows the estimation of a 2D rigid transformation T (translation + rotation) with subpixel accuracy. We noted $\theta_{ref}(x,y)$ and $M_{ref}(x,y)$ the edge orientation and the edge magnitude for the pixel (x,y) obtained using a Sobel edge detector on the reference image I_{ref}. Identically, let $\theta_{cur}(x,y)$ and $M_{cur}(x,y)$ be the edge orientation and the edge magnitude for the pixel (x,y) obtained on the current image to register I_{cur}. To the coordinate transformation T relating kidney motion, we used the edge-based consistency metric proposed by Sun et al. [2] as follows:

$$\gamma\left(I_{ref}(x,y), I_{cur}(T(x,y))\right) = \frac{\sum_{x,y\in m} M_{ref}(x,y).M_{cur}(T(x,y)).\cos\left(2\left(\theta_{ref}(x,y) - \theta_{cur}(T(x,y))\right)\right)}{\sum_{x,y\in m} M_{ref}(x,y).M_{cur}(T(x,y))}$$

An exhaustive search was performed to determine parameters of T that maximises γ. A multi-step scheme was used to perform a subpixel registration while reducing enumeration of possible solutions.

MRI Functional measurement: We used the Patlak-Rutland model in the period of 60-120 seconds post Gadolinium contrast injection (considering time zero the first rise of the signal from the baseline in the aorta or iliac artery) to asses glomerular filtration [1]. GFR was calculated on a voxel-by-voxel basis providing a 2D GFR map (noted K_p) within the cortex. Standard deviation of Patlak-Rutland model fitting errors was also evaluated. The standard deviation map obtained (noted $\sigma(K_p)$) relates the uncertainty on GFR computation and was thus used as a quality criterion in our study. These results were then compared between the uncorrected and movement corrected data.

Results

Figure 1 and 2 display results obtained on native and transplanted kidneys. Anatomical images are shown in (a), 2D GFR maps in (b) and (c) and 2D GFR standard deviation maps in (d) and (e) (arbitrary units). Figures (b) and (d) relate to results obtained without motion correction, (c) and (e) with motion correction. Kidney movement correction improved the Patlak-Rutland plots by decreasing the standard deviation of GFR values that relate to the uncertainty of GFR computation. The average reduction on GFR uncertainty in native kidneys was 30.9%±17.6 (max=60.8%) for the right kidney, and 31.8%±14 (max=55.3%) for the left kidney. This average reduction in transplanted kidneys was 6.9 %±6.9 (max=21.4%).

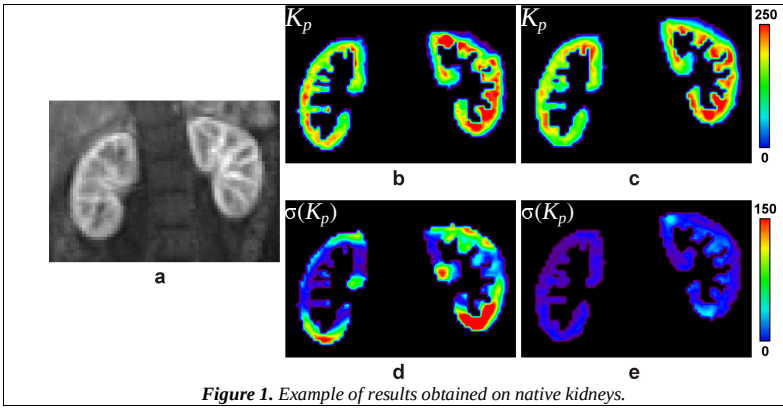

Figure 1. *Example of results obtained on native kidneys.*

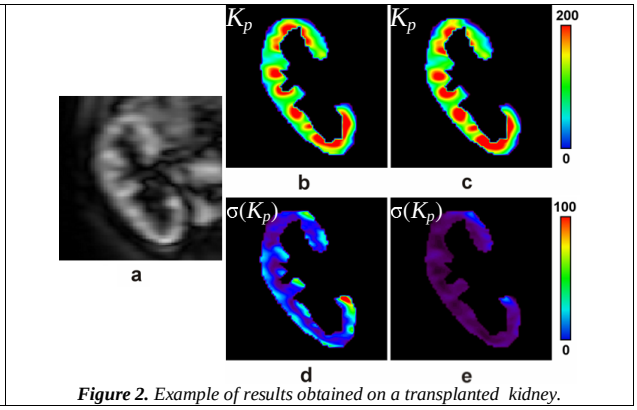

Figure 2. *Example of results obtained on a transplanted kidney.*

Conclusion and Perspectives

The implemented registration method appeared to be efficient for movement correction on Gadolinium-contrast enhanced dynamic MRI in both native and transplanted kidneys. This was independent of MR acquisition protocol (SNR, spatial resolution, and fat suppression) and operator intervention. Results showed that the correction of kidney displacements allowed a significant reduction of the error in estimation of the GFR using the Patlak-Rutland plot technique. Motion correction is a necessary prerequisite to improve any method of renal perfusion and GFR analysis, avoiding drift errors. We have shown an efficient technique to correct spontaneous motion and effects of motion drift for native (right and left) as well as transplanted kidneys. These results open great opportunities to evaluate kidney function in different conditions (diseased native kidneys, obstructed kidneys, infants) and for evaluation of its effect on quantification of renal filtration in comparison with a reference method.

References

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[2] Sun Y. et al. [2004], IEEE, International Conference on Image Processing.