

## Automatic registration of renal perfusion image sequences by mutual information and adaptive prediction

V. Positano<sup>1</sup>, I. Bernardeschi<sup>1</sup>, V. Zampa<sup>2</sup>, M. Marinelli<sup>3</sup>, M. Santarelli<sup>3</sup>, and L. Landini<sup>1,4</sup>

<sup>1</sup>MRI Lab, Fondazione G.Monasterio CNR-Regione Toscana, Pisa, Italy, <sup>2</sup>Department of Diagnostic and Interventional Radiology, University of Pisa, Pisa, Italy,  
<sup>3</sup>Institute of Clinical Physiology, Pisa, Italy, <sup>4</sup>Department of Information Engineering, University of Pisa, Pisa, Italy

**Introduction:** Perfusion technique is aimed to assess the effect of renal artery stenosis (RAS) on the kidney parenchyma. In clinical practice, kidney images are continuously acquired following the perfusion of a contrast media with high temporal resolution (about one image/sec) in a temporal interval of several minutes. In the image analysis phase, signal intensity-time curves are obtained from a ROI over the renal cortex. The signal curve is fitted to an appropriate model to extract semi-quantitative perfusion parameters, as maximum upslope (MUS), mean transit time (MTT), and time to peak (TTP) that was demonstrated to correlate with kidney perfusion [1,2]. The analysis is complicated by kidney motion due to respiration and patient movement, that may corrupt the shape of signal curve. Aim of this study is to develop an automatic image registration technique able to compensate kidney motion.

### Materials and methods:

Images from 20 patients (age 16-74 yr, mean 55) scheduled for renal perfusion study were acquired by a 1.5T scanner (Signa Excite HDx, GE). A 3D-FSPGR (LAVA) MR sequence was used (TR=2.9 ms, TE=1.2 ms, FA=15°, matrix=128x128, slice thickness=10 mm) to acquire coronal views encompassing both kidneys with a temporal resolution of 1 sec following the infusion of 2 ml Gd-BOPTA in a 160-200 sec frame. Acquisition was performed in free breathing. Image data were randomly divided in a training set and a validation set (10 patients each).

Image frames to be registered are characterized by change in MR signal due to the pass of the contrast medium, so the use of mutual information (MI) as registration metric seems to be appropriate [3]. However, experiments on training data set demonstrated that MI-based registration is robust and fast only if a reasonable guess is provided as input of the optimization procedure. Figure 1 schematize the registration procedure developed. The renal cortex was manually defined in the first frame of the sequence (1). The defined ROI was expanded by 0.6 factor to obtain a “ring” including the tissues around the cortex (2). The same ROI was propagated to the following frame (3). A preliminary registration was performed by minimizing the quadratic difference between images by a simplex optimization. The output of this step, fine registration was performed by maximizing the mutual information (MI) extending the ROI to the whole kidney region in both frames (4,5). Powell optimization algorithm was used, with a binsize=16 in MI histogram calculation. The process was iterated among all frames in the sequence. After the first ten frames, the starting point of the MI-based registration procedure was provided by an adaptive predictor (4). The adaptive predictor exploits a 10-frames window model of kidney movement inferred from analysis of the training image sequence:

$$f(x) = c + a_2 \sin(b_2 t) \quad (1)$$

the model in Eq. 1 is iteratively fitted to the ten previously obtained geometrical transformation. The use of the predictor allowed to improve both robustness and speed of the registration procedure.

Finally, renal cortex contour was traced by two independent observer on all frames in the validation data set to evaluate the effectiveness of the proposed approach. The distance between contours were evaluated by the Iterative Closest Point (ICP) algorithm [4].

**Results:** The mean distance between automatically and manually detected contours was 2.84 mm, not significantly different from the inter-observer variability of the manual registration procedure (2.36 mm, P=0.84). The mean processing time, measured on a standard PC (2 Ghz processor, 2 Gb RAM, Windows XP OS, procedure developed in IDL 6.3 environment) was 3.2 min. The use of the predictor saved about 30% of the processing time.

**Conclusions:** The developed method is able to automatically compensate kidney motion in perfusion studies, with a precision not significantly different from inter-observer variability of human operators. It may allow to avoid time-consuming manual image registration expanding the use of kidney perfusion imaging in the clinical practice.

**References:** [1] HJ Michaely et al. Radiology 2006 [2] V Zampa et al, RNSA 2009 [3] JPW Pluim IEEE TMI 2003 [4] PJ Besl IEEE PAMI 1992

