Automatic estimation of renal cortical thickness using MRI perfusion curves

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Introduction: The kidney is formed fundamentally by two zones: cortex and medulla [1]. The thinning of renal cortex has been recognized as a determinant of kidney function, in fact, in patients with chronic renal deseases the lost of cortical tissue is sign of a poor outcome [2]. For this reason it is important to have a tool that would allow measuring the cortical thickness. This could be useful to physicians for guiding and following-up therapies. Today cortical thickness is commonly measured by contrast enhanced MRI however this approach generally suffers from a small difference in signal intensity between the cortex and surrounding segments, resulting in a time-consuming, and potentially erroneous manual segmentation process [3]. We propose to use perfusion MRI data to better segment cortex from medulla, based on the differences in perfusion profiles between both tissues. Histological differences determine these differences even in patients with renovascular disease. The advantage of looking at the perfusion curves is that we do not rely only on image contrast between cortex and medulla which is sometimes diffuse.

Patients and Methods: We performed a contrast-enhanced MRI with a 1.5T system (Phillips Intera; Phillips Medical, Best, Netherlands) to one kidney. Low resolution multislice anatomical images were initially acquired to localize the kidneys. The contrast-agent method was performed using a dynamic three-dimensional (3D) gradient-spoiled turbo-gradient-echo sequence. Intravenous injection of 10 mL of gadolinium diethylenetrianminepentaacetatebis- methylamide (Gd-DTPA-BMA) (Omniscan; GE Healthcare, Oslo, Norway) was performed as a single bolus using a power injector (10 mL/second) during the dynamic MRI sequence with a single phase acquisition time of 15 seconds. Other sequence parameters were: frames = 39, frames/sec = 0.25, slice size = 1.06 mm, reconstruction matrix = 160 x 256, TR/TE = 5.16/2.56 msec. All MRI sequences were obtained without electrocardiograph (ECG) triggering, breath hold, or motion compensation. Informed consent was obtained from all patients.
The mechanism for segmenting the cortex and medulla from the kidney was as follows: (1) By averaging several late frames, when the contrast agent has already reached both cortex and medulla, we obtained a good anatomical image which was used as reference. (2) The kidney was segmented from this image by a semi-automatic method. Firstly, we did a coarse segmentation with a simple threshold, found with Otsu's method. Secondly we manually defined a polygon to select the kidney, polygon which does not need to be accurate. (3) To differentiate cortex from medulla we fit a step function to the perfusion curves for each pixel (Fig. 1 shows two typical profiles for one pixel in the cortex and another in the medulla). This gave us an estimate of the contrast arrival time. The arrival time in cortex pixels is markedly earlier than in medullar pixels. The fit was done with a step function that modelled the step with a sinusoidal function: $A(0.5 + 0.5\sin(\pi(t - t0)/dt))$, where A is the step amplitude, $t0$ the arrival time and dt the transition width. To estimate the relative renal cortex thickness we used a cortex / medulla ratio.

Results: As shown in Figure 3, we were able to correctly identify the cortex and the medulla. For such identification we classified pixels as belonging to the cortex if the arrival time was less than 25 seconds. In this particular case, the total number of cortex and medullar pixels was 1,964 and 276 respectively. The cortex/medulla ratio was 6.1.

Disscusion: We developed a semi-automatic tool to recognize the cortex of the kidney based on its features of perfusion. To the best of our knowledge there is no other method based on physiological features of the renal cortex. It has been demonstrated that the perfusion profile of the cortex is different in comparison with medulla because its histological features [4]. In the cortex are the glomerulli and in the medulla the tubules and where occurs the excretion of the gadolinium. Acquiring the entire kidney this method could permit a fast calculation of the volume (and even the mass) of the cortex and correlate it with the body size of the patient. This would be a good indicator to choose the most adequate treatment and for following-up the effect of the therapies applied.

References: [1] Mouinier-Vehier et al. Kidney Int 2002; 61: 591-598. [2] Van den Dool. Radiology 2005; 236: 189-195. [3] Kasrstoft et al. JMRI 2007; 26: 1564-1571. [4] Michaely et al. Radiology 2006; 238: 586-596.

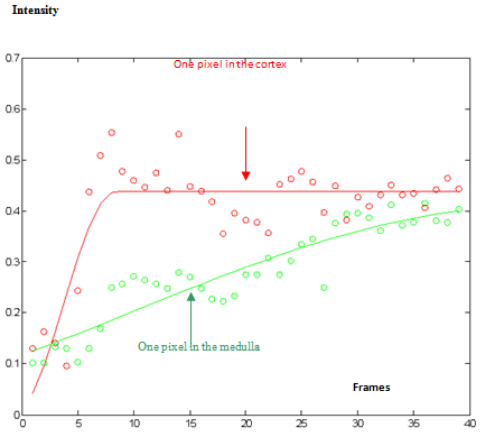

Figure 1: Perfusion profiles of pixels belonging to the cortex (red) and to the medulla (green). Using this difference we identified the tissue in cortex and medulla

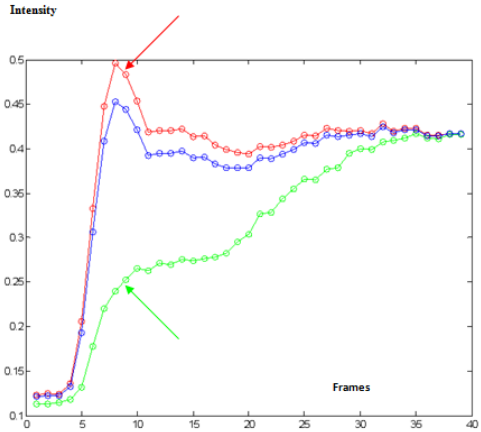

Figure 2: The mean of all pixels identified as cortex (red) and medulla (green). The cortex has an early peak (red arrow) due to the pass of the contrast through the glomerulli. The excretion of the gadolinium in the tubules is represented by a smooth increase in the intensity in the medulla (green arrow). In blue the mean in the entire

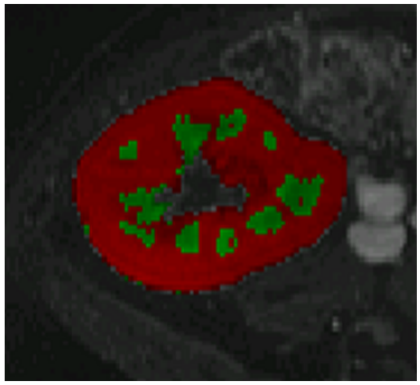

Figure 3: Graphic representation with the identification of the cortex and the medulla. In red cortex and in green medulla