Deconvolution-based MR imaging of renal perfusion and function using dynamic T1 contrast: a feasibility study

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Introduction:

Dynamic Contrast Enhanced MRI is a promising non-invasive method for imaging renal perfusion [1-3]. T1-weighted DCE images using standard Gadolinium chelates reflect the vascular as well as the excretory renal phase of the bolus transit [2]. It has been shown [1] that both phases can be separated after deconvolution of the tracer concentrations with an Arterial Input Function (AIF). Since deconvolution removes the dependency of the results on the shape and size of the bolus, this approach may provide a suitable method for quantifying both perfusion and filtration on the basis of the same data. Currently such an analysis has been applied in a rabbit model only, using a single signal averaged over the renal cortex. On the other hand, a pixel-by-pixel approach towards perfusion quantification was shown to be a useful tool for distinguishing normality from renal artery stenosis [2,3].

The primary objective of this study was to investigate whether deconvolution of T1-DCE data on a pixel-by-pixel basis in the kidney leads to acceptable regional parameters. More precisely, in view of the extreme sensitivity of deconvolution to noise [4], we investigate whether this procedure leads to data of diagnostic quality.

Materials and Methods:

In vivo perfusion measurements were performed on four normal human patients in the supine position using a 1.5 T scanner (Philips, Intera, The Netherlands). After injection of 0.1 mmol/kg Gd-DTPA at 2cc/ sec, axial images were acquired in breathhold condition during the first pass, using single slice Turboflash (180° preparatory pulse, TR 4.4 ms, TE 2.2 ms, FA 25°, slice thickness 4 mm, matrix 128/256). All experiments were approved by the local ethical board. Image post-processing was performed on a personal computer using software written in-house in IDL (Research Systems, Boulder, CO). All calculations were based on relative signal enhancement, without conversion to tracer concentration. An AIF was selected manually in the aorta and the tissue time courses were deconvolved using standard-form Tikhonov regularization and the L-curve criterion for selection of the regularisation parameter [4]. Parametric maps were calculated on the basis of the deconvolved time-courses, as well as on the original relative enhancement curves for comparison of the image quality. We calculated the following parameters: maximum (MAX), integral (INT) and integral/maximum (RATIO). No attempt was made to automatically separate the intravascular and excretory phase at this stage of the investigation.

Results:

Figure 1 illustrates a typical result for the deconvolved time courses. The first two peaks were observed throughout our data: they are assumed to reflect the contrast passage in respectively glomerulus and proximal convoluted tubule [1]. The passage through the distal convoluted tubuli (third peak) was not always distinguishable from the background. For the maximum of the time course after deconvolution average values of 1.7 ml/min/ml for the cortex and 0.5 ml/min/ml for the medulla were found, with standard deviations of, respectively, 0.6 ml/min/ml and 0.3 ml/min/ml. The height of the second peak was measured on a cortical ROI which, after correction for average cortical weight, led to a value of 67.9 ml/ min.

Figures 2 and 3 compare typical parametric maps before and after deconvolution. The image quality before and after deconvolution is comparable, except for a small number of isolated pixels where the instability in the deconvolution process led to deviating values (see also [4]).

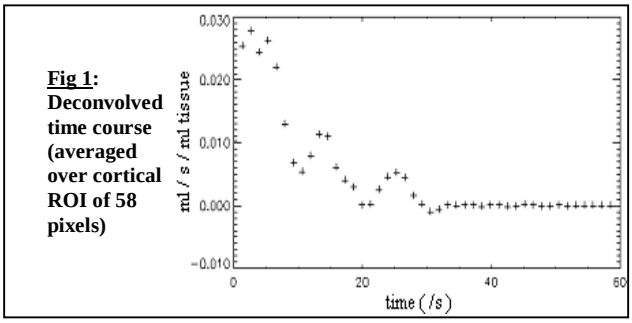

Fig 1: Deconvolved time course (averaged over cortical ROI of 58 pixels)

Discussion and conclusion:

Summary parameters are highly dependent on the AIF and therefore unreliable for follow up studies or comparison between patients. Deconvolution removes this dependency, but it is a procedure extremely sensitive to noise [4]. Our results show, however, that the amplification of noise by deconvolution has a negligible impact on image quality in kidney. In addition, deconvolution leads to improved delineation of anatomical structures, most notably on the RATIO maps.

An interpretation of the calculated maps cannot be made without a profound analysis of the tracer kinetics involved. However, a first approximation could be obtained by applying the tracer kinetic model for a linear and stationary system [1,2,4]. As such, the parameters MAX, INT and RATIO, when calculated after deconvolution, may be interpreted as renal perfusion (RBF), volume of distribution of the tracer (RDV), and mean transit time (MTT). We further interpret the maximum of the second peak in the deconvolved data as single kidney glomerular filtration rate (SKGFR).

Our data provide partial support for such hypotheses: the regions characterized by high MTT correspond to the renal medulla, as expected from physiological considerations. This is in strong contrast to the corresponding RATIO map made before deconvolution, where the cortex leads to higher values. From a quantitative point of view, we note that the ratio of cortical/medullary RBF (3.4) is near to the literature value of 4.0 [5] and the calculated SKGFR is close to the reference value of 62.5 ml/min[6].

On the other hand, measurements of absolute RBF values are typically underestimated by 60%. This illustrates the need for a further refinement of the procedure, eg. by using tracer concentrations, rather than relative enhancement, as a basis for deconvolution [1].

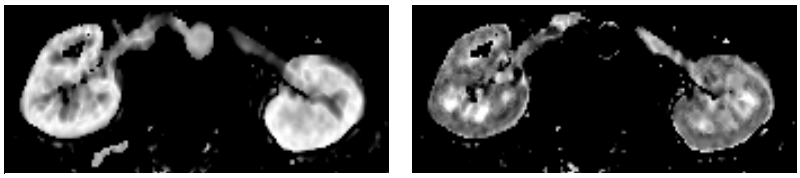

Fig 2: RATIO map before (left) and after deconvolution (right) in a normal male. Colour scale ranging left from 0 s (black) to 22 s (white) and right from 5 s (black) to 20 s (white). Note that only after deconvolution the medulla has higher values than the cortex, in agreement with the interpretation of such maps as Mean Transit Time.

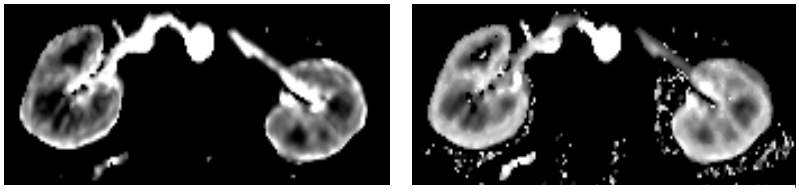

Fig 3: MAX map before (left) and after deconvolution (right) in the same patient. Colour scale ranging left from 1 (black) to 5 (white) and right from 0.060 ml/min/ml tissue (black) to 3 ml/min/ml tissue (white). Note the improved regional anatomical delineation, eg. in the posteromedian part of the right kidney

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