Ultra Low Dose Free breathing Quantitative Renal Perfusion and Filtration using 3D Through-time Radial GRAPPA

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Target Audience: Those interested in quantitative dynamic contrast-enhanced (DCE) MRI of the kidneys and applications of non-Cartesian parallel imaging.

Purpose: The purpose of this study was to perform a low dose, free-breathing exam for quantitative renal DCE MRI in order to provide a 3D high resolution measurement of perfusion and filtration. To achieve 3D coverage and high spatiotemporal resolution, data were acquired with a highly-accelerated stack-of-stars trajectory and reconstructed with 3D through-time radial GRAPPA[1].

Methods: ***Image Acquisition/Reconstruction:*** Renal DCE-MRI data were acquired in 10 asymptomatic volunteers after administration of Gd-DTPA (Magnevist, Bayer, Berlin, Germany) in this IRB-approved, HIPAA compliant study. Data were acquired in 5 volunteers after administration of a half dose of Gd-DTPA (0.05mmol/kg) and in 5 volunteers after administration of a quarter dose of Gd-DTPA (0.025mmol/kg). All imaging was performed at 3T (Magnetom Skyra, Siemens, Erlangen, Germany) with 30-34 receive channels. The acquisition was performed with a stack-of-stars trajectory and a FLASH readout. These data were accelerated in-plane by undersampling the radial trajectory by a factor of eight and with partial Fourier of 6/8 in the partition direction. This yielded a temporal resolution of 2.1-2.9s/frame and a spatial resolution of 2.2-2.3mm^3 with full 3D coverage of the kidneys and the aorta. Other scanning parameters include: TR/TE: 3.02-3.78/1.3 ms, flip angle: 12°, FoV: 350-370mm^2 x 79.2-92 mm, 160x160x36-40 matrix size, 20 projections/partition, number of frames: 135. Data were reconstructed using 3D through-time radial GRAPPA[1] and then gridded using the non-uniform fast Fourier transform[2]. GRAPPA weights were estimated using data from a fully-sampled acquisition with the following parameters: 160 projections/partition, 8 partitions, 16 repetitions, 8x4 (read x proj) segment size, free-breathing during calibration, acquisition time of 1-1.25min. ***Registration:*** All data were acquired without breath-holds. Thus, inter-frame motion must be corrected prior to DCE analysis. Here, an edge detection algorithm was used to determine the location of the kidneys over time, and several reference frames are selected where the kidney is at the same spatial location but at different points in enhancement[3]. The algorithm can then select the reference frame that is temporally nearest to each frame and use this as the reference for non-rigid registration using the FMRIB's FNIRT software[4]. This results in a fully registered time-series of 3D renal DCE data. ***DCE Analysis:*** A separable two-compartment pharmacokinetic model was used to quantitatively evaluate perfusion and filtration in the kidneys[5]. This model estimates perfusion (F_P, mL/100mL/min), filtration rate (F_T, mL/100mL/min), and mean transit times of the tracer in the tissue and renal tubular compartments (T_P and T_T, sec). An arterial input function was selected using an ROI in the aorta, and then normalized to account for hematocrit. Signal intensity values were converted to concentration, and the model applied to the concentration time-courses. DCE analysis was performed on an ROI and pixelwise basis. Whole kidney ROIs were drawn for each kidney, and parameter values reported for each kidney (10 kidneys for each dose). Pixelwise 3D mapping of all four parameters in the renal cortex was performed.

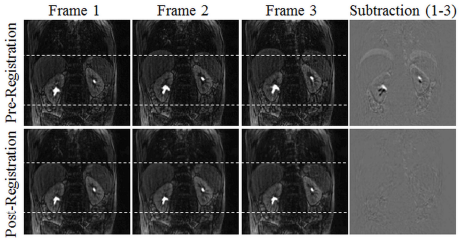

Figure 1. Images at 3 consecutive time points before and after registration. Last column shows subtraction of first and last images.

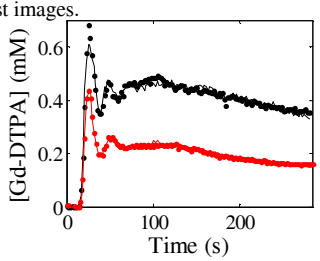

Figure 2. Concentration time-courses of whole kidney ROIs (½ dose: black dot, ¼ dose: red dot) and their model fits (½ dose: black -, ¼ dose: red -).

	Quarter Dose	Half Dose
F_p (ml/min/100ml)	212.5±47.6	218.1±57.1
T_p (seconds)	3.3±0.8	4.8±2.2
F_t (ml/min/100ml)	25.8±9.0	28.7±10.0
T_t (seconds)	124.2±36.3	131.1±60.2

Table 1: ROI analysis of kidneys using ½ dose (n=10 kidneys) and ¼ dose (n=10 kidneys) of Gd

Results: Data from 10 volunteers were successfully reconstructed and registered. An example reconstruction and registration result is seen in Figure 1. Figure 2 shows representative data and model fit from a single, whole kidney ROI after administration of a half and quarter dose. Low residual errors were seen between ROI data and the model fit with an average root mean squared error of 2.15% for half dose data and 1.3% for quarter dose data. The ROI analysis for half and quarter dose data is shown in Table 1, and pixelwise parameter maps for single partitions from the 3D data are shown in Figure 3 after a half and quarter dose of Gd-DTPA in two different volunteers.

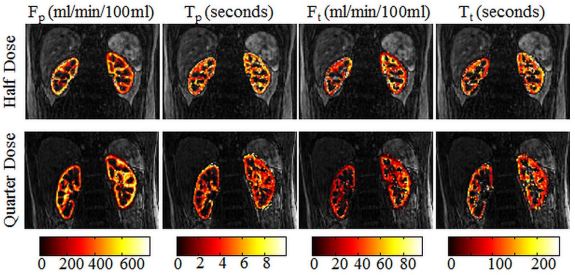

Figure 3. 3D parameter maps of perfusion, filtration, and mean transit times in the kidneys of 2 different volunteers after administering a ½ and ¼ dose of Gd.

Discussion: The goal of this study was to implement and evaluate a 3D DCE MRI protocol that used a very low dose of Gd-DTPA. Acquired data were highly undersampled to meet 3D coverage and high spatiotemporal needs of the exam, and aliasing artifacts were successfully removed by using 3D through-time radial GRAPPA. This allowed for 3D coverage and high spatial and temporal resolution of ~2.2mm^3 and < 3 s/frame. Data acquisition was completely free-breathing, and the registration algorithm successfully removed motion between each frame to allow for quantitative analysis. The renal pharmacokinetic model fit well to the concentration time-courses with low residual error, and the resulting parameter values for ROI and pixelwise analysis are similar to those in the literature[5]. Additionally, we successfully demonstrate this analysis with both a half dose and quarter dose of Gd-DTPA. This allows a low-dose quantitative exam and the remaining contrast dose could also be used for other indications such as MR angiography or evaluation of other organ systems.

References: [1]Wright KL, et al. Three-Dimensional Through-Time Radial GRAPPA for Renal MR Angiography. J Magn Reson Imag. In press. [2]http://www.eecs.umich.edu /~fessler/code/. [3]Chen Y, et al. Proc of the ISMRM 2013; 601. [4]http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSL. [5]Sourbron SP, et al. Invest Radiol 2008;43(1):40–8. **Acknowledgements**: Siemens Healthcare and NIH grants 1R01DK098503, and R00EB011527, 1R01EB017219.