Quantitative High Resolution Renal Perfusion Imaging using 3D Through-time Radial GRAPPA

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Target Audience: This work targets those interested in quantitative renal dynamic contrast-enhanced (DCE) MRI and in applications of 3D non-Cartesian parallel imaging techniques.

Purpose: The purpose of this study is to demonstrate a high spatiotemporal resolution, free-breathing, quantitative DCE MRI in the kidneys using highly-accelerated 3D through-time radial GRAPPA[1].

Methods: ***Image Acquisition/Reconstruction:*** A free-breathing, renal DCE MRI exam was performed on five asymptomatic volunteers following injection of Gd-DTPA (Magnevist, 0.1 mmol/kg, Bayer, Berlin, Germany) on a 3T Siemens Verio (Siemens Medical Solutions, Erlangen, Germany). Data were acquired using a 3D stack-of-stars trajectory, and were accelerated by undersampling each partition radially by a factor of 8 (acceleration factor of 12.6 with respect to Nyquist criterion). This acquisition yielded a temporal resolution of better than 3s/frame. Scanning parameters were tailored to fit the anatomy of each volunteer while maintaining a scan time of less than 3s/volume: FLASH readout; TR/TE/FA: 3.4-3.68ms/1.24-1.36ms/18°, FOV: 385-470mm^2 x 87-108mm, Spatial Resolution: 2.41-2.81mm^3, BW: 580-820Hz/pixel, 20-24 projections/partition, partial Fourier in partition direction: 6/8, acquisition time: 2.2-2.9 s/frame, 80 volumes acquired. GRAPPA weights were estimated using 3D through-time calibration with the following acquisition: 160-192 projections, 12-16 repetitions, 8 partitions, free-breathing during calibration, acquisition time 1-1.5 min. This calibration scheme was optimized via simulation and testing with normal volunteers. Data were reconstructed with 3D through-time radial GRAPPA[1] with an 8x4 (read x proj) segment size and then gridded using the non-uniform fast Fourier transform[2]. ***DCE Analysis:*** A separable two-compartment model[3] was used to obtain an estimate of 4 parameters: F_P (Perfusion, ml/min/100ml tissue), T_P (mean transit time in the plasma compartment, seconds), F_T (Tubular flow, ml/min/100ml tissue), and T_T (mean transit time in the tubular compartment, seconds). An ROI was placed in the aorta proximal to the renal arteries for the arterial input function. Based on the assumptions of the model[3], a ROI analysis was performed using a whole kidney and a cortical ROI. Pixelwise parameter mapping was performed on the renal cortex, which was segmented by thresholding signal intensity values in a frame during corticomedullary enhancement. The images were manually registered to correct for respiratory motion. Signal intensity values were converted to concentration of Gd-DTPA by including vials with known concentrations of Gd-DTPA for calibration[3]. Concentration time courses were then employed to estimate perfusion and filtration parameters with a non-linear least squares fit.

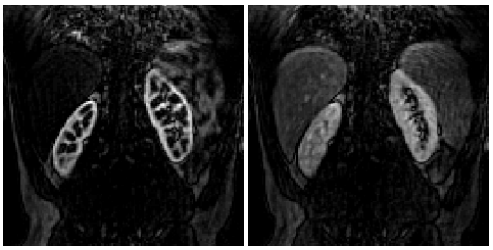

Figure 1. Representative single partition images through the kidneys during the corticomedullary and nephrographic phases of enhancement.

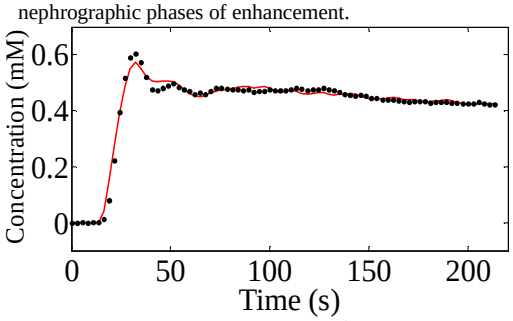

Figure 2. Concentration time-courses of renal parenchyma (black dotted line) and two-compartment model fit (red line).

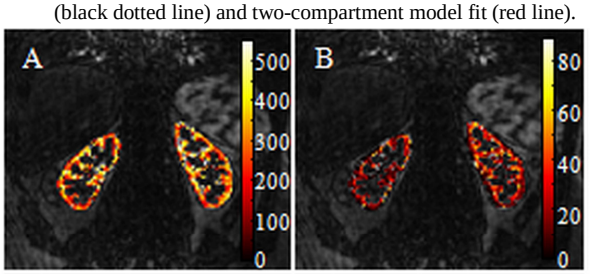

Figure 3. Parameter map of F_P and F_T (ml/min/100mltissue).

Results: Representative single partition images from a volume reconstructed using 3D through-time radial GRAPPA are shown in Figure 1 (single slice at ~30s and ~132s after injection). A concentration time-course of the renal parenchyma is shown in Figure 2, where data from a ROI analysis in a single volunteer are shown with its model fit. Whole kidney ROIs parameter measurements (n=10 kidneys) resulted in the following mean values ± standard deviation across the population: F_P= 225.0±40.0 ml/min/100ml-tissue, T_P=6.0±1.1s, F_T= 18.2±3.7 ml/min/100ml-tissue, T_T=133.7±27.9s. The model fit of the cortical ROIs resulted in the following mean values ± standard deviation (n=10 kidneys): F_P= 404.3±79.6 ml/min/100ml-tissue, T_P=6.5±1.0s, F_T= 20.6±9.1 ml/min/100ml-tissue, T_T=127.8±31.9s. Representative parameter maps of F_P and F_T from a pixelwise analysis are shown in Figure 3.

Discussion: 3D through-time radial GRAPPA was used to successfully reconstruct data with a temporal resolution of better than 3s/frame using an acceleration factor of 12.6 with respect to the Nyquist criterion and partial Fourier in the partition direction as demonstrated in Figure 1. No view-sharing was employed, thus guaranteeing a high fidelity reconstruction. This allows for an accurate, 3D functional evaluation of both kidneys including renal perfusion and filtration parameters using a DCE MRI analysis. Our estimated parameters from a ROI analysis of the renal parenchyma and cortex are in good agreement with those previously reported in the literature[3]. High resolution parameter mapping was also demonstrated in Figure 3. These results represent a significant improvement over previously reported results which were performed with thick 2D slices[3], thick 3D partitions[4], or with view-sharing and thus broad temporal footprints[5].

Conclusion: 3D through-time radial GRAPPA was used to acquire accurate, quantitative clinical estimate of renal function with high spatiotemporal resolution (2.2-2.9s/frame) in a free-breathing, 3D dynamic contrast-enhanced MRI exam of the kidneys.

References: [1]Seiberlich N, et al. In: *Proc. Int. Soc. Magn. Reson. Med.*, Melbourne, Australia, Electronic Poster 3838; 2012. [2]http://www.eecs.umich.edu/~fessler/code/. [3]Sourbron SP, et al. Invest Radiol 2008;43(1):40–8. [4]Lee VS, et al. Radiology 2003;227(1):289–94. [5]Gulani V, et al. In: *Proc. Int. Soc. Magn. Reson. Med.*, Honolulu, USA, Poster 2037; 2009. **Acknowledgements**: Siemens Healthcare and NIH grants R00EB011527, 1RO1HL094557, and 2KL2RR00040.