

3D high spatiotemporal resolution quantitative liver perfusion imaging using a stack-of-spirals acquisition and through-time non-Cartesian GRAPPA acceleration

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Target Audience This work targets those interested in high spatiotemporal resolution liver dynamic contrast-enhanced (DCE) MRI and perfusion quantification.

Purpose The goal of this work is to demonstrate high spatiotemporal resolution quantitative DCE liver MRI using a 3D stack-of-spirals acquisition, through-time non-Cartesian GRAPPA reconstruction, non-rigid body motion correction, and application of a dual-input single compartment model for quantitative perfusion mapping.

Introduction Combining liver DCE-MRI and quantitative perfusion modeling has shown promise in predicting treatment response in metastases¹. However, quantitative DCE-MRI in the liver poses several challenges. Most MR liver exams require a breath-hold to limit motion artifacts, and multiple acquisitions/breath-holds spanning the period of contrast enhancement, which are difficult for patients. Secondly, high spatial resolution is required to differentiate small lesions from normal tissues, a particular challenge in the liver as it is the largest organ in the body. Finally, high temporal resolution is required for accurate arterial input function characterization and perfusion model fitting. In this work, we demonstrate high spatiotemporal resolution 4D liver DCE imaging with quantitative dual-input single tissue compartment perfusion modeling, using a stack-of-spirals acquisition and through-time non-Cartesian GRAPPA acceleration². A high temporal resolution of 1.9 sec was achieved with high spatial resolution (1.9x1.9x3 mm³), which allows rapid measurement of contrast dynamics in the whole liver during **free breathing** and accurate model fitting of perfusion parameters. No view sharing is employed and therefore the acquisition time of the images is the true temporal footprint, ensuring high data fidelity.

Methods MRI experiments were performed on a Siemens 3T Verio scanner with a 12 coil array. The exam was performed on normal volunteers (N = 3), and 0.1 mmol/kg Gadobenate (Multihance, Bracco, NJ) was given. T₁-weighted 3D volumes were acquired using an interleaved variable-density stack-of-spirals gradient echo sequence with an option of fat suppression. 130 volumes were acquired with a temporal resolution of 1.9 seconds, while the subjects were breathing freely. To accelerate the acquisition, data were undersampled in-plane with a reduction factor of 6, and reconstructed using through-time non-Cartesian GRAPPA². To calculate the GRAPPA weights, a reference scan of 8 fully sampled 3D volumes (free breathing, ~77 s) was acquired at the end of the perfusion exam. Other parameters were: FOV=36x36 cm; matrix 192x192 (effective in-plane resolution 1.9 mm); TR/TE 4.5/0.6 ms; flip angle 10°; 60 partitions; slice thickness 3 mm; partial Fourier in partition direction=6/8. Images were reconstructed using Matlab. The reconstructed volumes were registered using FMRIB's Non-linear Image Registration Tool (FNIRT). A dual-input single-compartment model was established to retrieve liver perfusion parameters from DCE-MRI data³. Signal intensities were measured in the aorta, portal vein and liver parenchyma and then converted to contrast agent concentrations. Several perfusion parameters including arterial fraction, distribution volume and mean transit time were calculated with some fixed model parameters from the literature (T_{1,blood} 1800 ms (3T); T_{1,liver} 800 ms (3T); hematocrit 0.4).

Results and Discussion Figure 1 shows a single undersampled (R=6) and reconstructed partition acquired from a normal subject. Image quality is excellent and almost no residual aliasing artifacts are present after through-time non-Cartesian GRAPPA reconstruction. Figure 2 shows representative single slice images from a normal volunteer at four different phases of contrast enhancement. With the high imaging speed of 1.9 sec/volume, a free-breathing scan is achieved, and subtle dynamic changes in contrast enhancement are captured without interpolation or data gaps due to rests between scans. Figure 3 (left) shows signal time courses for the accelerated stack-of-spirals acquisition shown in Fig. 2, from the aorta, portal vein, and the hepatic parenchyma (average intensity from nine voxels), and the model fit to the parenchymal signal time-course (right). The model fitting yielded an arterial fraction of 16.3%, distribution volume of 16.6%, and mean transit time of 10.6 seconds, all in good agreement with published literature for CT and MR⁴. Representative liver perfusion maps from a single slice are shown in Fig. 4.

Conclusion In this study, a high spatiotemporal resolution 3D liver imaging technique was developed using a stack-of-spirals acquisition and through-time non-Cartesian GRAPPA acceleration. This technique allows fast imaging of the whole liver during free breathing and accurate quantification of liver perfusion.

References 1. Miyazaki K, et al. Radiol, 2012;263:139-148. 2. Seiberlich N, et al. MRM, 2011;66:1682-1688. 3. Materne R, et al. MRM, 2002;147:135-142. 4. Van Beers BE, et al. AJR, 2001;176:667-673.

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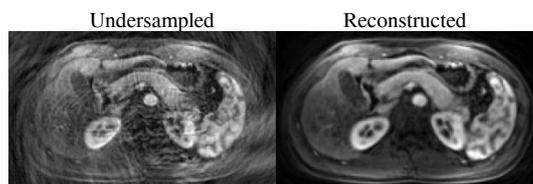


Fig. 1. Representative undersampled (R=6) and reconstructed spiral images acquired 28.5 seconds after contrast injection.

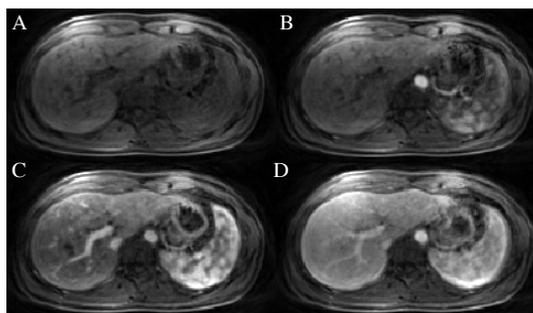


Fig. 2. Single slices from 3D liver DCE-MRI images of a normal subject acquired at different phases. The images shown are (a) 3.8 s (b) 22.8 s (c) 32.3s and (d) 41.8 s after contrast injection.

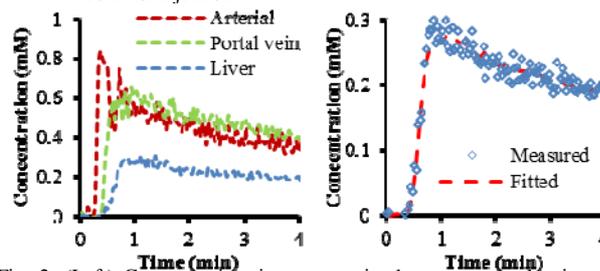


Fig. 3. (Left) Concentration-time curves in the aorta, portal vein and liver tissue (mean value of nine voxels). (Right) Measured and fitted data of liver tissue using a dual-input single compartment model. The model fitting yielded an arterial fraction of 16.3%, distribution volume of 16.6%, and mean transit time of 10.6 seconds.

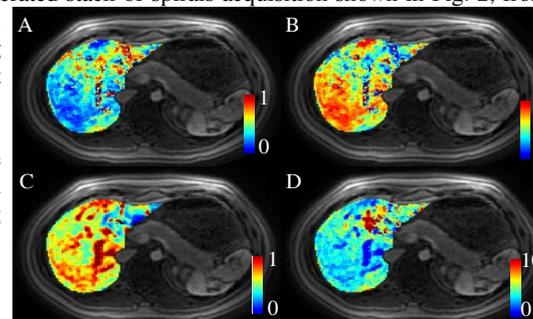


Fig. 4. Representative liver perfusion maps of (A) arterial fraction, (B) portal fraction, (C) distribution volume, and (D) mean transit time.