3D Through-Time Radial GRAPPA with In-Plane and Through-Plane Acceleration

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Target Audience: Scientists and clinicians interested in 3D non-Cartesian parallel imaging and its use in renal MR angiography.

Purpose: To demonstrate the use of 3D through-time non-Cartesian GRAPPA with a 3D radial stack-of-stars trajectory accelerated both in-plane and through-plane to achieve high spatiotemporal resolution images. Through-time radial GRAPPA and its 3D implementation have been shown to yield images with few residual artifacts even for high in-plane reduction factors [1, 2]. However, greater acceleration could also be achieved by undersampling along the partition direction. Here we present a method to reconstruct 3D radial contrast-enhanced renal MR angiography (MRA) data that have been undersampled both in-plane and through-plane to decrease the temporal footprint and improve the spatial resolution of the acquisition.

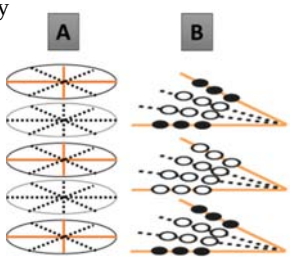

Fig 1. *(A) Undersampled stack-of-stars trajectory (B) 3D GRAPPA kernel with source (filled) and target points (open).*

Methods: Data were acquired along a 3D stack-of-stars trajectory that was undersampled in both the projection and partition directions (Fig 1A). The 3D through-time radial GRAPPA reconstruction was performed using a 3D kernel spanning three readout points, two projections, and two partitions (Fig 1B). To estimate the weight set, calibration data were accumulated by repeating the kernel not only through-k-space and through-time as in previous methods, but also through-partitions. Calibration was executed with a k-space segment of 4x1 (read x projection), 8 frames, and 16 partitions. Gridding was performed after reconstruction using the non-uniform fast Fourier Transform [3].

Two healthy volunteers were recruited for renal MRA on a 3T MR scanner (MAGNETOM Verio, Siemens HealthCare, Erlangen, Germany) in this IRB approved study. A free breathing calibration dataset (1m44s) was acquired prior to contrast injection, with a 15 channel body array, 228 projections, 448 read points, 224^2 grid, 16 partitions, TR/TE/FA=3.55ms/1.44ms/19°, and FOV 325x325x48 mm^3. After contrast injection (0.01 mmol/kg, Multihance, 3 mL/s), undersampled data (scan length 28s, 4 s/volume, 448 read points, 224^2 grid, 40 partitions, TR/TE/FA=3.55ms/1.44ms/19°, FOV 325x325x120 mm^3) were acquired during a breath-hold with 38 projections (R=6) and retrospectively undersampled along the partition encoding direction by a factor of 2 to yield a temporal resolution of 2 s/volume.

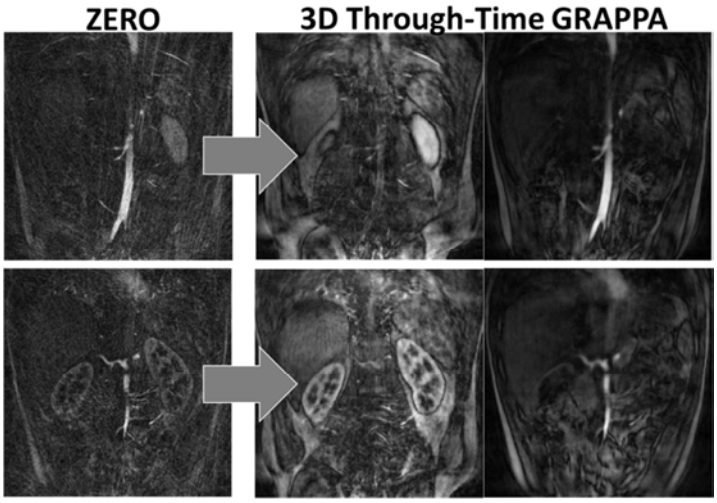

Fig 2. *Renal MRA images 16s after contrast injection with total R=12 (R=6 in-plane, R=2 through-plane), zero-filled and reconstructed using 3D through-time radial GRAPPA with a 3D kernel. Partitions are indicated in the insets.*

Results: Representative single partition renal MRA source images with total acceleration R=12 (R=6 in-plane and R=2 through-plane) are displayed in Fig 2. Anatomical details in the zero-filled images are obscured by radial streaking and fold-over artifacts from partition undersampling that are resolved by applying 3D through-time radial GRAPPA with a 3D kernel. In particular, the anterior contour of the left kidney and origin of the right renal artery are aliased into the same partition (top left) in the zero-filled images, while they are resolved into their appropriate partitions (top right) after GRAPPA reconstruction. Similarly, the celiac, hepatic, and superior mesenteric arteries from the anterior of the imaged volume appear in the same partition as the kidneys from a posterior partition (bottom left) in the zero-filled images, while they are seen at their proper through-plane locations (bottom right) after GRAPPA reconstruction. A maximum intensity projection (MIP) computed after reconstruction with 3D through-time radial GRAPPA is shown in Fig 3; note the removal of streak artifacts visible in Fig 2 (left) despite the high in-plane acceleration (R=6).

Discussion: We have demonstrated that 3D through-time radial GRAPPA can achieve high total reduction factors by undersampling in all three spatial dimensions (R=6 in the radial direction and R=2 in the partition direction, R=12 total). Due to the accurate GRAPPA weights calculated using the through-time approach, the reconstructed images successfully alleviate much of the radial streaking and fold-over artifacts in the zero-filled images without using view-sharing or model-based reconstruction approaches. Despite the free-breathing nature of the calibration data, it was possible to reconstruct images with high acceleration factors after contrast injection to yield spatial and temporal resolutions of 1.45x1.45x3.00 mm^3 and 2s/volume (after retrospective undersampling). While a 3D through-time GRAPPA approach was employed here, it is possible that a two-step GRAPPA reconstruction using 2D kernels (first a Cartesian GRAPPA reconstruction in the partition direction followed by 2D through-time radial GRAPPA) may be better suited in cases where there is significant motion between partitions and may lead to reduced spatial blurring.

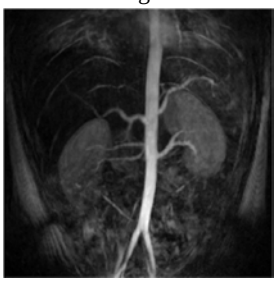

Fig 3. *MIP computed from images reconstructed with through-time 3D radial GRAPPA.*

Conclusion: High in-plane (R=6) and through-plane (R=2) acceleration for 3D scans, resulting in a total R=12, can be realized using 3D through-time radial GRAPPA with a 3D reconstruction kernel. This method can potentially mitigate radial aliasing and wraparound artifacts for 3D dynamic imaging applications with high spatiotemporal resolutions.

Acknowledgements: Funding for the project was received from Siemens Medical Solutions, Case Western Reserve University/Cleveland Clinic CTSA UL1 RR024989 and NIH/NIBIB R00EB011527. ***References***: 1. Griswold MA, et al. In: *Proceedings of the 11th Annual Meeting of the ISMRM*, 2003:2349. 2. Seiberlich N, et al. Magn Res Med 2011;65(2):492–505. 3. Fessler JA. J Magn Reson. 2007;188(2):191–195.