

# A Self-Calibrated Through-time radial GRAPPA Method

Ozan Sayin<sup>1</sup>, Haris Saybasili<sup>2</sup>, M. Muz Zviman<sup>3</sup>, Mark Griswold<sup>4,5</sup>, Nicole Seiberlich<sup>5</sup>, and Daniel A. Herzka<sup>1</sup>

<sup>1</sup>Department of Biomedical Engineering, Johns Hopkins University School of Medicine, Baltimore, MD, United States, <sup>2</sup>Siemens Healthcare USA, Inc., Chicago, IL, United States, <sup>3</sup>Department of Medicine, Cardiology, Johns Hopkins University School of Medicine, Baltimore, MD, United States, <sup>4</sup>Department of Radiology, Case Western Reserve University, Cleveland, OH, United States, <sup>5</sup>Department of Biomedical Engineering, Case Western Reserve University, Cleveland, OH, United States

**Target Audience:** Scientists and clinicians interested in highly accelerated cardiac imaging.

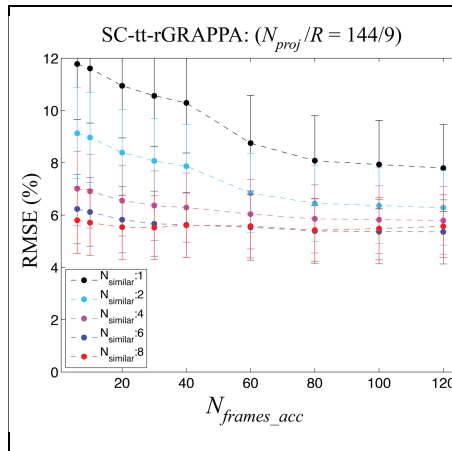
**Purpose:** High acceleration factors with undersampled radial trajectories have previously been demonstrated in cardiac MRI with through-time radial GRAPPA (tt-rGRAPPA).<sup>1</sup> This method estimates the radial GRAPPA (rGRAPPA) weights from a calibration pre-scan, consisting of multiple fully sampled reference frames, with a separate scan required per imaging plane.<sup>2-4</sup> This work aims to remove the need for a calibration scan. Several self-calibrating methods for radial GRAPPA have previously been proposed,<sup>5-8</sup> however, none have realized acceleration factors high enough to enable real-time acquisition with good image quality. An alternative self-calibration scheme for undersampled radial trajectories is proposed and demonstrated including quantitative comparison to the reference gold standard of through-time radial GRAPPA.<sup>1</sup>

**Theory:** Self-calibrated rGRAPPA (SC-tt-rGRAPPA) is derived from the original rGRAPPA formulation,<sup>9</sup> which uses a unique GRAPPA kernel for each missing k-space sample, and calibration for weight calculation is derived from multiple kernel occurrences with similar geometries over small segments of a fully sampled k-space (i.e. through-k-space calibration) (Fig. 1a). tt-rGRAPPA increases kernel occurrences by also using data from additional fully sampled frames.<sup>1</sup> Here, we use a one-sided kernel instead of a standard two-sided kernel (i.e. 3x1 instead of 3x2), which we refer to as “half-block” (HB) rGRAPPA (Fig. 1b). Finally, kernel occurrences with matching geometries are collected from the undersampled k-space (Fig. 1). Choosing the most geometrically similar  $N_{\text{similar}}$  kernel occurrences from  $N_{\text{frames\_acc}}$  consecutive undersampled frames, yields  $N_{\text{similar}} \times N_{\text{frames\_acc}}$  kernels for calibration. To obtain kernel occurrences with better geometric similarity, the azimuthal indices of the  $N_{\text{proj}}/R$  acquired projections were shifted by  $\text{floor}(R/2)$  on alternating frames where  $N_{\text{proj}}$  is the number of projections and  $R$  is the undersampling factor.

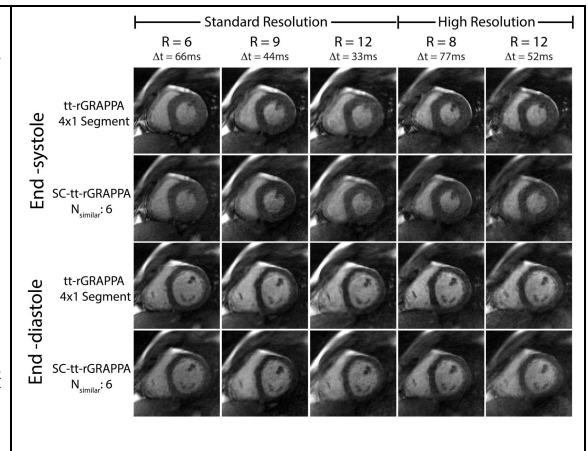
**Methods:** One swine and two healthy subjects were imaged with ACUC and IRB approval, at 1.5T (Avanto, Siemens Medical Systems, Erlangen, Germany) using standard coils (15 channels). Imaging included a free-breathing balanced steady-state free precession sequence (BW=1184 Hz/pixel, FoV=250 mm<sup>2</sup>) at two resolutions with varying acceleration rates. *Standard:*  $N_{\text{proj}}=144$ , matrix=128x128, TE/TR=1.4/2.8 ms,  $R=[6, 9, 12]$ . *High-Res:*  $N_{\text{proj}}=192$ , matrix=192x192, TE/TR=1.5/3.1 ms,  $R=[8, 12]$ . Slice thickness was 7.0 and 8.0 mm for animal and human scans, respectively. Since rGRAPPA calibration requires motion, the animal study was carried out to serve as a comprehensive “phantom” experiment during which gold standard reference images were reconstructed with 400 fully sampled calibration frames with a 1 x 1 segment (i.e. no through-k-space calibration).<sup>1</sup> RMSE values were computed for both tt-rGRAPPA and SC-tt-rGRAPPA for 3 short axis slices (SAX) and one long axis (LAX) slice. The effects of  $N_{\text{frames\_acc}}$  and  $N_{\text{similar}}$  on image quality were explored. In humans a complete stack of 12 SAX was acquired with each slice imaged for 5-10 sec, yielding 200 undersampled frames. SC-tt-rGRAPPA was compared to tt-rGRAPPA with 80 fully sampled frames per slice with a 4x1 segment.

**Results:** Figure 2 shows the performance of the self-calibrated reconstructions. As either  $N_{\text{similar}}$  or  $N_{\text{frames\_acc}}$  increased, RMSE decreased.  $N_{\text{similar}}=6$  demonstrated optimal results though with some variation with imaging resolution. Increasing  $N_{\text{similar}}$  too much (>8) lead to an increase in RMSE. Figure 3 displays images from a healthy subject reconstructed with both tt-rGRAPPA and SC-tt-rGRAPPA at various resolutions. High acceleration rates ( $R=12$ ) were supported and achieved acquisitions speeds of ~20 frames/second.

**Discussion/Conclusion:** A novel self-calibrated rGRAPPA technique is proposed. Image quality is comparable



**Figure 2:** RMSE for self-calibrated reconstructions from a swine SAX slice.



**Figure 3:** Example images from a human SAX slice reconstructed with tt-rGRAPPA and SC-tt-rGRAPPA.

to that of the state-of-the-art tt-rGRAPPA techniques as shown by RMSE. The performance of this method may enable more efficient clinical imaging by removing the need of pre-scan calibration. Eliminating a calibration in non-Cartesian scans may also increase flexibility in image-guided procedures where slice orientation may need to be altered on the fly. **References:**[1] Seiberlich et al., *MRM* 2011. [2] Sayin et al., *ISMRM 2013*. [3] Sayin et al., *SCMR 2014*. [4] Saybasili et al., *Magn Reson Imaging 2014*. [5] Arunachalam et al., *MRM* 2007. [6] Huang et al., *MRM* 2007. [7] Codella et al., *NMR in Biomed* 2011. [8] Hamilton et al., *ISMRM 2013*. [9] Griswold et al., *ISMRM* 2003. **Funding:** AHA11SDG5280025, R00EB011527, R01EB018108, 1R01HL094557.