

A Novel Profile/View Ordering (NINJA-STAR) for High-Resolution 3D Volumetric T1 Mapping

Sui-Cheng Wang^{1,2}, Amit R. Patel², Akiko Tanaka³, Hui Wang⁴, Xiang Zhu⁵, Dianwen Zhang⁶, Takeyoshi Ota³, Roberto M. Lang², and Keigo Kawaiji²

¹Biomedical Engineering, Northwestern University, Evanston, Illinois, United States, ²Medicine, Section of Cardiology, The University of Chicago, Chicago, Illinois, United States, ³Surgery, The University of Chicago, Chicago, Illinois, United States, ⁴Philips Medical Systems, Cleveland, Ohio, United States, ⁵College of Information and Electrical Engineering, and College of Economics & Management, China Agricultural University, Beijing, China, ⁶Imaging Technology group, Beckman Institute for Advanced Science and Technology, University of Illinois at Urbana-Champaign, Urbana, Illinois, United States

Target Audience: For MR Physicists and Clinicians interested in novel cardiac relaxometry techniques.

Introduction: Myocardial T1 mapping for the detection of myocardial fibrosis is commonly performed in 2D using a linear sweep profile/view order in which the central k-space lines are sampled at the acquisition window midpoints. This acquisition scheme provides both accurate contrast specific to the inversion time and also minimizes balanced SSFP eddy current artifacts. 3D T1 mapping is highly desirable as it can improve spatial resolution or coverage [1-3], and ensure earlier detection of diseases to improve patient outcomes. A FAN-type ordering [3-6] can acquire central k-space at acquisition midpoints and also suppress eddy currents. In this study, we propose a new acquisition scheme (NINJA-STAR or NJS) based on FAN-type ordering for 3D T1 mapping to reduce the total number of breath-holds (BHs).

Methods: The proposed 3D NJS acquisition employs a Cartesian projection of radial sectors that are partitioned by the number of total breath-holds. Each opposite sector pair is acquired in a single readout, while k-space center is acquired at the acquisition window midpoint. This acquisition employed both partial kz (~62%) and circular shutter Field-of-View (FOV) (~27% reduction) to create a circular mask. The proposed NJS ordering scheme additionally includes the following design specifications:

- 1) Linear sweep of the central kz data is performed during the first breath-hold, and the inversion times are aligned to these parameters for all subsequent breath-holds, regardless of heart rate variability in subsequent acquisitions.
- 2) Cropping of outer k-space is performed as determined by the NJS breath-hold reduction factor (k/n), defined as the actual number of breath-holds k out of n total breath-holds necessary for a fully sampled acquisition, while compatible with Sensitivity Encoding (SENSE) acceleration.
- 3) Array sorting using Cartesian ky and kz coordinate positions is performed to minimize k-space jumps between each readout, hence reducing eddy current artifacts that may arise due to rapid balanced SSFP sampling.

Fig 1 shows a ky-kz phase and slice encoding table of the NJS acquisition using a $k/n = 6/8$ BH reduction factor with SENSE R=2, yielding two (25%) fewer BHs.

Imaging was performed using 1.5T MRI (Philips Achieva) with a 5-channel cardiac array in a phantom experiment and *in-vivo* (5 swine). The 3D acquisition employed a 5-(3sec)-3 Modified Look-Locker Inversion Recovery (MOLLI) over 11 heart beats per breath-hold. The following scan parameters were used for all experiments: FOV: 330x330x80 mm³; Spatial Resolution: 1.7x2.1x4.4 mm. TR=2.5 ms, TE = 1.1ms, 78 TRs per heart beat. In a phantom experiment, the NJS BH factor was first varied between $k=4-7$ while n was set to 8, and were also compared to SENSE acceleration matched by scan time (R=3,4; using 5 channels, matched to NJS factors $k/n=6/8$ and 4/8). The optimal NJS factor k/n was employed in *in-vivo* imaging of 5 swine with respirator controlled breath-holding. An equivalent 2D MOLLI was also acquired. An AHA 16 segment model analysis of the LV [7] was performed with both 2D and 3D T1 measurements.

Results: In the phantom experiment, NJS factors 6/8 and 4/8 (SENSE R=2) yielded superior images compared to time-matched SENSE R=3,4 accelerations, as these yielded significantly more reconstruction artifacts. NJS factor $k=6/8$ yielded the optimal trade-off in the BH reduction and image quality (Fig 2). Fig 3 shows an example of the acquired *in-vivo* T1 map in the swine heart. Each scan was performed over 6 breath-holds in 2~3 minutes; where the total 3D MOLLI acquisition was ~45 seconds at a typical swine heart rate of ~90 BPM. The reported T1 values from the LV AHA segments between 2D and 3D MOLLI ROIs were 992 ± 42 vs 1041 ± 51 (n=80 segments). Across the five pigs, the average T1 values were $5.0 \pm 0.7\%$ greater with the proposed method than the 2D measurements, suggesting that the proposed method yielded slightly larger T1 measurements with comparable precision as the 2D MOLLI reference.

Discussion: We demonstrate the feasibility of the NINJA-STAR profile/view ordering scheme that is compatible with SENSE-accelerated reconstructions for 3D myocardial T1 mapping. NJS allows 3D imaging with higher through-plane spatial resolution in a reduced number of breath-holds compared to the FAN-type ordering [3], which has previously been shown to yield robust 3D T1 measurements of small tissue samples even under influence of motion as determined by a respiratory motion phantom. Clinically diagnostic T1 maps with slightly higher T1 measurements and comparable precision as 2D MOLLI references were acquired in swine hearts without any additional motion correction. Future work includes further scan time reduction and incorporating motion correction strategies to improve overall image quality of the 3D T1 maps.

References: [1] Weingartner et al. MRM 2014. In Press. [2] Kvernby et al. Proc. ISMRM 2014. pp 2422. [3] Kawaiji et al. SCMR 2015. Abstract Accepted. [4] Spincemaille et al. MRM 2004. 52(3). [5] Haider et al. MRM 2010. 64(4). [6] Klobitsch et al. MRM 2011. 66(4). [7] Tarroni et al. Radiology 2012, 265(2).

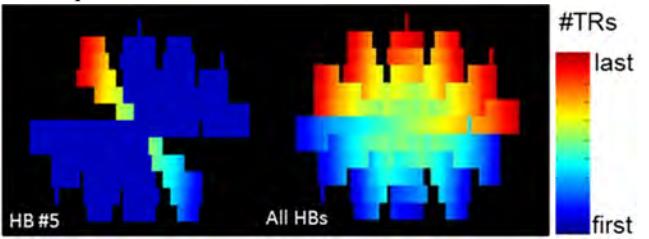


Figure 1. Slice vs phase encoding coordinate map of proposed NJS scheme. Color map (blue → red) shows sampling order within each acquisition window during mid-diastole of an R-R interval.

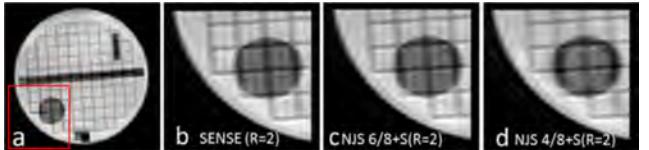


Figure 2. Phantom experiment: a) shows the (SENSE R=2), while b) zooms into the ROI (red box). c), d) shows $k/n = 6/8$ and $4/8$, respectively. $k=6$ was used for subsequent *in-vivo* imaging.

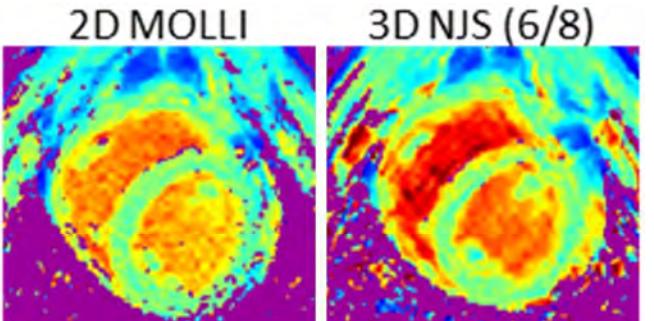


Figure 3. Example of a matched slice in 3D vs 2D MOLLI of a swine heart. NINJA-STAR allows 3D imaging with increased spatial resolution in a reduced number of breath-holds ($k=6$) in ~3mins; yielding 3-fold increase in slices/BH (3D: 18 slices/6BHs vs 2D: 8slices/8BHs) (4.4 vs 10mm thickness). This example demonstrates that 3D MOLLI T1 map volumes exhibited some motion blurring, while the matched 2D MOLLI slice yielded erroneous fits. Both results were clinically diagnostic for AHA segments analysis. K-space/image space motion correction can potentially improve image quality, but was not applied in this study.