

A Method for non-Cartesian Parallel Imaging Reconstruction with Improved Calibration

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Reconstructing non-Cartesian parallel imaging scans by synthesizing unacquired k-space data from neighboring acquired data (1-4) is a straightforward non-iterative approach that has shown promising results. However, accurate calibration remains a challenge. One approach (1) requires coil sensitivity estimates, which can be difficult to obtain in the presence of noise or motion. Autocalibrating methods (2-4) do not need to estimate coil sensitivities but are trajectory-specific, designed to work with either radial or spiral trajectories. In addition, these methods use a segmented k-space approach that does not use all of the fully sampled calibration data in generating the reconstruction weights for each segment. Because of this, additional calibration data can be required: for example, radial GRAPPA (2) does not use the inherently over-sampled central region for calibration, but must acquire additional calibration spokes.

In this work, we present an approach that has *all* of the following properties: 1) does not need to estimate coil sensitivities 2) not trajectory-specific 3) uses the entire unaccelerated calibration region to generate each set of reconstruction weights. The feasibility of the proposed method, called APPEAR (Anti-aliasing Partially Parallel Encoded Acquisition Reconstruction), is demonstrated, showing that the method is able to suppress residual aliasing artifacts and achieve good image quality. Compared to segmented autocalibrating methods, APPEAR can improve the net acceleration by reducing the amount of calibration data that needs to be acquired.

Theory Autocalibrating methods generate reconstruction weights by fitting calibration ‘source’ data to ‘target’ data using generalized matrix inversion. APPEAR uses an indirect calibration procedure that eliminates the need for calibration data to be acquired in a similar pattern to the accelerated data. Figure 1 shows a schematic of APPEAR. The calibration data on each coil is gridded and used to generate a grid of ‘correlation values’ that relate k-space kernel locations on the grid between all coils. Figure 2 explains how correlation values are computed from the gridded calibration data. Reconstruction weights are then generated to synthesize a datum at a target location by solving $w = C_{ss}^{-1}C_{st}$. C_{ss} is an $N_s \times N_s$ matrix, where N_s is the number of source points on all coils. It is formed from correlation values relating all source locations on all coils. C_{st} is an $N_s \times N_c$ matrix, where N_c is the number of coils (one target per coil). C_{st} is also formed from correlation values, relating source locations on all coils to each target location. It can be shown that the correlation value function $c(j_1, k_1; j_2, k_2)$ is bandwidth limited, allowing correlation values to be accurately interpolated, for arbitrary source/target patterns, from the grid of correlation values.

Methods Scans were performed on a 1.5T scanner (Signa® HDx, GE Healthcare, Waukesha, WI) using a variable-density stack-of-spirals trajectory (16 interleaves per spiral, 5.5 ms readout duration, 64 slices) designed for an in-plane acceleration of two. First, a resolution phantom was scanned with an 8-channel cardiac array and imaging parameters: FOV=12 cm, resolution=0.6x0.6 mm, slice thickness=1.2 mm, TR=50 ms. Next, a brain scan was performed on a volunteer with an 8-channel head coil and imaging parameters: FOV=20 cm, resolution=1.0x1.0 mm, slice thickness=2.0 mm, TR=50 ms.

To evaluate APPEAR for 2-D scans, an FFT was performed in the stack direction and each slice was treated as a separately acquired spiral scan. Slices were reconstructed using APPEAR and standard gridding (5) to show aliasing artifacts. For APPEAR, the target locations were chosen to directly synthesize data on a Cartesian grid. The reconstruction weights for each target location were computed independently, resulting in over 30,000 source/target patterns. Reconstructions were performed on a 3 GHz Intel Pentium computer.

Results Typical reconstruction results are shown in Figs. 3 and 4. The proposed method was able to suppress the aliasing artifacts and did not introduce any shading artifacts seen in previous autocalibrating spiral reconstructions (4). A single 2-D reconstruction took about 3 minutes, the bulk of which were spent generating reconstruction weights (generating correlation values and applying the weights took only a few seconds).

Discussion This work demonstrates the feasibility of the APPEAR method. Data was acquired using variable-density spiral scans, however APPEAR can be used to reconstruct other non-Cartesian scans without modification and can use the inherently over-sampled central region of k-space in radial scans for calibration. Reconstruction time is still a challenge, mainly due to the large number of source/target patterns in the current implementation. Algorithm optimization and parallelization should further reduce the computation time, which can also be reduced by taking advantage of techniques for reducing the number of source/target patterns (6). For time-series acquisitions, the time consuming process of generating weights needs to be performed only once, allowing subsequent reconstructions at several time points to be much faster. APPEAR is a straightforward non-iterative method that achieves good image quality; it does not use coil sensitivity estimates, is not trajectory-specific and uses the entire unaccelerated calibration region to generate reconstruction weights, thereby increasing the robustness of the calibration procedure.

References (1) Yeh et al. 2005, MRM 53:1383-94 (2) Griswold et al. Proc ISMRM 2003, p2349 (3) Heidemann et al. 2004, 2nd Workshop on Parallel MRI (4) Heberlein and Hu 2006, MRM 55:619-25 (5) Beatty et al. 2005, IEEE TMI 24(6):799-808 (6) Samsonov et al. 2006, MRM 55:431-8

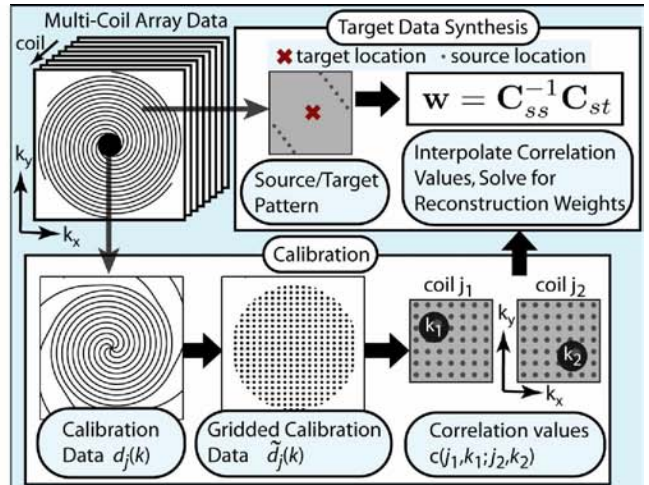


Figure 1: Schematic of APPEAR calibration and target data synthesis. *Calibration:* Data is interpolated onto a grid; correlation values are then generated, relating k-space kernel locations on all coils (Fig. 2). *Target Data Synthesis:* The matrices C_{ss} and C_{st} are formed by interpolating correlation values. The reconstruction weights, w , are generated and applied to synthesize the target datum.

$$c(j_1, k_1; j_2, k_2) = \sum_{i=1}^N \tilde{d}_{j_1}^*(k'_i + k_1) \tilde{d}_{j_2}(k'_i + k_2)$$

Figure 2: (a) Correlation value $c(j_1, k_1; j_2, k_2)$ relates k-space kernel location k_1 on coil j_1 to k-space kernel location k_2 on coil j_2 . (b) For APPEAR, a correlation value can be written as the given sum, where N is the number of fit locations, k'_i is center of fit location i in the gridded calibration data and $\tilde{d}_j(k)$ is the gridded datum on coil j at k-space location k . Every element of C_{ss} and C_{st} can be expressed as a correlation value.

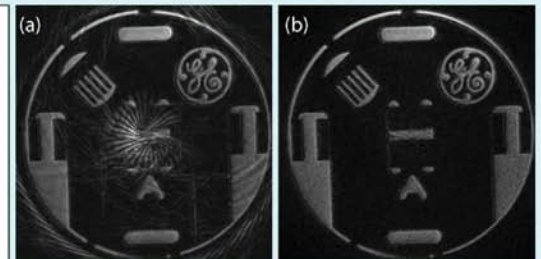


Figure 3: Axial slice of phantom scan. (a) Gridding reconstruction shows aliasing artifacts and (b) APPEAR reconstruction is able to suppress the aliasing artifacts.

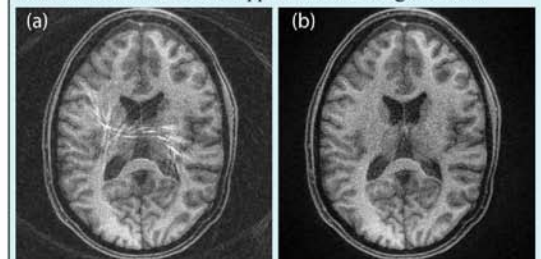


Figure 4: Axial slice of brain scan. (a) Gridding reconstruction shows aliasing artifacts and (b) APPEAR reconstruction is able to suppress the aliasing artifacts.