Correlation Imaging for Multi-Scan Acceleration in Clinical MRI

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Introduction: Parallel imaging provides a generic solution to accelerating a single MRI scan using multi-channel coil sensitivity information. A clinical MRI protocol for patient screening, however, typically needs a series of MRI scans for acquiring a number of images with different contrast and geometry. It is our expectation that since all of the data in a clinical protocol are acquired from the same patient with the same coil array, the shared information among all the scans can be used to optimize multi-scan imaging in aggregate. In the presented work, we propose an approach to multi-scan acceleration by combining multi-channel acceleration mechanisms underlying parallel imaging and the shared information of a multi-scan acquisition. Since the synergy of these mechanisms relies on the estimate of auto- and cross-channel correlation functions from multi-channel and multi-scan imaging data, the proposed approach is called "correlation imaging". In this work, we describe an anatomical correlation imaging strategy that speeds up a three-scan imaging protocol beyond the capability of conventional parallel imaging techniques optimized for single-scan MRI.

Theory: Figure 1(a) illustrates how multi-scan MRI is accelerated using a conventional single-scan optimization strategy with SENSE on clinical MRI scanners. The reconstruction for every scan can be depicted as **v**=**U****a**, where **v** is the reconstructed full-FOV image, **U** is the unfolding matrix calculated from the calibration scan, and **a** is the folded image [1]. It should be noted that the unfolding matrix **U** associated with a previously determined undersampling trajectory depends only on coil sensitivity shared by all the scans. By assembling the reconstruction equations for multi-scan images together, we can form a set of linear equations with the shared unfolding matrix as unknowns and the multi-scan images as the coefficients, providing an approach to finding the optimum reconstruction relationship in the sense of least square error from multi-scan imaging data. It should be noted that since the coefficients of these linear equations are images (not coil sensitivity), the resolved reconstruction relationship will not be equivalent to that in SENSE. Following this thought, we developed a multi-scan imaging acceleration strategy in this work: As shown in Figure 1(b), this strategy follows the same scan sequence as in SENSE. We found that the reconstruction relationship from undersampled data to an aliasing-free image in each scan can be found by resolving the following linear equations:

$$\sum_{i=1}^{N}\left[\sum_{r'} C_{ij}(-r-r')\,T_s(r')\right] U_i(r) = C_{mj}(-r),\ j=1,2,...,N \qquad (1),$$

where r and r' represent the image-space position, N is the channel number, $T_s(r)$ is the point spread function of a previously determined undersampling trajectory, $\{U_i(r),\ i=1,2,\ldots,N\}$ gives the channel weightings (analogous to the row vector of SENSE unfolding matrix) for the reconstruction of an arbitrary channel m, and $C_{ij}(r)$ is the image-space representation of k-space correlation functions between channels i and j. Since the solution to Eq. 1 is completely dependent on $C_{ij}(r)$, the estimate of auto-channel (i=j) and cross-channel (i≠j) correlation functions plays a critical role in correlation imaging. In the presented work, correlation functions are estimated from each scan using acquired or reconstructed aliasing-free images. During the run of a series of clinical scans, the ensemble summation of the estimated correlation functions over all previous scans are used in Eq. 1 to resolve the channel weightings $U_i(r)$'s for reconstruction of the current scan (Figure 1b). This ensemble summation suppresses the incoherent contrast information across scans and brings the shared information into image reconstruction. Since the amount of shared information increases as imaging proceeds, correlation imaging allows for the increase of acceleration factor in subsequent scans.

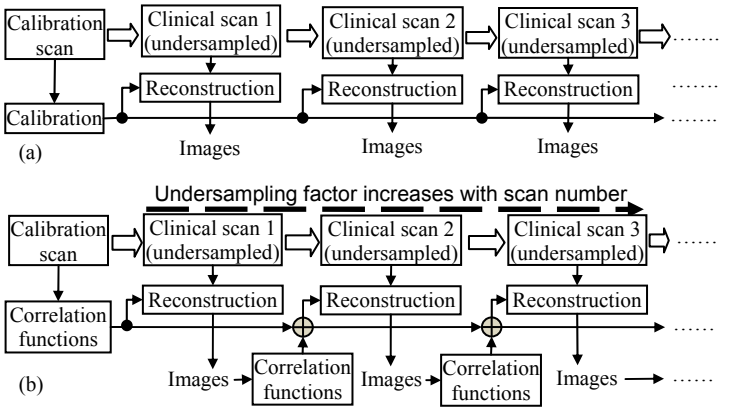

Figure 1. *(a) Conventional single-scan optimization strategy with SENSE. (b) Proposed multi-scan optimization strategy using information sharing.*

Methods and Materials: A series of brain anatomical scans was run using an 8-channel head coil array. A calibration scan was performed at the beginning of this protocol using a T1-weighted 3D FFE sequence (FOV=240×240×240 mm, matrix=64×64×64, TR/TE=3.6/1.7 ms, flip angle=6°). Following calibration, three high-resolution scans were conducted: 1) T1-weighted 2D axial IR TSE scan (FOV=240×240 mm, matrix=256×256, TR/TE=3248/8 ms, TI=800 ms, TSE factor=16, 10 slices with 4 mm thickness and 8 mm gap, phase encoding left-right). 2) T2-weighted 2D axial TSE scan (FOV=240×240 mm, matrix=256×256, TR/TE=3000/80 ms, TSE factor=16, flip angle=90°, 10 slices with 4 mm thickness and 8 mm gap, phase encoding left-right). 3) T1-weighted 3D sagittal TFE scan (FOV=240×240×240 mm, matrix=128×128×64, TR/TE=7.9/3.9 ms, TSE factor=256, flip angle=8°, phase encoding anterior-posterior, slice encoding left-right). These high-resolution imaging data were undersampled in post-processing for reconstruction. The single- and multi-scan optimization strategies shown in Figure 1 were compared. The calibration data were used to generate coil sensitivity profiles for SENSE in single-scan optimization and calculate the initial correlation functions for multi-scan optimization.

Results: Figure 2 shows the results using two different optimization strategies. It can be seen that multi-scan optimization strategy allows for the increase of acceleration factors as imaging proceeds (5 for the first, 8 for the second, 16 for the third scans). The reconstruction is comparable to that using SENSE optimized for single-scan MRI with lower but maximum acceleration factors allowed on clinical scanners (4 for the 2D scans and 8 for the 3D scan). It is also shown that conventional SENSE with the same acceleration factors as multi-scan optimization gives higher noise and artifacts.

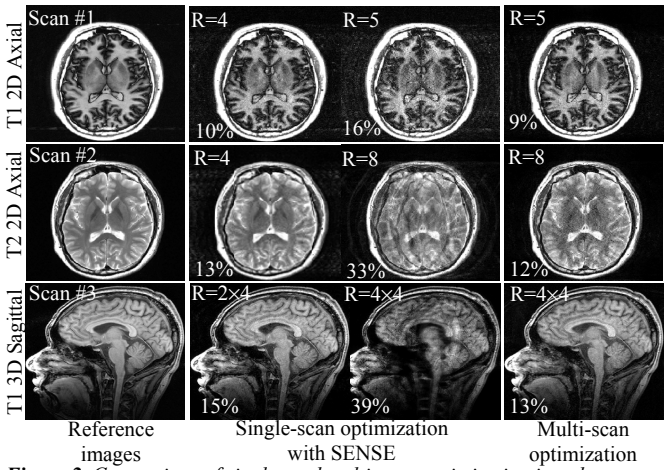

Figure 2. *Comparison of single- and multi-scan optimization in a three-scan anatomical MRI protocol. R represents reduction or acceleration factor. The percentage numbers are root mean square errors in reconstruction.*

Conclusion: Correlation imaging for multi-scan optimization offers the potential to accelerate a clinical MRI protocol beyond the acceleration limit in parallel imaging optimized for single-scan imaging.

Reference: [1]. Prussmann, K.P. et al., MRM 1999, 42: 952-962.