KerNL: Parallel imaging reconstruction using Kernel-based NonLinear method

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Target audience: Scientists and clinicians interested in new and improved parallel imaging techniques

Purpose: Parallel imaging (PI) has been used routinely for many clinical MR applications. The conventional calibration-based parallel imaging method (e.g., GRAPPA [1] and SPIRIT [2]) assumes a linear relationship between the acquired undersampled k-space data and the unacquired missing k-space data, where the linear coefficients are estimated using some auto-calibration signal (ACS). Such a linear model is valid in the ideal case but not in practice because both the ACS data and the undersampled data contain measurement noise. As a result, the model error leads to poor reconstruction at high accelerations. NL-GRAPPA [3] has used a truncated 2nd-order polynomial model to describe the nonlinear relationship between the missing and acquired k-space data and shown improved reconstruction quality. In this work, a much more general nonlinear framework is proposed for auto-calibrated parallel imaging. In this framework, kernel tricks are employed to represent the general nonlinear relationship between acquired and unacquired k-space data without increasing the computational complexity. Identification of the nonlinear relationship is still performed by solving linear equations. We name the proposed method Kernel-based NonLinear (KerNL) reconstruction method. Experimental results demonstrate that the proposed method can achieve reconstruction quality superior to GRAPPA and NL-GRAPPA at high net reduction factors.

Theory and Methods: In k-space-based parallel imaging methods [1,2], we need to find the relationship between each unacquired k-space data point y and its neighboring acquired data points x from all coils for reconstruction. The relationship is usually estimated using some additionally acquired auto-calibration data (ACS). Conventional methods assume a linear relationship between y and x: y = x*b, where b is estimated through calibration using the ACS. In this work, we propose a general nonlinear relationship f(*) between x and y such that y = f(x). With all the x and y pairs obtained from the auto-calibration data, finding the nonlinear relationship can be formulated as finding a function f(*) such that \( \sum (y_i - f(x_i))^2 + \lambda \|f\|_H \) (1) is minimized, where \( \|f\|_H \) defines a norm in the Hilbert space. According to the Representer’s theorem [4], the minimizer f(*) of (1) always takes the form of f(x) = \( \sum m \alpha_i k(x_i, x) \) (2), where k(•) is a positive definite kernel function. The significance of the theorem is that although we are searching for functions in an infinite-dimensional Hilbert space, it states that the solution lies in the span of m particular kernels – those centered on the calibration data points x. Given the ACS, the coefficients (4) can be found analytically by \( \alpha = (K + \lambda I)^{-1} y \) (3), where the kernel matrix K is calculated by \( K_{ij} = k(x_i, x_j) \) from the calibration data (as illustrated in Fig. 1), I is the identity matrix, and \( \lambda \) is the regularization parameter. After we obtain the coefficient \( \alpha \), the missing k-space data is reconstructed by y = \( \sum m \alpha_i k(x_i, x) \), which is a nonlinear function of x. Although many different kernel functions (e.g., Gaussian) are applicable, here we use a polynomial kernel \( k(x, x) = (\alpha^T x + a)^2 \) (4), where a is a constant, and (•)^H denotes the Hermitian transpose. Here we choose a to be equal to the maximum of \( x_i^T x_i \) for all i and j. To speed up calculation, random projection [5] is used in solving Eq. (3).

Results: To evaluate the performance of the proposed method, a set of brain data was acquired from a multiple sclerosis patient on a GE 3T scanner (GE Healthcare, Waukesha, WI) with an 8-channel head coil. The dataset was an axial brain image acquired using a 2D spin echo sequence (TE/TR=11/700 ms, matrix size=256x256, FOV=220x220 mm²). The data were fully acquired and then retrospectively undersampled to simulate the partial acquisition. The proposed KerNL method, GRAPPA and NL-GRAPPA were used to reconstruct the image. All code were written in MATLAB and run on a PC with 3.4GHz CPU and 16GB memory. Fig. 2 compares the reconstructed images from GRAPPA, NL-GRAPPA, and KerNL. Experimental results demonstrate that, compared with GRAPPA and NL-GRAPPA, KerNL achieves lower NMSEs and better image quality for all net reduction factors. The proposed KerNL method is also more efficient computationally.

Discussion: NL-GRAPPA has shown to significantly improve the SNR over GRAPPA. However, it might fail when too few ACS are acquired to solve for the increased number of unknown weights. As a new nonlinear method, the proposed KerNL addresses this issue by introducing kernel functions. As seen in Fig. 2, when NL-GRAPPA fails at very few ACS (16 lines), the proposed method is still superior to GRAPPA.

Conclusion: We have proposed a nonlinear, non-iterative approach to parallel imaging reconstruction, named KerNL. The method is able to improve both image quality and computation efficiency at high reduction factors, compared with GRAPPA and NL-GRAPPA.