

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 \mathbf{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 \mathbf{x} : $y = \mathbf{x}^T \mathbf{b}$, where \mathbf{b} is estimated through calibration using the ACS. In this work, we propose a general nonlinear relationship $f(\bullet)$ between \mathbf{x} and y such that $y = f(\mathbf{x})$. With all the \mathbf{x}_i and y_i pairs obtained from the auto-calibration data, finding the nonlinear relationship can be formulated as finding a function $f(\bullet)$ such that $\sum_i (y_i - f(\mathbf{x}_i))^2 + \lambda \|\mathbf{f}\|_H$ (1) is minimized, where $\|\bullet\|_H$ defines a norm in the Hilbert space. According to the Representer's theorem [4], the minimizer $f(\bullet)$ of (1) always takes the form of $f(\mathbf{x}) = \sum_{i=1}^m \alpha_i k(\mathbf{x}_i, \mathbf{x})$ (2), where $k(\cdot, \cdot)$ 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 \mathbf{x}_i . Given the ACS, the coefficients $\alpha = [\alpha_1, \alpha_2, \dots, \alpha_m]^T$ in (2) can be found analytically by $\alpha = (\mathbf{K} + \lambda \mathbf{I})^{-1} \mathbf{y}$ (3), where the kernel matrix \mathbf{K} is calculated by $\mathbf{K}_{i,j} = k(\mathbf{x}_i, \mathbf{x}_j)$ from the calibration data (as illustrated in Fig. 1), \mathbf{I} is the identity matrix, and λ is the regularization parameter. After we obtain the coefficient α , the missing k-space data is reconstructed by $y = \sum_{i=1}^m \alpha_i k(\mathbf{x}_i, \mathbf{x})$, which is a nonlinear function of \mathbf{x} . Although many different kernel functions (e.g., Gaussian) are applicable, here we use a polynomial kernel $k(\mathbf{x}_i, \mathbf{x}_j) = (\mathbf{x}_i^H \mathbf{x}_j + a)^2$ (4), where a is a constant, and $(\bullet)^H$ denotes the Hermitian transpose. Here we choose a to be equal to the maximum of $\mathbf{x}_i^H \mathbf{x}_j$ 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=256×256, FOV=220×220 mm²). The data were fully acquired and then retrospectively under-sampled 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.

References: [1] Griswold MA, et al., MRM, 47(6):1202-1210, 2012. [2] Lustig M, et al., MRM, 64(2):457-471, 2010. [3] Chang Y, et al., MRM, 68(3): 730-740, 2012. [4] Kimeldorf GS, et al., J of Math. Anal. and Appl., 33: 82-95, 1971. [5] Lyu J, et al., MRM, DOI: 10.1002/mrm.25373, 2014.

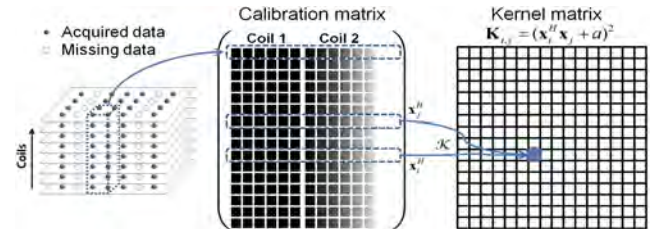


Fig. 1. Illustration of calculation of the kernel matrix

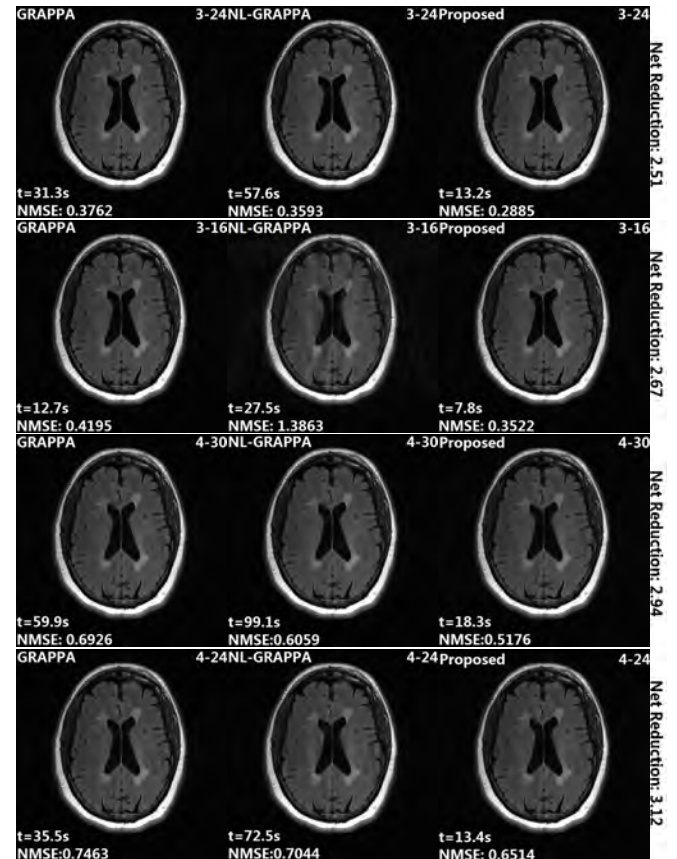


Fig. 2. Comparison of proposed method with GRAPPA and NL-GRAPPA