Kernel GRAPPA: A GENERAL NONLINEAR FRAMEWORK FOR GRAPPA REGULARIZATION

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INTRODUCTION:

The conventional GRAPPA method [1] reconstructs the missing *k*-space data by a linear combination of the acquired data. The method can suffer from severe noise at high accelerations. Some methods use regularization [2,3] or iterative reweighted least-squares (IRLS) [4] to reduce noise. The kernel method has recently been studied for regression and prediction problems and shown to outperform linear models [5,6,7]. The idea of kernel method is to transform the data nonlinearly to a higher dimensional space such that linear combination in the new space can approximate a broader class of nonlinear functions. Due to the improved accuracy in the regression model, the kernel method can improve the regression and prediction accuracy. In this abstract, we propose a kernel method to improve the conventional GRAPPA model and reduce the reconstruction error. We study both polynomial and Gaussian kernels for the nonlinear mapping and formulate the problem of reconstructing the missing *k*-space data as a nonlinear combination of the acquired *k*-space data. Experimental results demonstrate that the proposed method outperforms the conventional GRAPPA, regularized GRAPPA, and IRLS methods in suppressing the spatial-varying noise.

THEORY AND METHOD:

In conventional GRAPPA, the reconstruction is formulated as $\mathbf{b}=\mathbf{A}\mathbf{x}$ (1), where $\mathbf{A}$ represents the matrix comprised of the acquired data, $\mathbf{b}$ denotes the vector of the missing data (or ACS when calibrating), and $\mathbf{x}$ represents the coefficient. In proposed kernel GRAPPA, we apply a nonlinear mapping Φ over the acquired undersampled *k*-space data. Under such a mapping, we will need to solve a linear system: $\mathbf{b}=\Phi(\mathbf{A})\mathbf{x}$ (2), where $\Phi(\mathbf{A})=\left[\Phi(\mathbf{a}_1),\Phi(\mathbf{a}_2),\cdots,\Phi(\mathbf{a}_M)\right]^T$ is an $M\times N_K$ matrix, *M is* the number of acquired ACS data, N_K is the dimension in the reproducing kernel Hilbert space (RKHS) [8] which is usually much higher than *M*, and $\mathbf{a}_i$'s are row vectors of the matrix $\mathbf{A}$. A kernel is a continuous, symmetric and positive-definite function, and is related to the mapping Φ in that $\kappa(\mathbf{a}_1,\mathbf{a}_2)=<\Phi(\mathbf{a}_1),\Phi(\mathbf{a}_2)>,\ \forall\mathbf{a}_1,\mathbf{a}_2\in\mathbf{A}$ (3), where <,> represents the inner product. It is seen that calibration using ACS is still to solve a linear equation: $\hat{\mathbf{x}}=\left(\left(\Phi(\mathbf{A})\right)^H\left(\Phi(\mathbf{A})\right)\right)^{-1}\left(\Phi(\mathbf{A})\right)^H\mathbf{b}$ (4), avoiding any iterative steps required in most nonlinear approaches. Once the coefficients are estimated in Eq. (4), they are used in reconstruction to find the missing data in outer *k*-space, like the conventional GRAPPA does.

We investigate the generally used polynomial kernel [9] and Gaussian kernel [10]. A polynomial kernel takes the form of $\kappa(\mathbf{a}_i,\mathbf{a}_j)=\left(\gamma\mathbf{a}_i^T\mathbf{a}_j+r\right)^d$, (5) where γ and *r* are scalars and *d* is the degree of the polynomial and the Gaussian kernel is $\kappa(\mathbf{a}_i,\mathbf{a}_j)=\exp(-\|\mathbf{a}_i-\mathbf{a}_j\|_2^2/\sigma^2)$ (6). The kernels are the inner product between two vectors $\Phi(\mathbf{a}_i)$ and $\Phi(\mathbf{a}_j)$. For the polynomial kernel with $\gamma = r = 1$ and $d = 2$, to reduce the computational complexity, we keep the first-order components $1,\sqrt{2}\mathbf{a}_1,\ldots,\sqrt{2}\mathbf{a}_K$, and randomly and sparsely choose the second-order components to construct a nonlinear mapping $\mathbf{\Phi}(\mathbf{a})=\left[1,\sqrt{2}a_1,\sqrt{2}a_2,\cdots,\sqrt{2}a_K,a_{i_1}a_{j_1},a_{i_2}a_{j_2},\cdots\right]$, where $a_1, a_2, \ldots, a_K$ are components of the vector $\mathbf{a}$ and *i*, *j* are randomly chosen from 1, 2,…, *K*, such that the size of $\mathbf{\Phi}(\mathbf{a})$ is equal to the desired dimension N_K. With the polynomial kernel, the proposed kernel GRAPPA method is thereby formulated as

$$S_j\left(k_y+r\Delta k_y,k_x\right)=w_{j,r}^{(0)}\times 1+\sum_{l=1}^{L}\sum_{b=B_1}^{B_2}\sum_{h=H_1}^{H_2}w_{j,r}^{(1)}(l,b,h)\times S_l\left(k_y+bR\Delta k_y,k_x+h\Delta k_x\right)+\sum_{n=1}^{N}w_{j,r}^{(2)}(n)\times P(n)\times Q(n) \quad (7)$$

where S_j, S_l and *w* represent the missing (or ACS) data, acquired undersampled data and coefficients, respectively, and $P(n)$ and $Q(n)$ are randomly chosen from the acquired data and *N* is the number of randomly selected second-order terms. For the Gaussian kernel, the nonlinear mapping to the RKHS is a collection of $\Phi_n(a_k)=\sqrt{2^n/n!\sigma^{2n}}a_k^n e^{-(a_k/\sigma)^2}$ (8) for all integer *n* and *k* = 1, 2,…, *K*. The above kernel formulation represents a more general model for GRAPPA, which includes the conventional GRAPPA as a special case. It is seen that the second part of kernel GRAPPA in Eq. (7) is equivalent to the conventional GRAPPA, which mainly captures the linear relationship between the missing and acquired signals in absent of noise and approximations. The first and third parts of the Eq. (7) can be used to characterize other nonlinear effects in practice such that noise and approximation errors are suppressed.

RESULTS AND DISCUSSION:

Kernel GRAPPA method was evaluated on a set of *in vivo* human brain data acquired using a SE pulse sequence (TE/TR = 10/550 ms, 31.25 kHz bandwidth, 256×256 pixels, FOV = 220 mm^2) on a 3T scanner (GE Healthcare, Waukesha, WI, USA) with an 8-channel head coils (Invivo Corporation, Gainesville, FL, USA). The number of the second-order terms (*N* in Eq. (7)) was chosen to be 4 times of that of the first-order terms. The reconstructed images with an outer reduction factor (ORF) of 5 and 52 ACS lines are shown in Fig. 1. Conventional GRAPPA, regularized GRAPPA [2], and IRLS [4] methods are also shown. They demonstrate that Kernel GRAPPA can suppress the noise in GRAPPA with the same outer reduction factors and ACS lines, without introducing aliasing artifacts as other regularization methods do. We also studied the effects of *N* in reconstruction quality and found that the result is generally good when *N* is 3-12 times of the number of the first-order terms. Within this range, the reconstruction is not sensitive to the changes in *N* and smaller values are preferred for reduced computational complexity.

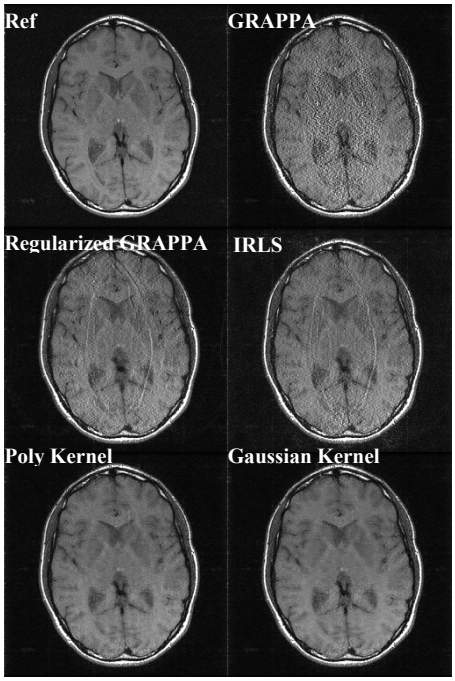

Figure 1 Original, GRAPPA, regularized GRAPPA, IRLS, and Kernel GRAPPA with polynomial and Gaussian kernels when ORF = 5 and ACS = 52.

CONCLUSION:

We propose a novel kernel-based method to improve conventional GRAPPA. The method maps the data onto a higher dimensional space through a nonlinear transformation such that the nonlinear model can characterize the relationship between the acquired and missing data more accurately. The experimental results demonstrate that the proposed method is superior to the conventional GRAPPA and other improved GRAPPA methods in suppressing noise.

REFERENCES:

[1] Griswold MA, et al, MRM 47: 1202-1210, 2002. [2] Qu P, et al, JRMI 24:248-255, 2006. [3] Lin FH, ISMRM 2006. [4] Huo D, et al, JMRI 27:1412-1420, 2008. [5] Tomaso P, et al, Notices of AMS, 50:537-533, 2003. [6] Liu W, et al, IEEE Trans. Sig. Proc. 56: 543-554. [7] Camps-Valls G, et al, IGP, 2007. [8] Berlinet A, et al, Springer-Verlag, 2003. [9] Frieb T, et al, ESANN, 245-250, 1999. [10] Steinwart I, et al., IEEE Tran. Info. Theory 52:4635-4643, 2006.