

Image Domain Based Fast GRAPPA Reconstruction and relative SNR degradation Factor

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Introduction

GRAPPA [1] is a very successful k-space parallel imaging reconstruction method, which but requires a very long reconstruction time for MRI system with up to 32 receiver channels. In this paper, we present an equivalent image space based GRAPPA algorithm, which reconstructs the parallel imaging raw data in the image domain. In this way, the image reconstruction time can be reduced. Because we can calculate the weighting function in the image domain, it is very easy for us to calculate the relative SNR degradation due to parallel imaging, which is equivalent to the inverse of the g-factor for SENSE reconstruction. We present here for the first time the relative SNR degradation of the k-space reconstruction method and show that the relative SNR degradation of the k-space fitting method is image content dependent and is not only a value given by the geometry of the coil elements.

Image domain GRAPPA Algorithm

GRAPPA uses the k-space fitting method to reconstruct the images from each receiver channel and the single channel reconstructed images are combined together by using the sum-of-the-square method. Mathematically this procedure can be expressed as a sum of the convolution of the undersampled k-space data $rawdata_{iCh}^{ppa}$ (denoted as ppa data) with the convolution kernel $F_{iCh,kCh}$. Usually the length of the convolution kernel should be

an odd number, with the center component set to 1. Depending on the acceleration factors, some zeros should be defined in the convolution kernel to perform a normal k-space fitting algorithm. After the undersampled raw data of each single channel is fitted to full sampled data, they need to be Fourier transformed to get the data in the image domain $image_{kCh}^{full}$. GRAPPA uses then sum-of-the-square to combine single channel images into one complete result $image^{sos}$

Because we know that a convolution in k-space is equivalent to a point-by-point multiplication in the image domain [2], we can write the GRAPPA method also in the image domain (see equation on the right side), with $image_{iCh}^{full}$ represent the fitted image of the channel kCh , $image_{iCh}^{ppa}$ image data of undersampled raw data of the channel iCh and $f_{iCh,kCh}$ the fitting coefficient, which is obtained by the Fourier transform of the convolution kernel in k-space $F_{iCh,kCh}$. To calculate the sum-of-the-square image $image^{sos}$, we use the calculated sum-of-the-square profile P_{kCh} , which can be calculated from the reference lines of the parallel acquisition.

It is obvious that the result sum-of-the-square image must be identical to the k-space domain GRAPPA algorithm. The only difference between the two methods is the different convolution definition in the boundary area of the raw data, which is very small. In this way, we derived an expression for the weighting function w_{kCh} , which can be used for the image reconstruction in the image space domain.

SNR degradation factor due to iPAT reconstruction

Without losing generality, we can simply assume that all receiver channels are not correlated and the noise power is equal to unit. The relative SNR degradation compared to the sum-of-the-square algorithm can be calculated according to [3]. The inverse of the relative SNR is equivalent to the g-factor in the sense related paper [4].

Results

The raw data of Fig.1 is acquired from the Siemens Trio system with 8-channel head coil array in Beijing MR Center for Brain Research. The images have been reconstructed by using both k-space and image domain GRAPPA methods. No difference can be observed between the two algorithms. The calculation time for the image domain method should be much faster than the k-space method. We present also, for the first time to the knowledge of the authors, the SNR degradation of k-space parallel imaging methods (Fig. 2, 1/SNR is shown for easy comparison with g-factor). The relative SNR degradation is similar to the inverse of the g-factor for Sense method. Generally, fitting coefficients used for k-space reconstruction method is not only coil sensitivity profiles determined, when the number of channels is larger than the acceleration factor. Because GRAPPA reconstruction is done with segmentation in the readout direction, we see therefore strong SNR difference between neighboring segments. We avoid using the g-factor definition, just because in the k-space method, the SNR degradation is image content dependent and is not only a factor of the coil geometry.

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Reference

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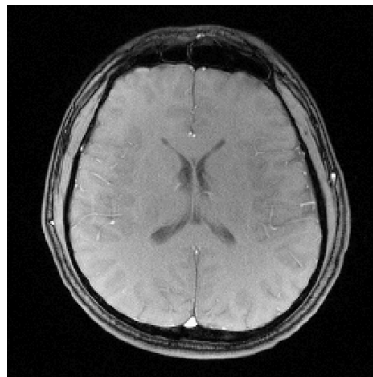


Fig.1

$$rawdata_{kCh}^{full} = \sum_{iCh=1..nCh} rawdata_{iCh}^{ppa} \otimes F_{iCh,kCh}$$

$$image^{sos} = \sqrt{\sum_{kCh=1..nCh} |image_{kCh}^{full}|^2}$$

with the convolution kernel $F_{iCh,kCh}$. Usually the length of the convolution kernel should be an odd number, with the center component set to 1. Depending on the acceleration factors, some zeros should be defined in the convolution kernel to perform a normal k-space fitting algorithm. After the undersampled raw data of each single channel is fitted to full sampled data, they need to be Fourier transformed to get the data in the image domain $image_{kCh}^{full}$. GRAPPA uses then sum-of-the-square to combine single channel images into one complete result $image^{sos}$

$$image_{kCh}^{full} = \sum_{iCh=1..nCh} image_{iCh}^{ppa} \cdot f_{iCh,kCh}$$

$$image^{sos} = \sum_{kCh=1..nCh} image_{kCh}^{full} \cdot P_{kCh}^*$$

$$= \sum_{iCh=1..nCh} image_{iCh}^{ppa} \cdot w_{kCh}$$

with the weighting function w_{kCh} defined as:

$$w_{kCh} = \sum_{iCh=1..nCh} f_{iCh,kCh} \cdot P_{kCh}^*$$

$$SNR^{rel} = \frac{\sum_{k=1..nCh} w_{kCh} \cdot P_{kCh}}{\sqrt{\sum_{k=1..nCh} |P_{kCh}|^2} \cdot \sqrt{\sum_{k=1..nCh} |w_{kCh}|^2}}$$

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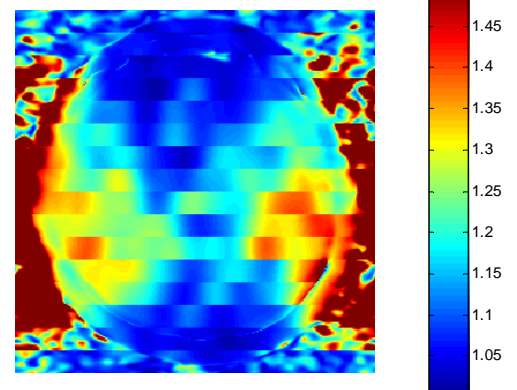


Fig.2