A 3D GRAPPA algorithm for volumetric parallel imaging

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Introduction:

In volumetric parallel imaging, data reduction is carried out along two phase encoding directions, thereby exploiting sensitivity variations in two spatial dimensions and yielding improved parallel imaging reconstruction performance. In previous work, imagedomain based two-dimensional SENSE reconstruction methods have been presented for rectangular [1] and 2D CAIPIRINHA-type reductions [2]. However, it appears that in applications where sensitivity maps, as required for SENSE reconstruction, are hard to obtain, the GRAPPA method is beneficial. Aliasing in the full-FOV reconstructed image has also been reported to work only with GRAPPA [3]. Recently, a GRAPPA algorithm for volumetric parallel imaging has been presented [4], which operates by applying the GRAPPA operator [5] in two successive steps in each direction separately. However this strategy is suboptimal because, data points reconstructed in the first step are used in the second reconstruction step. For this reason, a 3D GRAPPA formalism for volumetric parallel imaging is presented which works in three dimensional k-space, allowing the reconstruction of both rectangular and 2D-CAIPIRINHA-type reduced data sets.

Methods: In vivo abdomen 3D FLASH experiments were performed on a 1.5T clinical Scanner (Avanto, Siemens) equipped with a 12 channel body array for signal reception. The experiment was accelerated using conventional rectangular reduction (R=2x2) and 2D CAIPIRINHA -type reduction (R=4). A low-resolution fully-encoded reference scan was used as autocalibration (ACS) to calculate the 3D GRAPPA reconstruction weights. To this end, a small threedimensional reconstruction kernel (eg. 5x5x3) is chosen from the ACS data, where source points are selected according to the reduced 2D sampling scheme (here CAIPIRINHA-type (see Fig. 1 left)). In this schematic,





only the middle section of the three dimensional kernel is displayed, containing the (R-1) target points selected according to the missing points (see Fig. 1a). By sliding the 3D kernel through the 3D ACS data, multiple repetitions of the kernel can be found and assembled in a source \hat{S}_{src} and target matrix \hat{S}_{trg} . By fitting the source matrix to the target matrix via generalized matrix inversion (pinv), three-dimensional GRAPPA reconstruction weights \hat{w} are derived (see Fig. 1a). These weights are applied to the acquired data, which are then assembled in a source vector \vec{S}_{acq} and used to directly solve for the missing data \vec{S}_{clc} (see Fig. 1b). By sliding the 3D pattern through the undersampled three-dimensional data, all the missing points can be calculated. Following this procedure, the data must be reordered according to the correct sampling positions in each coil, thereby arriving at the full 3D k-space in each coil.

<u>Results:</u> In Fig.2 3D GRAPPA reconstruction results are presented after four-fold (b) rectangular (R=2x2) and (c) CAIPIRINHA-type reductions, showing one partition from the 3D data set. As a reference (a) the fully encoded unaccelerated corresponding partition is given. As can be seen, the 3D GRAPPA algorithm provides good image quality for both rectangular and 2D CAIPIRINHA-type reductions. However, the latter sampling scheme performs better because sensitivity variations provided by the coil array are exploited more efficiently.



Figure 2: 3D GRAPPA reconstructions after R=4 (b) rectangular (R=2x2) and (c) 2D CAIPIRINHA-type (R=4) undersampling and (a) the unaccelerated reference.

Discussion: A 3D GRAPPA algorithm for volumetric parallel imaging has been presented. In contrast to previous reported k-space based strategies, the method presented here solves directly for the missing data points in three dimensional k-space and therefore is applicable to arbitrary Cartesian sampling schemes.

References:

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