

Improved parallel imaging with GRAPPA with large virtual coils arrays for time-resolved applications

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Introduction: Parallel imaging [1,2] is based on the simultaneous measurement of the MR signal with multiple receiver coils. The different sensitivity profiles of the coils modulate the signal of the object in different ways. It is thus possible to accelerate the measurement by compensating a reduction of the number of phase encodings by using spatial information derived from the coils sensitivity profiles without loss of information. The motion of an object can also be seen as a modulation of the object and of its MR-signal. Therefore, a time resolved measurement of a moving object can be considered as an acquisition with multiple (virtual) receiver coils along the temporal dimension. Assuming a N -element receive array and M time frames, parallel imaging reconstruction can then be performed by treating each element and time frame as an independent virtual coil resulting in a large virtual $N \times M$ coil array. In this work we investigated this hypothesis for time-resolved (CINE) phantom and an in-vivo cardiac measurement and compared the results to standard GRAPPA [2] reconstructions.

Methods: Phantom and in-vivo measurements were performed on a 3T system (Trio, Siemens, Germany) with full k-space sampling. To obtain undersampled data, phase encoding lines were retrospectively removed and set to zero according to a standard GRAPPA sampling scheme, i.e. the identical undersampling patterns for all time points (central calibration lines and undersampling of outer regions by R). The phantom measurement was performed with a $N=12$ channel body coil using an rf-spoiled CINE gradient echo sequence (matrix size = 256×256 , spatial resolution = 0.94×0.94 mm, temporal resolution 16.8 ms ($M=68$ time frames)). The phantom consisted of a moving object filled with agarose gel and a static water bottle. The moving phantom oscillated with a frequency of approximately 1Hz. Additionally, in-vivo short axis cardiac images were acquired during breathhold with $N=15$ coil elements. A 2D CINE balanced SSFP sequence was used with matrix size = 202×198 , spatial resolution = 1.4×1.4 mm and temporal resolution = 33 ms ($M=26$ time frames). All GRAPPA reconstructions were performed with the same number of auto calibration lines $N_{ACS} = 24$ and a kernel size of $b_x = 5$ and $b_y = 4$ for the undersampling factors $R = 2, 4$. Two different reconstruction pathways were tested. The first was a standard GRAPPA reconstruction, i.e. GRAPPA weight calculation and image reconstruction was performed for each time point separately using ACS data from N coils. Secondly, the time and coil dimension were treated equally as a virtual coil dimension with $N_{VC} = N \times M = 816$ for the phantom and $N_{VC} = N \times M = 390$ for the cardiac data. ACS data from all N_{VC} measurements were used to estimate a single set of coil weights for the entire CINE data set which was then used to reconstruct all time frames. All reconstructions were performed in Matlab using the same GRAPPA reconstruction code for the two reconstruction pathways. The ACS data were not copied back after the reconstruction. The coil combination was performed with the sum-of-squares method. To estimate the image quality of the different reconstructions the root-mean-square-errors (RMSE) compared to the fully sampled reference images were computed for each time frame and then averaged.

Results: The phantom results in Fig. 1 show a clear improvement in image quality for GRAPPA reconstructions based on the large virtual coil array compared to standard GRAPPA, especially for $R = 4$. In the difference images a small improvement is also visible for $R = 2$. Figure 2 shows the results for in-vivo cardiac imaging. For $R = 2$, similar image quality was obtained for both reconstruction methods, whereas for $R = 4$ virtual coil reconstruction resulted in improved image quality. The results of the RMSE analysis for the phantom and the cardiac data are summarized in Fig. 3 and confirm the visual impressions in Fig. 1 and 2.

Discussion: The findings of this feasibility study clearly show that the time domain can have similar encoding properties as the coil dimension. The comparison of the phantom and the cardiac measurement also shows that the encoding potential clearly depends on the object and the motion. The main difference to other methods which incorporate the temporal domain into the reconstruction process such as UNFOLD [3], k-t SENSE [4], k-t GRAPPA [5] and k-t PARS [6] is that the undersampling pattern was not shifted in time. Simply by combining the coil and the time dimension into one dimension an improved reconstruction could be achieved by using the same sampling pattern and the same reconstruction algorithm as for standard GRAPPA. The method is especially useful for high reduction factors. However, as there is no penalty for using the virtual coil reconstruction, the method may be useful for imaging with any acceleration factor. Future work is needed to investigate the behavior of the virtual coil reconstruction for other objects and motion patterns. Also the dependency of the image quality on the GRAPPA parameters such as the amount of calibration data and the kernel size is important.

Acknowledgements: Grant support by the Deutsche Forschungsgemeinschaft (DFG), Grant # MA 2383/5-1 and the Bundesministerium für Bildung und Forschung (BMBF), Grant # 01EV0706.

References: [1] Pruessmann et al. MRM 1999; 42:952-62 [2] Griswold et al. MRM 2002; 47:1202-10 [3] Madore et al. MRM 1999; 42:813-28 [4] Tsao et al. MRM 2003; 50:1031-42 [5] Huang et al. MRM 2005; 54:1172-84 [6] Samsonov et al. MR Angio Club 2007

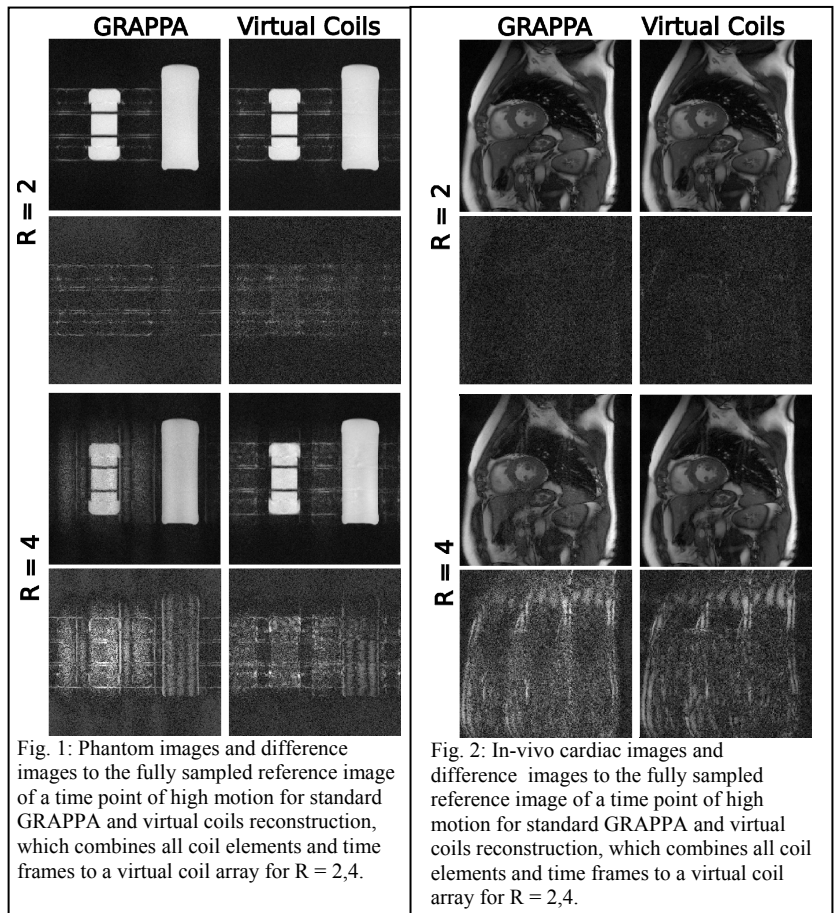


Fig. 1: Phantom images and difference images to the fully sampled reference image of a time point of high motion for standard GRAPPA and virtual coils reconstruction, which combines all coil elements and time frames to a virtual coil array for $R = 2, 4$.

Fig. 2: In-vivo cardiac images and difference images to the fully sampled reference image of a time point of high motion for standard GRAPPA and virtual coils reconstruction, which combines all coil elements and time frames to a virtual coil array for $R = 2, 4$.

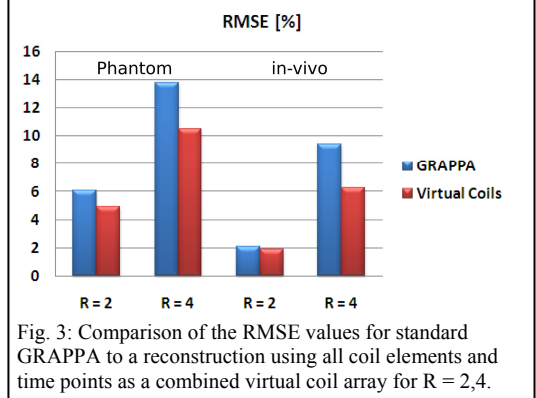


Fig. 3: Comparison of the RMSE values for standard GRAPPA to a reconstruction using all coil elements and time points as a combined virtual coil array for $R = 2, 4$.