A parallel computing framework for motion-compensated reconstruction based on the motion point-spread function.

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INTRODUCTION

Generalized reconstruction frameworks allowing correction of nonrigid displacements during MR acquisition (inter-view motion) have been proposed recently [1,2]. Their main drawback is their computational complexity which makes them currently impractical for clinical use. Based on the properties of the point-spread function (PSF) describing the occurrence of motion-artifacts, we propose a method for splitting the reconstruction process into several reconstruction tasks of smaller size. This allows easier and more efficient implementation of these algorithms on a parallel architecture such as a cluster of workstation, both in terms of reconstruction time and memory requirement.
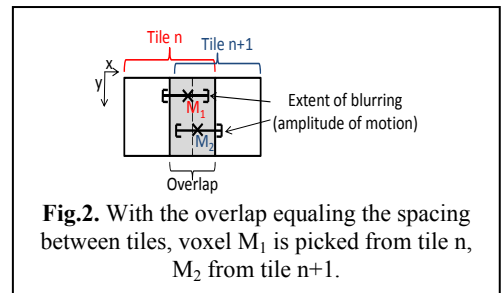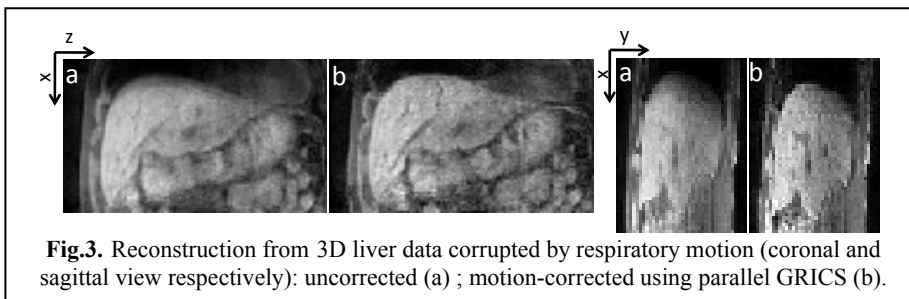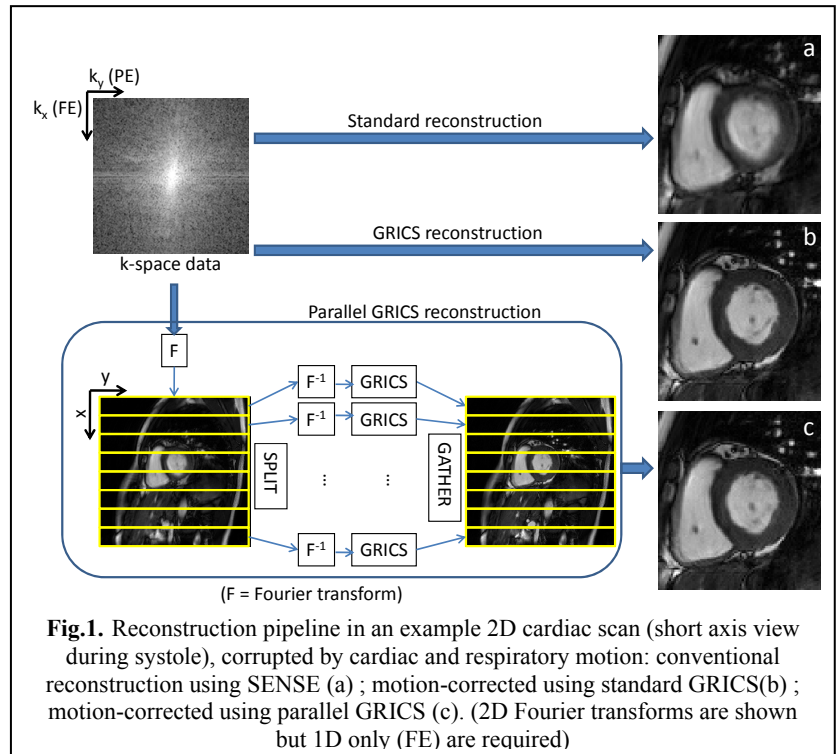
METHODS

The analytical PSF describing motion artifacts was given in [3], in the simplified case of a periodic (sine wave) translational motion in both frequency-encoding (FE) and phase-encoding (PE) direction(s), in a spin echo experiment. This PSF results in a blurring in the FE direction and a combination of ghosting and blurring in the PE direction(s). Since artifacts in the FE direction are well localized, we propose to split the field-of-view into tiles of reduced width in 2D (or thin slabs in 3D), by linearity of the acquisition system (see Fig. 1). Then data from the different tiles (or slabs) are reconstructed independently, enabling coarse grain parallelization. Finally the results are gathered to form the final image. To avoid side effects near the edges of the tiles, overlapping is employed. If the maximal amplitude of motion in FE direction is A, then both the spacing between tiles and the overlapping can be set to A. This ensures that, for each voxel, the artifact signal (the blurring) is entirely contained in at least one tile, and thereby can be corrected (see Fig.2). The GRICS algorithm [2] with the splitting technique was tested on a 240 core cluster of workstations with real motion-corrupted 2D cardiac cine images and 3D liver images, acquired on a 1.5T Philips Achieva clinical scanner (Best, The Netherlands), with a 32 channel cardiac coil array. The reconstruction framework was the same as described in [4], and 1D navigators provided us with the prior knowledge about motion (i.e. the "driving signals" of the motion model in GRICS). Results were compared to the single-threaded reconstruction of the full slice or volume.

RESULTS

In a typical 3D liver dataset, the computation time was reduced from 5.3 hours to 17.4 min (18-fold speed-up), with a splitting into 59 slabs of 13.6 mm thickness (6.8 mm spacing between slabs + 6.8 mm overlapping). The images reconstructed without and with the splitting technique were visually similar and showed efficient artifact reduction (see Fig. 1 and Fig.3).

DISCUSSION AND CONCLUSION

In the case of arbitrary motion, artifacts are not described in terms of a simple PSF as for a periodic translation, but in the FE direction they can still be described by a local blurring (no ghosts are produced in FE direction). This makes the splitting technique applicable to real motion-corrupted data, as shown in our results. The choice of the width of each tile (or slab), as well as the amount of overlapping, is important and is related to the maximal amplitude of motion in FE. This information might be derived from the data themselves.

Fig.1. Reconstruction pipeline in an example 2D cardiac scan (short axis view during systole), corrupted by cardiac and respiratory motion: conventional reconstruction using SENSE (a) ; motion-corrected using standard GRICS(b) ; motion-corrected using parallel GRICS (c). (2D Fourier transforms are shown but 1D only (FE) are required)

Fig.2. With the overlap equaling the spacing between tiles, voxel M_1 is picked from tile n, M_2 from tile n+1.

Fig.3. Reconstruction from 3D liver data corrupted by respiratory motion (coronal and sagittal view respectively): uncorrected (a) ; motion-corrected using parallel GRICS (b).

REFERENCES

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