

RANDOM-PROJECTION GRAPPA: AN EFFICIENT COMPUTATIONAL METHOD FOR PARALLEL MRI RECONSTRUCTION

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Description:

As a data-driven technique, GRAPPA has been widely used for parallel MRI reconstruction. In GRAPPA, a large amount of calibration data is desirable for accurate calibration and thus estimation. However, the computational time increases with the large number of equations to be solved, which is especially serious in 3-D reconstruction. To address this issue, a number of approaches have been developed to compress the large number of physical channels to fewer virtual channels. The hardware approaches are cumbersome and the software approaches have other optimization issues addressed by the novel method developed by UB researchers in this invention.

This novel technology uses random projections to reduce the dimension of the problem in the calibration step. Our unique technology acquires Parallel MRI ("pMRI") (a method of collecting data using multiple detector coils allowing for decreased collection times) signals simultaneously through a number of receiving coils, where each coil has localized sensitivity respective to an imaged volume combine with auto calibrating pMRI signals to fast estimate the fitting coefficients for each coil with random projection. The technology is a fast algorithm to process the data acquired from MRI scanners with massive array coils and reconstruct the final high quality images for diagnosis.

The technology is potentially able to save the processing and reconstruction time of the existing commercial method by at least two to ten orders of magnitude, without use of any supercomputing hardware. Such a saving will allow all massive data being fully utilized in processing such that the image quality is significantly improved for better diagnosis.

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