Comparison of Pre-reconstruction Interpolation Methods for Rapid Compressed Sensing Reconstruction of Non-Cartesian *k*-Space

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Purpose

Compressed sensing and other iterative reconstruction algorithms are greatly improving MRI capabilities. Non-Cartesian *k*-Space trajectories, however, result in slower iterative algorithms since an algorithm such as the non-uniform fast Fourier transform (NUFFT)[1] is needed at each iteration. Some researchers have instead interpolated onto nearby Cartesian grid points prior to the iterative reconstruction, and used a fast Fourier transform algorithm for reconstruction. In this study we compare three fast pre-reconstruction interpolation (also termed pre-interpolation) methods to the more standard iterative reconstruction using NUFFT.

Methods

The three interpolation methods we selected to compare are: 3-point interpolation (implemented as MATLAB's griddata[2]), nearest-neighbor interpolation (NN), and GRAPPA Operator Gridding (GROG)[3]. The first two methods pre-interpolate data one coil at a time whereas the last (GROG) uses all coils simultaneously via a set of GRAPPA coefficients which are directly calculated from the measured data.

These three methods and NUFFT were used to reconstruct golden-ratio radial perfusion datasets that were acquired previous to this study. These datasets were derived from a variety of acquisition sequences (20, 24 and 30 ray, gated and ungated dynamic contrast enhanced cardiac perfusion) to test for robustness of the method. The datasets were first interpolated by each method under study to Cartesian points (see Fig. 1) and then reconstructed by 100 iterations of spatiotemporal constrained reconstruction (STCR)[8]. The same STCR weight parameters were used for all three interpolation methods but the NUFFT weights were independently tuned.

Additionally, to explore the effect that undersampling has on each interpolation method, we artificially undersampled a 30-ray ungated perfusion golden-ratio dataset by sequentially dropping rays from the acquisition in each frame.

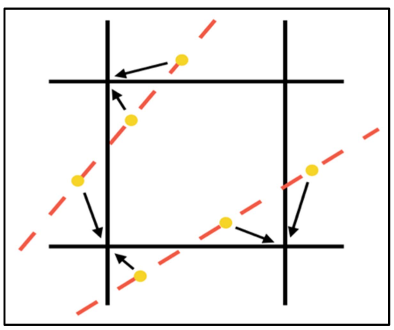

Figure 1. Along each ray (red dashed lines) there are many data points which do not fall on a Cartesian coordinate (yellow circles). All three pre-interpolation methods map existing data to nearby Cartesian locations (black arrows).

Results

Fig. 2 shows difference images for each of the interpolation methods compared to NUFFT. These images are rescaled and normalized so that values represent percent difference from NUFFT. Fig. 3 shows the root mean square difference (RMSD) of each image plotted as a function of time during the sequence. Fig. 4 shows the result of simulated undersampling, again using RMSD to quantify the similarity between reconstructed images.

Discussion

The difference images show that of the three, the multi-coil method (GROG) is the most similar to NUFFT. The RMSD vs Time plot shows that despite relatively large variation in accuracy across a dataset, from point to point, the GROG method is able to consistently outperform the single-coil methods in terms of reproducing an NUFFT-like image.

We also see in Figure 4 that the two single-coil methods perform more similarly as the data set becomes more undersampled, whereas the GROG method consistently performs well even down to 10 rays.

These methods permit significant speedups since we timed MATLAB's FFT algorithm to be on average 5.7 times faster than the NUFFT algorithm[1].

Conclusion

A collection of data sets were reconstructed to demonstrate that RMSD values of images gridded with GROG are lower than those for images gridded using NN interpolation or 3-point interpolation when evaluated with NUFFT reconstruction as the reference standard.

Sources

[1] Fessler, J.A; Sutton, B.P. Sig Proc, IEEE Trans 2003;51(2):560-74. [2] The MathWorks, Inc. U.S.A. [3] Seiberlich N, et. al. Magn Reson Med. 2007;58(6):1257-65.

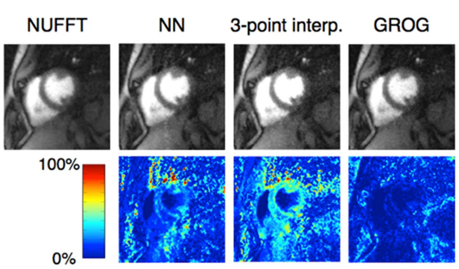

Figure 2. One time frame shown, 24-ray, golden-ratio, ungated perfusion dataset. Top: Reconstructed imags from each method. Bottom: Normalized difference images between method and NUFFT.

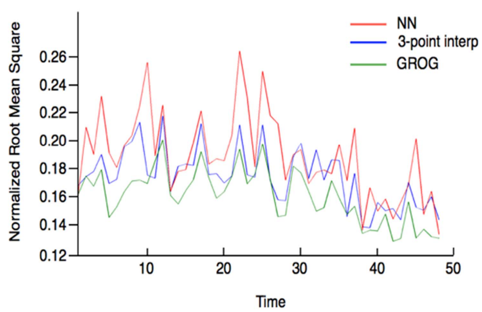

Figure 3. RMSD as a function of time for a 24-ray golden-ratio ungated perfusion dataset.

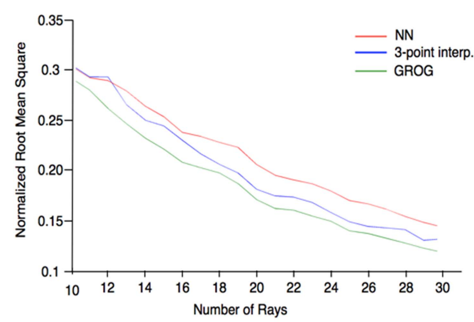

Figure 4. RMSD as a function of undersampling-rate for a 30-ray golden-ratio ungated perfusion dataset for one time frame.