Technical Note: Evaluation of pre-reconstruction interpolation methods for iterative reconstruction of radial k -space data

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Purpose: To evaluate the use of three different pre-reconstruction interpolation methods to convert non-Cartesian k -space data to Cartesian samples such that iterative reconstructions can be performed more simply and more rapidly.

Methods: Phantom as well as cardiac perfusion radial datasets were reconstructed by four different methods. Three of the methods used pre-reconstruction interpolation once followed by a fast Fourier transform (FFT) at each iteration. The methods were: bilinear interpolation of nearest-neighbor points (BINN), 3-point interpolation, and a multi-coil interpolator called GROG Operator Gridding (GROG). The fourth method performed a full non-Uniform FFT (NUFFT) at each iteration. An iterative reconstruction with spatiotemporal total variation constraints was used with each method. Differences in the images were quantified and compared.

Results: The GROG multicoil interpolation, the 3-point interpolation, and the NUFFT-at-each-iteration approaches produced high quality images compared to BINN, with the GROG-derived images having the fewest streaks among the three preinterpolation approaches. However, all reconstruction methods produced approximately equal results when applied to perfusion quantitation tasks. Pre-reconstruction interpolation gave approximately an 83% reduction in reconstruction time.

Conclusion: Image quality suffers little from using a pre-reconstruction interpolation approach compared to the more accurate NUFFT-based approach. GROG-based pre-reconstruction interpolation appears to offer the best compromise by using multicoil information to perform the interpolation to Cartesian sample points prior to image reconstruction. Speed gains depend on the implementation and relatively standard optimizations on a MATLAB platform result in preinterpolation speedups of ~ 6 compared to using NUFFT at every iteration, reducing the reconstruction time from around 42 min to 7 min. © 2017 American Association of Physicists in Medicine [https://doi.org/10.1002/mp.12357]

Key words: constrained reconstruction, GROG, interpolation, iterative, MRI, non-Cartesian, NUFFT

1. INTRODUCTION

Iterative algorithms for image reconstruction are greatly improving MRI capabilities. Many of these algorithms require one or more Fourier transforms at each iteration and are

therefore well-suited to Cartesian data, thanks to highly optimized implementations of the fast Fourier transform algorithm (FFT). When applied to the problem of reconstructing non-Cartesian data, however, iterative reconstruction can be time consuming because the FFT does not process non-Cartesian data

therefore a full Fourier summation must be performed instead.¹ Because non-Cartesian acquisition schemes benefit a wide variety of applications including cardiac perfusion,² angiography,³ and quantitative oncological imaging,⁴ faster alternatives to a direct Fourier sum have been explored.

Popular methods for avoiding a direct $O(n^2)$ Fourier summation include the nonuniform fast Fourier transform (NUFFT) provided by Fessler and Sutton⁵ and the nonequispaced fast Fourier transform (NFFT) provided by Keiner et al.⁶ In both implementations, Kaiser-Bessel interpolation⁷ is followed by a standard FFT to approximate the sum. Fessler and Sutton reported this interpolation step requires roughly twice as much time as the FFT step in their implementation leading to an expected threefold time requirement when reconstructing non-Cartesian data compared to Cartesian because both the interpolation and FFT steps must be performed at each iteration of reconstruction.

To avoid this, some researchers have instead converted their non-Cartesian MRI data into Cartesian data prior to reconstruction by interpolating onto nearby Cartesian grid points. This pre-reconstruction interpolation (also called preinterpolation) replaces the measured non-Cartesian data with a similar number of points on Cartesian grid locations. The new undersampled Cartesian data can then be used with iterative algorithms, to avoid the need of estimating non-Cartesian values at each iteration. This is an approximation, but may still provide useful reconstructions. For example, in 2010 Uecker et al. reported real-time MRI with high temporal resolution by interpolating non-Cartesian data prior to iterative reconstruction.⁸ Likewise, Adluru et al.⁹ interpolated undersampled radial data onto Cartesian grid points that were within 0.5 units of a measured sample before performing iterative reconstruction. Another approach, replacing gridding with a pre-computed point-spread function on a $2\times$ oversampled grid, is also possible,^{10,11} but is not studied in this work.

In this paper, we compare three pre-reconstruction interpolators to the NUFFT implementation by Fessler and Sutton⁵ in terms of speed and accuracy, treating NUFFT (with its concomitant interpolation at each iteration) as the gold-standard in this type of reconstruction problem.

2. MATERIALS AND METHODS

For this study, we used the multicoil spatiotemporal constrained reconstruction (STCR)⁹ algorithm for image reconstruction. This method reconstructs the image by iteratively minimizing a cost function with tunable weight parameters α_1 and α_2 :

$$c(m) = \sum_i \|WFS_i m - d_i\|_2^2 + \alpha_1 \left\| \sqrt{(\nabla_x m)^2 + \varepsilon} \right\|_1 + \alpha_2 \left\| \sqrt{(\nabla_x m)^2 + (\nabla_y m)^2 + \varepsilon} \right\|_1. \quad (1)$$

This equation is described in detail in Ref. [9], so here we explain only the first term that requires Fourier transforms at

each iteration. This term is the data fidelity term where $\mathcal{F}$ is a Fourier transform operator, W represents a binary mask of sampled locations and S_i is the coil sensitivity map for coil element i . These three terms simulate the sampling process of the estimated image m . To derive the fidelity term, the difference between the forward projection of the estimated image and the acquired (for NUFFT implementation) or preinterpolated k -space data d_i for each coil is first computed, then a summation of the l_2 -norms squared of the differences gives the cost of the fidelity term. For preinterpolation reconstructions, the estimated image is not compared to the actually acquired data but to a Cartesian k -space estimation of the acquired data, hence the reconstruction using NUFFT (which includes interpolation and FFTs) at every iteration is the gold-standard for non-Cartesian k -space.

Since the FFT estimates an intensity for every point on the Cartesian grid based on the estimated image, a binary mask W representing the radial sampling points on Cartesian grid is necessary. Such a mask is not necessary for NUFFT reconstruction since the NUFFT algorithm only estimates the intensities on desired points. That means at each execution of the forward NUFFT, an FFT followed by interpolation to the desired points takes place (or for the inverse NUFFT, interpolate first then inverse FFT). Therefore, the computational difference between the NUFFT approach and the preinterpolation approach at each iteration is that NUFFT computes two interpolations and performs an FFT and an inverse FFT, whereas the preinterpolation strategy performs an FFT followed by multiplication of a sampling mask and an inverse FFT.

A complex sensitivity map S_i of each coil is estimated before the iterative reconstruction, by projecting all k -space data into a set of coil images using the corresponding NUFFT or preinterpolation method, then calculating S_i from these coil images using an eigenvector method.¹² This sensitivity map is used to map the estimated image onto each coil for comparing with the k -space data d_i , and to recombine the update images from all coils.

2.A. Bilinear interpolation

We created a hybrid algorithm between nearest-neighbor and bilinear interpolation, termed Bilinear Interpolation of Nearest-Neighbor points (BINN). This algorithm calculates a weighted average of nearest (unit distance) points based on distance:

$$\frac{\sum_i^N S_i w_i}{\sum_i^N w_i}. \quad (2)$$

Where S_i is the signal from non-Cartesian location i and w_i is one minus the distance between non-Cartesian location i and the new Cartesian location. This way no samples go unused (a shortcoming of simple nearest-neighbor interpolation), and if more than one sample is within 0.5 units of a Cartesian location, they are each given weight proportional to their proximity to the desired point and then averaged.

2.B. 3-point interpolation

The 3-point interpolator we used was MATLAB's (MATLAB version 9.1.0.441655, R2016B, MathWorks, Natick, MA, USA) `griddata` function and in this paper will be referred to as Grid3. This algorithm fits a surface function based on triangulation to the data points at the sampled locations given in the trajectory. Then, griddata uses that surface function to compute new values at the desired (Cartesian) points.

However, the use of only the nearest three samples can be limiting when Grid3 is used where sample points are dense, such as the center of k -space when using radial or spiral trajectories. This issue makes the Grid3 perform relatively poorly when k -space is sampled with a large number of rays. To overcome this disadvantage, we interpolated the acquired radial k -space data onto a finer Cartesian grid, and define an overinterpolation factor (OIF) as

$$OIF = \frac{N_c}{N_r}, \quad (3)$$

where the N_c is number of points on each side of the overinterpolated grid and N_r is the number of data points on each radial ray. The "oversampled Cartesian" k -space was then resampled to the standard size k -space by sinc interpolation implemented by Fourier transforming to image space, cropping the image to be of size $N_r \times N_r$, and applying an inverse Fourier transform. This k -space data were multiplied by the sampling mask to be the k -space data used in the fidelity term of Eq. (1).

2.C. GROG interpolation

The third method we investigated was a multicoil method called GRAPPA Operator Gridding (GROG).¹³ This method uses GRAPPA operator theory¹⁴ to map data values from measured locations in k -space (k_x, k_y) to unmeasured locations a distance ($\Delta k_x, \Delta k_y$) away,

$$S'(k_x + \Delta k_x, k_y + \Delta k_y) = G_x^{\Delta k_x} G_y^{\Delta k_y} S(k_x, k_y). \quad (4)$$

In the above equation, G_x and G_y are $N_c \times N_c$ GRAPPA coefficient matrices where N_c is the number of coils. $S(k_x, k_y)$ is the $N_c \times 1$ vector of acquired data at location (k_x, k_y) and $S'(k_x + \Delta k_x, k_y + \Delta k_y)$ is the shifted data vector at location ($k_x + \Delta k_x, k_y + \Delta k_y$). G_y computes a unit shift in the positive k_y direction and G_x computes a unit shift in the positive k_x direction. As explained in Seiberlich et al.,¹³ a GRAPPA matrix of unit shift distance (like G_x and G_y) can be raised to a power to obtain a shift matrix for any shift distance in k -space.

Though G_x and G_y can be obtained in a normal GRAPPA-like manner from a fully sampled part of k -space (such as auto-calibration signal lines), they can also be obtained directly from radial data itself as in the self-calibrating GROG (scGROG) method.¹⁵ In this study, we used scGROG to compute G_x and G_y and then shifted non-Cartesian values from their original locations to Cartesian locations using the formula given above.

2.D. NUFFT interpolation

We compared the above methods to the well-studied convolution-based interpolation employed by the NUFFT algorithm. The inverse NUFFT takes as input the data and trajectory and then transforms the non-Cartesian k -space into Cartesian image space with minimal error,⁵ and the resultant images from NUFFT can be further reconstructed with an iterative algorithm which includes forward and inverse NUFFT operations at each iteration. The radial k -space was filtered by a Ram-Lak filter as density compensation before each inverse NUFFT operation. The NUFFT software we used was obtained from <http://web.eecs.umich.edu/~fessler/irt/irt/nufft> and then modified to fit this study. We used the default parameters: interpolation kernel = 6×6 and over-sampling factor = 1.5. MATLAB code of the four reconstruction methods used in this paper is available at <https://github.com/edibella> with the 24-ray ungated dataset described below.

2.E. Data

We acquired a 24-ray, golden-ratio radial, saturation recovery phantom dataset for 100 time frames on a 3T Prisma MRI scanner (Siemens Medical Solutions, Erlangen, Germany) with a 20 channel phased-array receive coil. The first 420 rays were selected to be the test dataset. The scan parameters were: slice thickness = 7 mm, flip angle = 5 degrees, pixel size = 1.8 mm $\times$ 1.8 mm, TE = 1.3 ms, matrix size 288 $\times$ 24 rays, and a saturation preparation pulse was used before each time frame.

Additionally, we chose two human cardiac perfusion datasets for comparative reconstructions. These cardiac studies were approved by the University of Utah Institutional Review Board. Both were acquired on a 3T Verio MRI scanner (Siemens Medical Solutions, Erlangen, Germany) with a 32 channel phased-array receive coil, and used a 0.05 mmol/kg dose of gadoteridol for contrast.

The first dataset, which we will refer to as the gated dataset, was from a 34-yr-old normal volunteer and consisted of 30 ray, golden-ratio radial, saturation recovery, ECG gated, cardiac perfusion data. The scan parameters were as follows: slice thickness = 7 mm, 7 slices, flip angle = 10 degrees, pixel size = 1.8 mm $\times$ 1.8 mm, TE = 1.37 ms, matrix size 144 $\times$ 30 rays. We used a saturation preparation pulse repeated every five slices and used slice five for comparative reconstruction.

The second dataset was from a 23-yr-old normal volunteer and consisted of 24-ray, golden-ratio, radial, saturation recovery, non-ECG gated, cardiac regadenoson stress perfusion dataset with the following scan parameters: TR = 2.2 ms, TE = 1.25 ms, matrix size 144 $\times$ 24 rays, slice thickness = 8 mm, 4 slices, flip angle = 10 degrees, pixel size = 1.9 mm $\times$ 1.9 mm. Slice three was used for comparative reconstruction.

Before creating the reconstructions for the comparisons, the ungated dataset was reconstructed using the Grid3

method and binned into near-systolic and near-diastolic time frames using a self-gating method.¹⁶ Only the k -space near-systolic frames were then used for reconstruction and hence this dataset will be referred to as the self-gated dataset.

All of the datasets were first scaled, so that the mean absolute intensity had a magnitude of order 10 and then were compressed in the coil dimension via principal component analysis to give the eight most representative virtual coils for reconstruction.¹⁷

The reference image for the phantom was created by combining all 420 rays into a single-frame dataset and then reconstructed using an iterative spatial total variation constrained algorithm with NUFFT. The constraint weight was chosen based on visual comparison of reconstruction images from different weights, by selecting a weight that removes most of noise yet retains most of the details in the images. The weights for the other undersampled images were linearly decreased according to the number of rays used. Reference images for the other two datasets were selected the same way by visual comparison of reconstructed images using NUFFT, and weights for preinterpolation algorithms were kept the same. Due to scaling differences between the Fourier transform operations in interpolation algorithms and the NUFFT algorithm, we rescaled the WFS_m in fidelity term for NUFFT algorithm to have the same mean absolute value as that of the other algorithms for the first iteration, and kept the same scale factor for the rest of the iterations.

For the 420-ray phantom dataset, we used OIF = 15 for Grid3 to improve its reconstruction accuracy. However, for the two cardiac perfusion datasets with relatively fewer rays, we found no significant improvement in image quality based on NRMSE and SSIM of using OIF higher than 1, so we used OIF = 1 for Grid3 when reconstructing those two datasets. Experimental results on how OIF affects reconstruction are discussed in Appendix B.

Lastly, we performed perfusion quantification analysis on the reconstructed images. The reconstructed images were segmented and processed using the software package myocardial perfusion imaging 2D (mpi2D).¹⁸ The boundaries of the epicardium and endocardium were manually defined. To process a given dataset, the heart was divided into six azimuthal regions of interest. The average signal intensity from the blood pool and from each region was converted to gadolinium concentration using Bloch equations. The gadolinium converted tissue curves and arterial input function was then fit to a Fermi function model.¹⁹ The Fermi model only requires the time frames tracking the initial gadolinium bolus, and thus only a subset of the acquired time frames was reconstructed.

2.F. Error analysis

We used the normalized root-mean-square error (NRMSE) metric to compare one-time pre-reconstruction interpolation to every-iteration interpolation (NUFFT). The NRMSE was calculated as follows

$$\begin{aligned} \text{RMSE} &= \sqrt{\frac{\sum_i^N (f_i - g_i)^2}{N}}, \\ \text{NRMSE} &= \frac{\text{RMSE}}{\bar{f}}, \end{aligned} \quad (5)$$

f is the NUFFT-derived image volume (all slices and time frames), g is the pre-reconstruction interpolation-derived image volume, and the index i runs over all of the pixels in the volume N . We also used the structural similarity index (SSIM)²⁰ to compare preinterpolation images to the NUFFT standard.

Because of differences between reconstruction methods, the final images produced by each method were on different intensity scales making them poorly suited to RMSE and SSIM comparison without selecting a compensating scale factor. To increase the relevancy of this kind of analysis, the images were scaled to minimize their RMSE in an ROI. That scale factor was calculated as described in Appendix C.

Additionally, we generated difference images for visual comparison. The pixel intensities were computed as

$$h = \frac{|f - g|}{\bar{f}}, \quad (6)$$

where the definitions of f , g , and $\bar{f}$ are as before.

2.G. Undersampling simulation

To further compare methods, we simulated undersampling on the 420-ray phantom. This process involved dropping a certain number of rays from the end of the dataset and then proceeding with the normal reconstruction algorithm. NRMSE and SSIM analysis were used to determine how undersampling affects reconstruction quality for each method.

3. RESULTS

3.A. Reconstructed images

The top row of Fig. 1 shows one time frame of the reconstructed images from each method for the self-gated dataset. By convention, the acquired field of view (FOV) is doubled in the readout direction during acquisition from 144 readout samples to 288. In Fig. 1, we display the full FOV acquired to clearly show the intensity of the streaking-artifact outside of the body.

The bottom row shows difference image comparisons for the same dataset. The normalized difference images were calculated as described in Eq. (6). Because the difference is sensitive to the cropping region, two choices for different cropping regions are shown. The blue box outlines the field of view (FOV) cropping and the orange box outlines the region of interest (ROI) cropping. Figure 2 shows the reconstructed images for the gated dataset.

3.B. NRMSE and SSIM plots

While the difference images give a visual comparison of the methods, they show only one time frame. In Figs. 3 and 4

Self-Gated Dataset Result

FIG. 1. Top row shows final reconstructed images for all four methods on the 24-ray self-gated dataset. The smaller (orange) box indicates the region of interest (ROI) used in the comparison. Bottom row shows normalized difference images when compared to NUFFT (in the larger region (blue), in the top row of images). In Fig. 3, we see that NRMSE and SSIM values are dependent on cropping. This is due to a large difference in signal intensity estimates for regions outside the body, mainly caused by streaking artifacts. The methods are more similar within the smaller ROI (orange box). [Color figure can be viewed at wileyonlinelibrary.com]

Gated Dataset Result

FIG. 2. Same as Fig. 1 for the gated dataset. The top row shows final reconstructed images for all four methods. The larger box indicates the field of view (FOV) cropping and the smaller box indicates the region of interest (ROI) cropping. The bottom row shows normalized difference images when compared to NUFFT of FOV. The difference is less between methods in the gated dataset as can be seen from the numerical analysis of NRMSE and SSIM below. [Color figure can be viewed at wileyonlinelibrary.com]

FIG. 3. Plot showing how NRMSE and SSIM vary across time frames for the self-gated dataset. FOV: The dashed lines indicate NRMSE values of dataset when a maximum amount of the image is used while excluding bright regions as explained in the text. ROI: The solid lines show NRMSE values obtained when cropping tightly to the cardiac portion of the image. The steep cliff of solid lines at time frame 20 is when the contrast agent enters into the left ventricular (LV), resulting in an increase of the signal intensity. [Color figure can be viewed at wileyonlinelibrary.com]

FIG. 4. Same as Fig. 3 for the gated dataset. Contrast agent enters the LV at time frame 6. [Color figure can be viewed at wileyonlinelibrary.com]

we show the NRMSE and SSIM of each time frame for the two different croppings (FOV and ROI) when comparing each image to an NUFFT-based reconstruction for the self-gated and gated datasets, respectively.

The NRMSE values are strongly affected by the choice of cropping region. This is due to a significant difference between methods being able to suppress artifacts outside the body, and difference in contrast and intensity when estimating certain areas of the images. In the self-gated dataset for example, the rib area (visible in the bottom-left quadrant of Fig. 1 bottom row) has the following mean intensities (in arbitrary units): BINN = 1.41, Grid3 = 1.53, GROG = 1.72,

NUFFT = 1.79, after rescaling according to the formula in Appendix C. Hence, we chose the FOV to exclude most of the bright portions that were not of interest, and chose the ROI to include only the heart.

3.C. Simulated undersampling plots

Figure 5 shows the results of the simulated undersampling experiments. The horizontal axis shows the number of rays used and vertical axis shows the NRMSE or SSIM between the reconstructed image and the 420-ray NUFFT reconstructed reference image as described above.

FIG. 5. NRMSE (left plot) and SSIM (right plot) values from simulated undersampling. The horizontal axis gives the number of rays that were used to reconstruct the image. [Color figure can be viewed at wileyonlinelibrary.com]

FIG. 6. Self-gated perfusion time curves as calculated by the MPI2D software package. These curves show the concentration of the gadolinium-based contrast agent $[(\text{Gd})]$ in the arterial input function (AIF) in the left plot, and in a region of interest in the myocardial tissue in the right plot. [Color figure can be viewed at wileyonlinelibrary.com]

3.D. Perfusion time curves

Perfusion quantification analysis showed similar results for all methods. Figure 6 shows plots of the arterial input function and the tissue curves (averaged over the six ROIs) converted to gadolinium concentration.

3.E. Timing

The total time to reconstruct the self-gated dataset using 150 iterations on a 2.4 GHz 16 core Intel Xeon E5620 processor, and 96 GB 2400 MHz DDR3 RAM was as

follows – BINN: 415.45 s, Grid3: 437.79 s, GROG: 415.45 s, NUFFT: 2506.24 s. The data size for those times was 288 readout samples $\times$ 24 rays $\times$ 99 time frames $\times$ 8 coils. Thus, the pre-reconstruction interpolation methods were 83% faster than the NUFFT method, and had a speedup factor $\sim$ 6. More detailed analysis and further results running on GPU ($\sim$ 20 fold speed-up) are given in Appendix A.

4. DISCUSSION

These pre-reconstruction interpolation methods can be applied broadly to non-Cartesian image reconstruction in a

variety of applications, such as spiral trajectory MR images and 3D MR images. The primary reason to use a preinterpolation approach is to save image reconstruction time by interpolating only once, prior to reconstruction, instead of at each iteration, where we found an 83% reduction of the entire reconstruction time. It can also be simpler to work with undersampled Cartesian data within the iterations. In this work, the quality of the images that result from replacing measured data with interpolated values at nearby Cartesian points was evaluated. Among the three pre-reconstruction interpolation methods, the multicoil-based method GROG produced results most similar to the NUFFT reconstructions even though all methods were taking benefit from the multicoil acquisition. This was evidenced by the difference images and NRMSE/SSIM calculations that showed a closer match between GROG and NUFFT than the other methods.

The simulated undersampling trials further demonstrated that all three methods perform similarly but again GROG was best able to produce the fully sampled images among the three preinterpolation methods.

In perfusion quantification analysis of regions, the streaking artifacts and low SNR had little impact. The signal intensity curves appeared similar for all of the methods.

There is an expected timing advantage gained by switching from NUFFTs to FFTs in each iteration. Intuitively, it would be at most 3 since computing time for an NUFFT execution is approximately three times of that of an FFT execution, however we found a speed-up factor of ~ 6 . The actual speed-up can be significantly different due to computational platform, implementation issues and datasets used. We further discuss these issues in Appendix A. Generally speaking, replacing the inverse and forward NUFFT at every iteration by inverse and forward FFT using a pre-reconstruction interpolated Cartesian k -space can speed up the reconstruction, as well as maintaining reconstructed images very close to the NUFFT standard when using a reconstruction algorithm with spatiotemporal TV constraints. Future work is warranted to compare to the Toeplitz method with gridding only once but using $2\times$ oversampling.^{10,11}

5. CONCLUSION

In this paper, we evaluated three pre-reconstruction interpolation approaches to iterative reconstruction of radially sampled datasets. The slower NUFFT method, when coupled with an iterative method, consistently produced excellent results. However, faster FFT-based reconstruction can be performed at the cost of first approximating the measured k -space data on a Cartesian grid with a pre-reconstruction interpolation step. When comparing the results of these pre-reconstruction interpolation methods, we found that the multicoil GROG approach consistently produced the best images.

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CONFLICTS OF INTEREST

The authors have no relevant conflicts of interest to disclose.

APPENDIX A

SPEED-UP FACTOR

The speed-up factor between NUFFT and pre-reconstruction interpolation methods can be written as

$$\text{speed-up} = \frac{T_{\text{NUFFT}}}{T_{\text{pre}}} = \frac{T_{\text{p-NUFFT}} + N(2\tau_{\text{NUFFT}} + \tau_{\text{recon-NUFFT}})}{T_{\text{p-pre}} + n(2\tau_{\text{fft}} + \tau_{\text{recon-fft}})}, \quad (7)$$

TABLE I. Comparisons of computation time and speed-up factors compared to NUFFT. For GPU tests, we only measured the total time for the iteration portion of STCR. We demonstrated here by taking advantages of parallel computation, a faster reconstruction can be achieved.

		T	T_p	τ_{recon}	τ_{FT}	Speed-up to NUFFT	Speed-up to NUFFT iteration portion
Algorithm 1 150 iterations	BINN	2241.05	11.26	1696.77	533.02	1.76	1.76
	GROG	2539.82	317.62	1689.98	532.22	1.55	1.77
	Grid3	2305.18	49.34	1731.01	524.83	1.71	1.74
	NUFFT	3935.16	9.53	1659.63	2266.00	1	1
Algorithm 2 150 iterations	BINN	415.45	14.18	255.15	146.12	6.03	6.00
	Grid3	437.79	32.08	254.31	150.40	5.72	5.95
	GROG	438.40	35.62	253.22	149.56	5.72	5.97
	BINN GPU	112.86	14.23	98.63	22.21	24.40	
	Grid3 GPU	131.05	32.36	98.69	19.12	24.38	
	GROG GPU	134.32	35.68	98.64	18.67	24.39	
	NUFFT	2506.24	26.51	219.05	2187.27	1	1

where $T_{p\text{-NUFFT}}$ and $T_{p\text{-pre}}$ are total time spent before iterative reconstruction for each methods, N is number of iterations, τ_{NUFFT} and τ_{fft} are the times spent to perform one Fourier transform (backward or forward) and $\tau_{\text{recon-NUFFT}}$ and $\tau_{\text{recon-fft}}$ are the times spent on other operations at each iteration, mostly enforcing total variation constraints. If there is a dominant term among them, we can theoretically estimate the speed-up factor based on that term of the two methods, however every term in the above equation is strongly related to the computer platform, data size and the algorithm, making estimation of this speed-up factor challenging. In Table I, we show the time spent for two different algorithms on the same platform described in the paper. Algorithm 1 uses loops to go through coils and time frames, and is a single-coil reconstruction that after reconstruction combines the images from every coil by the square root of sum of squares. Algorithm 2 is a multicoil reconstruction algorithm used in this paper and processes all coils and time frames together in parallel. Algorithm 2 can be considered a generalized SENSE method with total variation constraints. We also report the time when using a GPU to compute the iterative portion of STCR (Nvidia Tesla C2070 with 6 GB 1.5 GHz DDR5 RAM). Though we did not test NUFFT algorithm on GPU, there are existing

GPU NUFFT methods that can significantly speed-up NUFFT operation, like stated in Sørensen et al.²¹ In general, parallel computation can benefit both daily clinical use and research purposes.

APPENDIX B
OIF FOR GRID3

We did experiments on both the 420-ray phantom and the 24-ray cardiac data to test how the OIF of Grid3 affects reconstructed images. For the 420-ray phantom, using OIF = 1 did not yield images with acceptable quality, especially for higher numbers of rays. Grid3 with OIF = 10 still yielded images poorer than BINN at high numbers of rays and OIF = 12 was very close to BINN. When using OIF = 15, the images were closer to the NUFFT standard than those from BINN, however the time spent for interpolation was close to that of GROG. These results are shown in Fig. 7.

While using higher OIF in the 420-ray dataset led to significantly improvement in image quality, no such evidence was seen in the 24-ray cardiac perfusion dataset. OIF = 2, 4, and 8 gave similar NRSME and SSIM numbers. Results are shown in Table II. And for OIF = 8, the time spent on

FIG. 7. Experiment results for comparing different OIF of Grid3 with the other methods. The test was from using the 420-ray phantom dataset. We can see from these curves that Grid3 with OIF = 1 cannot reproduce images close to the standard, especially at higher number of rays. [Color figure can be viewed at wileyonlinelibrary.com]

TABLE II. Experiment results for comparing different OIF of Grid3 with the other methods. The table shows the average values of all frames of the 24-ray cardiac perfusion dataset. No improvement of image quality was seen when using OIF greater than 1 for Grid3 for this dataset.

	BINN	GROG	Grid3 OIF = 1	Grid3 OIF = 2	Grid3 OIF = 4	Grid3 OIF = 8
NRMSE FOV	0.26	0.15	0.21	0.23	0.24	0.23
NRMSE ROI	0.11	0.09	0.10	0.11	0.11	0.11
SSIM FOV	0.80	0.87	0.84	0.83	0.82	0.83
SSIM ROI	0.90	0.92	0.92	0.91	0.91	0.91

interpolation was more than that of GROG, making Grid3 with high OIF a less efficient method.

APPENDIX C

CALCULATION OF NRMSE AND SCALE FACTOR

First, we note that the sum-term inside the square-root is just the l_2 -norm-squared difference between the images:

$$\|f - g\|_2^2 \quad (8)$$

The goal is to find a λ which scales g to minimize this difference. Because the values of this function are always positive and it is of second order, the minimum can be found by setting the first derivative with respect to λ to zero.

$$\frac{\partial}{\partial \lambda} \|f - \lambda g\|_2^2 = 0, \quad (9)$$

$$2(-g)^T(f - \lambda g) = 0, \quad (10)$$

$$\lambda = \frac{g^T f}{g^T g}. \quad (11)$$

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