A Framework for Inline Parallel Multi-Sequence Reconstructions: A Head Motion Correction Application

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Synopsis

Motivation: Offline MRI reconstruction limits clinical applicability due to lengthy processing times and lack of on-scanner preview. While Gadgetron enables customised inline reconstruction implementation, it may introduce scanner-reconstruction delays with multi-sequence implementation and time-consuming methods.

Goal(s): To develop a generalized framework for inline reconstruction capable of parallel multi-sequence operation without interrupting subsequent scans or scanner-reconstructions.

Approach: A Gadgetron-based, multi-GPU framework was developed and implemented with DISORDER motion correction reconstruction across three 3D neuroimaging sequences to validate feasibility and robustness.

Results: The framework demonstrated feasibility and high robustness (success in 271/273 cases) with DISORDER reconstruction implementation, effectively reducing motion artifacts while maintaining high image quality.

Impact: This generalized inline framework enables advanced but time-consuming, customised multi-sequence reconstructions within an MR examination without acquisition or scanner-reconstruction delays. It demonstrated high robustness and is extensible for future integration of customised methods across scanners via a centralized server.

INTRODUCTION

Advanced MR reconstruction and processing methods are emerging, but the slow transition to commercial solutions often necessitates offline computation, limiting clinical and large-cohort-study applications. The Gadgetron platform[1] provides a powerful capability for inline, customised reconstruction, but algorithms requiring long processing times can delay subsequent scanner-reconstructions. This issue is exacerbated when customised reconstructions for multiple sequences are required within a single exam.

We developed a generalized inline asynchronous reconstruction framework based on Gadgetron[1], leveraging multi-GPU parallel processing for multi-sequence protocols. We validated its feasibility and robustness within the TwinsUK[2] neuroimaging protocol, using a customised retrospective head motion correction method, DISORDER reconstruction[3].

METHODS

The proposed inline framework (Fig.1) has been implemented on Siemens scanners running XA50 software. It automates raw data management and runs customised reconstructions alongside scans without interrupting the scanner's standard processes Multiple reconstructions can run in parallel using multi-GPU resources, and can include scanner-based bias field and distortion corrections to ensure data consistency. Results are retrievable on scanners for reviewing and unified management, with options for retrieval during the same examination or afterwards.

Inline Reconstruction Framework:

The inline framework has three components (Fig.2).

1-Data transfer and scanner reconstruction: During scanning, k-space data is sent to both the scanner Measurement and Reconstruction System (MARS) for scanner-reconstruction and to the Gadgetron server for customised reconstruction. For Gadgetron processing, the raw data is converted to ISMRMRD format[4]. After scanning, the Gadgetron pipeline executes preprocessing (e.g., asymmetric echo handling), saves data on the server using the 'save_raw' MATLAB 'gadget'. Then a standalone bash script is triggered to allocate a GPU for customised reconstruction, while simultaneously, the Gadgetron processing chain reintegrates with the scanner without waiting for customised reconstruction results (only scanner-reconstructed images returned), releasing the Image Computation Environment (ICE) for subsequent reconstructions.

2-Standalone customised reconstruction: The bash script monitors until an idle GPU and sufficient computational resources are available. Once detected, it launches the customized program to read saved raw, perform computations, and save results, allowing multiple programs to run in parallel on different GPUs. Customised post-processing programs can be triggered afterwards (e.g., Gibbs ringing reduction using Mrtrix3[5]). Predicted resource usage logged before and after each customized program and real-time system monitoring inform the bash script's launch decisions.

3-Image retrieval: Reconstructed images can be retrieved flexibly through a dummy sequence or retrospective reconstruction during the same examination or afterward. Additional postprocessing tools from Gadgetron or the scanner (e.g., bias field and distortion correction) can be applied as needed.

Head Motion Correction Reconstruction (DISORDER[3]) Implementation:

To validate the framework's feasibility and robustness, DISORDER[3] reconstruction was implemented within the framework and applied to 3D neuroimaging sequences in the TwinsUK project[2]. MR scans were acquired on a 3T MR scanner (MAGNETOM Vida, Siemens Healthineers, Forchheim, Germany) using a 64-channel head/neck coil. The Gadgetron server has an Intel(R) Xeon(R) Silver 4314 CPU, 125GB RAM+32GB swap, and three GeForce GTX A6000 GPUs. Three 3D imaging sequences (FLAIR, MPRAGE and SWI) within the neuroimaging protocol can deploy the DISORDER trajectory and inline reconstruction (detailed parameters in Fig.3).

Implementation success rate of the framework was evaluated. To validate image quality we evaluated the signal-to-noise ratio (SNR), contrast-to-noise ratio (CNR), normalized gradient square (NGS)6 and overall image quality scores (2-no artifact to 0-severe artifact) in three MPRAGE reconstructions : conventional linear Cartesian trajectory with scanner reconstruction (MPRAGE_Lin_scanner), DISORDER trajectory with scanner reconstruction (MPRAGE_DIS_scanner) and DISORDER inline reconstruction (MPRAGE_DIS_MoCo).

RESULTS

The framework's feasibility and robustness were validated in the TwinsUK project by successfully implementing the MPRAGE sequence for 273 subjects, achieving 271 successful reconstructions with timely image retrieval (Fig.4); the two failures were due to temporary server internet connectivity issues. In a multi-sequence scenario, FLAIR, MPRAGE and SWI with DISORDER reconstructions were run inline for two volunteers (both 28-year-old, 1 female) (Fig.5), achieving feasible parallel reconstruction within 25-minutes during continuous scanning (Fig.1).

Forty-six subjects (66.9±8.3 years, 40 females) from the TwinsUK cohort were randomly selected for the image quality evaluation. SNR did not differ significantly across MPRAGE_Lin_scanner, MPRAGE_DIS_scanner, and MPRAGE_DIS_MoCo (all $p>0.05$). However, MPRAGE_DIS_MoCo showed improved CNR, NGS, and image quality scores (all $p<0.005$), indicating that the framework with DISORDER implementation reduces motion artifacts while maintaining SNR compared to the scanner-reconstruction.

CONCLUSION

The proposed inline reconstruction framework enables parallel multi-sequence implementation of advanced, time-consuming reconstructions, without interrupting scanning or scanner-reconstruction. It is feasible for large-cohort studies and demonstrates high robustness and image quality consistent with standard scanner-reconstructions. The framework also extensible, supporting future integration of diverse reconstruction methods across multi-scanners via centralized servers.

Acknowledgements

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Figures

Figure 1. The diagram of inline reconstruction framework implemented with a retrospective head motion correction reconstruction (DISORDER[3]) for three 3D neuroimaging sequences (FLAIR, MPRAGE and SWI). The duration of each section was measured from one scan from a 28-year-old male healthy volunteer. The customised reconstruction duration may vary according to motion severity by approximately ±5 minutes.
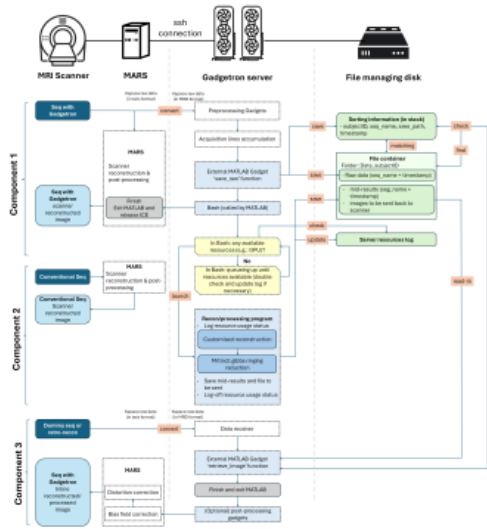
Figure 2. The detailed workflow of the inline reconstruction framework. Seq, sequence; ICE, image computation environment; Mrtrix3[5], a Gibbs ringing reduction method based on image domain.

Sequence parameters	MPRAGE	SWI	FLAIR
Sequence type	tfl	Multi-echo GRE	SPACE
TE, ms	1.97	9.42 and 19.70	394
TR, ms	2000	27.0	8000
FOV, mm³	256*256*208	230*205*144	250*250*208
Resolution, mm³	1*1*1	1*1*3	1*1*1.3
TI, ms	880	NA	2300
FA, deg	8	15	T2 Var
BW, Hz/Px	240	140	751
Turbo factor	208	NA	278
Averages	1	1	2
Acceleration factor	2*1 GRAPPA	2*1 GRAPPA	2*2 CAIPIRINHA
Partial Fourier	7/8 in RO direction	7/8 in PE and 3D directions	NA
DISORDER tile size*, [PE, 3D]	[15, 9]	[5, 8]	[8, 3]
DISORDER shot ordering*	Random-checkered	Random-checkered	Random
Reconstruction parameters	MPRAGE	SWI	FLAIR
Number of iterations†	15	15 for each echo	7 for each inversion
Outlier rejection†	Yes	Yes	Yes

* The DISORDER trajectory divides the Cartesian grid of the phase encoding into tiles[3]

† The maximum iterations for motion estimation[3]

Figure 3 The sequence parameters of the three 3D neuroimaging sequences (FLAIR, MPRAGE and SWI) which were applied to the inline reconstruction framework with a head motion correction reconstruction (DISORDER[3]).

Figure 4. Screenshot of the 3T MR system viewing tab displaying inline DISORDER reconstruction results for a 56-year-old female subject from the TwinsUK cohort. Following the MPRAGE sequence with the DISORDER trajectory (sequence (1)), the scanner immediately provides the scanner-reconstructed image (MPRAGE_DIS_scanner, left). The motion-corrected inline reconstructed image (MPRAGE_DIS_MoCo, right) retrieved by a 3-second dummy sequence (sequence (2)). The scans and reconstructions of the in-between sequences are not delayed.
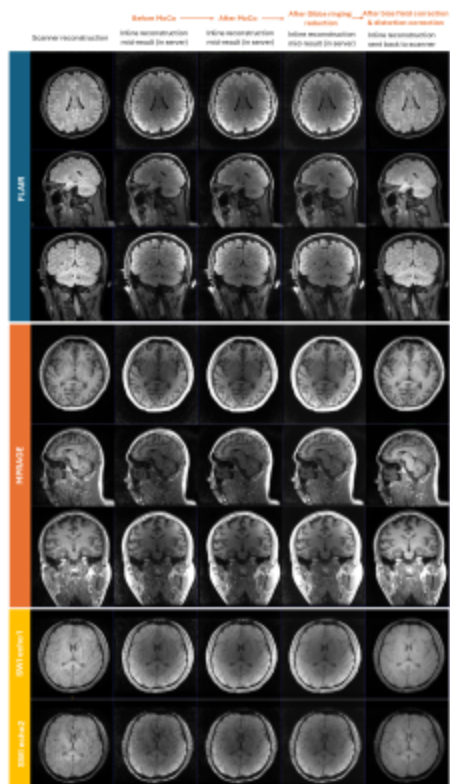
Figure 5 Scanner-reconstructed images (first column), intermediate results (columns 2–4), and inline DISORDER-reconstructed images (fifth column) for FLAIR, MPRAGE, and SWI sequences of a healthy 28-year-old male subject. Compared to the scanner-reconstructed images, the inline DISORDER reconstructions retrieved to scanner reduced motion artifacts and maintain data consistency following Gibbs ringing reduction, bias field correction, and distortion correction.