

A low-cost flexible non-linear parallelized MR image reconstruction system

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Introduction: Despite tremendous recent advances in non-linear image reconstruction methods, their clinical utility has been significantly held back by the limited computational power that is provided by the MRI system manufacturers and lack of flexibility in customizing the image reconstruction function pipeline such that the image reconstruction time of the state-of-the-art non-linear algorithms can be prohibitively long. To address this issue, we developed a MR image reconstruction framework in which any custom made algorithms can be implemented on custom built computer nodes connected to the MR scanner such that k-space data is sent to the nodes for calculation and reconstructed images are sent back to the scanner system as part of the default pipeline. Different levels of parallel computing are possible, including multiple nodes, multi-thread CPU and multi-core GPU. In this work, we demonstrate the benefit of this framework on 12 pediatric congenital heart disease patients who underwent cardiac MRI using a recently described 4D cardiac phase-resolved contrast-enhanced MRA (MUSIC) sequence^[1].

Architecture and Implementation: Fig.1 shows the schematic outline of the proposed framework. Two TCP/IP communication modules were inserted to default reconstruction pipeline to bypass operation like FFT, GRAPPA coil combination etc. Other vendor-provided modules, such as pre-reconstruction k-space filters and post-reconstruction image filters remain in the pipeline. One or more computer nodes are connected via Ethernet that receives the k-space data, perform the non-linear reconstruction and push the image data back into the scan's recon pipeline so that any post-recon image filters can be applied. CPU and GPU based acceleration is possible depending on hardware and software availability. We implement the proposed framework with a clinical MR scanner (MAGNETOM Trio, Siemens) and a Linux PC (CPU: 4core/4GHz, Memory: 32GB, GPU, Cost: \$1000). Two reconstruction algorithms were made available, including CPU and GPU accelerated L1-ESPIRiT^[2] based on the open-source Berkley Advanced Reconstruction Toolbox^[3] and our own implementation of CLEAR^[4], an image-domain, calibration-free image reconstruction method.

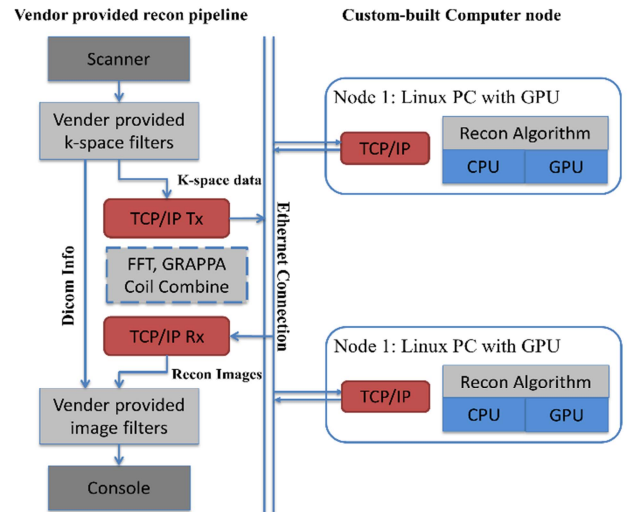
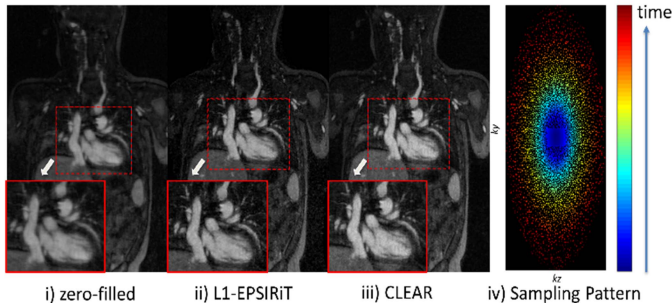


Fig1. The proposed reconstruction framework where one or more custom-built computer node are connected to the default recon pipeline via TCP/IP. Standard operation like FFT, GRAPPA and coil combination is bypassed but other vendor provided k-space and image-space filters are remained in the pipeline.

a) Comparison of zero-filled, L1-ESPIRiT and CLEAR reconstruction (selected 2D slice)



b) Reformatted multi-phase L1-ESPIRiT and CLEAR reconstruction

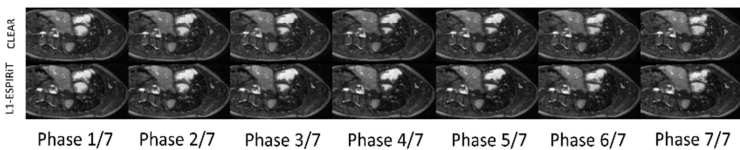


Fig.2 a) selected 2D slices reconstructed by zero-filling, L1-ESPIRiT and CLEAR. Images reconstructed by non-linear algorithm had improved sharpness and vessel definition than the one by zero-filling; b) The reformatted multi-phase cardiac cine images demonstrate the uniform quality throughout the 4D reconstructed images. It took 4-6 minutes to reconstruct the 4D dataset using L1-ESPIRiT with CPU and GPU acceleration and ~20 minutes using CLEAR for CPU acceleration only.

Conclusion: The proposed reconstruction framework significantly increased the computational power and development flexibility of the existing MR image reconstruction system at a very low cost (~\$1000) and enables inline non-linear image reconstruction within acceptable time. Our demonstration using pediatric 4D MRA further evaluate the feasibility, reliability and performance of using the proposed framework in a clinical environment, although the framework is independent from specific MRI applications or reconstruction algorithms.

Reference: [1] F Han et al, MRM 2014. [2] M Uecker et al, MRM 2014. [3] BART: version 0.2.04. [4] JD Trzasko et al, IEEE ACSSC, 2011.

Clinical Test: The proposed framework was tested on 12 pediatric patients with congenital heart diseases that are referred for contrast enhanced cardiovascular MRI. An accelerated cardiac and respiratory gated 4D MRA^[4] sequence with variable-density Poisson-Disk under-sampling pattern (Fig.2a.iv) was included in the scanning protocol after the contrast ejection and followed by a series of post-contrast 2D CINEs and flow quantification scans. Sequence parameters include: GRE readout, TE/TR=0.9/2.9ms, FA=25, isotropic resolution 0.9mm, matrix size: 500x300x120, 5-8 cardiac phases, scan time: 3-6 minutes. L1-ESPIRiT algorithm with both CPU and GPU acceleration was used for online reconstruction and additional retrospective reconstruction is performed after the scan using both CLEAR and L1-ESPIRiT with different configuration.

Result: All scans were completed and the 7-9 reconstructed DICOM volumes were available at the scanner console 4-6 minutes after the scan. Since most of the calculation took place on the computer node and did not use the vendor provided resources, additional scans like 2D CINE and flow quantification MRI could be performed during the time when the image reconstruction was performed on the computer node such that there was no dead time during the workflow of the scans as shown in Fig.3. The selected 2D slices of the reconstructed images shown in Fig.2 illustrate noticeable improvement in image quality using non-linear image reconstruction algorithm (both L1-ESPIRiT and CLEAR).

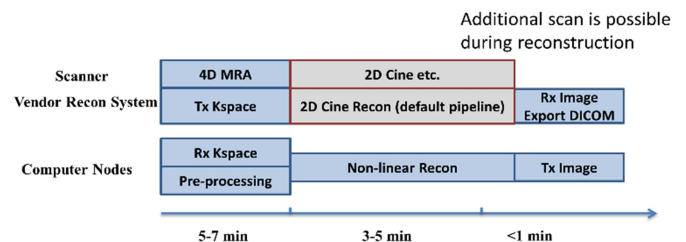


Fig.3 Timeline of the 4D MRA reconstruction process. K-space data are sent to the computer nodes during the scan which takes 5-7 minutes. Some pre-processing, including coil sensitivity map estimation are performed in parallel. It takes 3-5 minutes to reconstructed the 4D dataset (matrix size: 500x300x120x8) and additional 1 minutes to send back the images, during which time additional scan like 2D CINE is possible because the non-linear reconstruction does not use the resources of vendor-provided scanner system