Faster-than-acquisition 4D sparse reconstruction for Cartesian 2D SENSE-type acquisition

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PURPOSE:

MR imaging protocols must balance the competing goals of spatial resolution, signal-to-noise ratio (SNR), and acquisition time. Accelerated parallel imaging (SENSE[1], GRAPPA[2]) techniques make use of side information, in the form of the sensitivity profiles of the receiver coils, to permit multiple spatial locations to be imaged together (aliased), reducing the acquisition time while maintaining spatial resolution, at the expense of SNR. Sparse reconstruction techniques make use of additional constraints (a priori knowledge of output image characteristics) to improve the SNR of the output image, with the additional cost of increased computational time. As there is always a desire for faster, sharper, and higher SNR imaging, combining parallel imaging with a sparse reconstruction is a promising technique to move towards this ideal, but extended processing times can limit its clinical utility.

By leveraging a novel sparse reconstruction algorithm[3] that takes advantage of the known features of a view-shared 2D SENSE-accelerated acquisition[4] to reduce computational burden, and implementing this algorithm within an existing[5] parallel computation framework, we have deployed into the clinic a faster-than-acquisition reconstruction for time-resolved 3D datasets, providing improved results in a clinically relevant time frame.

METHODS:

A novel sparse reconstruction targeting Cartesian 2D-accelerated SENSE-type acquisitions has been developed. This reconstruction uses an iterative alternating direction method-of-multipliers (ADMM) strategy with multiple variable splitting, resulting in solving four closed-form quadratic or less sub-problems and three Lagrange multiplier updates per iteration. At a high level, these four sub-problems consist of: (A) constraining the Fourier transform of the current image estimate with the original acquisition data, (B) a 2D SENSE-type unfolding of an aliased image estimate, (C) a deconvolution of the effects of the 2D total-variation based sparsifying transform, and (D) a denoising or thresholding sparsifying transformation. See reference 3 for further discussion of the mathematical foundation for this reconstruction.

A number of these operations can have a portion of the computation performed once and then applied over multiple iterations or time frames. The unfolding (inversion) matrices for 2D SENSE-style reconstruction, for example, are constant over time or iteration for (B), so they can be calculated once, and then repeatedly applied. Similarly, the weights required for (C) can be calculated once and subsequently reused.

An additional benefit of this design is that there is no change required to the acquisition approach; the same k-space data can be reconstructed with a standard SENSE reconstruction.

After Fourier transforming along the frequency encoding dimension, this algorithm is applied on a slice-by-slice basis, permitting the first level of reconstruction parallelization — each remaining 2D time-resolved series can be solved separately (in parallel) from all others. This parallelization can be done over a set of independent computers, via a Message Passing Interface (MPI), or within a multi-processor machine (OpenMP or MPI); both have been implemented and are used as appropriate. Within a slice, most of the calculations operate on a voxel or subset of voxels (e.g. 2D SENSE unfolding) at a time, and can, if advantageous to the computing platform, be split via OpenMP to provide a second level of parallelism to the reconstruction.

This method was applied to dynamic-contrast-enhanced (DCE) perfusion imaging of the prostate. High spatial resolution ($256 \times 384 \times 38$; frequency × phase × slice) 3D image sets were formed every 6.2 seconds over almost 6 minutes, with a total of 55 timeframes. The data was acquired with 12 receiver coils and R=2.8 2D SENSE, net R=5.5 after corner removal; both traditional SENSE and ADMM reconstructions were performed.

RESULTS AND DISCUSSION:

This acquired dataset was reconstructed (with 25 ADMM iterations) on a single workstation with two 8-core Intel Xeon E5-2670 processors (2.6GHz, 20MB L2 cache each) in under 5 minutes, with an effective throughput of less than 5 seconds per 3D time frame. (Averaged over the entire execution, individual volumes are slightly faster; timing includes gradient correction and file I/O time.) This is 4-8x faster (in voxels reconstructed per second) than modern compressed sensing/sparse reconstruction algorithms leveraging GPUs[6], other accelerators[7], or more powerful traditional computers[8], and 40x faster than an earlier demonstration with a computing cluster[9]. ADMM parameters were chosen to yield fixed condition numbers for the quadratic sub-problems, and the regularization parameter was set globally for the exam style based on radiologist preference. We achieved effective scaling with parallelization (Figure 1) of the reconstruction. Examples of traditional 2D SENSE (left) and ADMM reconstruction (right) results are shown in Figure 2. This ADMM/sparse reconstruction technique has been integrated into a deployed SENSE reconstruction process, leveraging the capabilities previously integrated (grad-warp correction, DICOM generation, etc.) for easy interaction with our workflow. If desired, a traditional SENSE reconstruction of the time-series (~15 seconds total for 55 3D image sets) can be performed first for rapid confirmation of acquisition success.

CONCLUSIONS:

We have implemented and deployed a novel ADMM-based sparse reconstruction algorithm designed to leverage the characteristics of the acquisition for time-resolved reconstructions. This time-resolved reconstruction is applicable to both contrast-enhanced MR angiography (CE-MRA) and DCE perfusion acquisitions. The implementation provides faster-than-acquisition reconstructions, in addition to requiring no change to the imaging protocol, enabling integration with our imaging workflow while providing results in a clinically relevant time frame. Future work includes further reduction of the reconstruction time, likely by offloading (task-parallelism) portions of the reconstruction work to a Xeon PHI coprocessor.
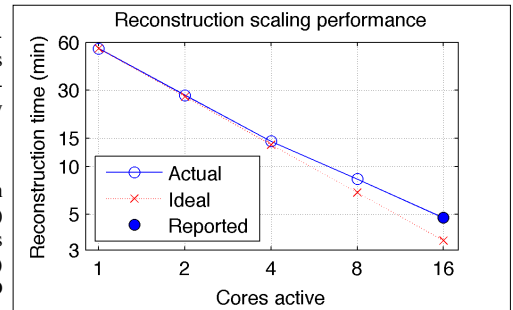

Figure 1: Reconstruction time (for 55-frame 3D time series) scaling vs. number of active cores. Departure from ideal scaling at high core counts is primarily due to increased memory bandwidth pressure and workload balance.
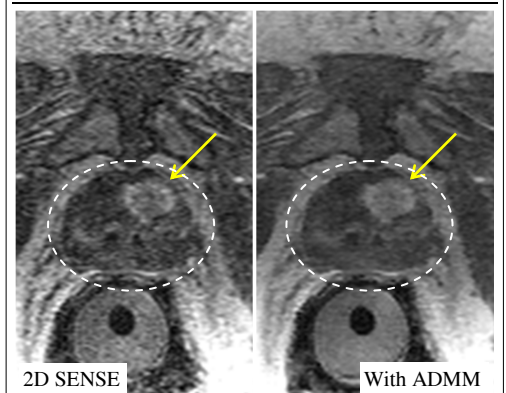

2D SENSE   With ADMM

Figure 2: Example DCE prostate MR reconstructions with identical source data. Central portion of axial slice from 3D time-resolved exam showing bright early enhancement region (arrow). ADMM shows improved SNR and similar sharpness. The prostate is indicated with a dashed border.

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