

Accelerated HYPR Reconstruction

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Introduction:

The use of highly constrained backprojection (HYPR) [1] in time-resolved contrast-enhanced MR angiography (CE-MRA) allows for a dramatic increase in the reconstructed temporal frame rate without the normal penalties in SNR and/or spatial resolution. Unfortunately, the increase in the computational requirements and data throughput can result in long reconstruction times, reducing the clinical viability of the technique. One approach to achieve shorter reconstruction times is to detect contrast dynamics from the k-space data and tailor the reconstruction to start with the contrast arrival and to reduce the temporal resolution during the venous phase [2], but even with the use of this technique typical reconstruction times still require minutes to hours to process a single dynamic 3D dataset.

In the past, clusters of networked computers have been used to solve computationally intensive problems that were impractical using a single computer. The degree of acceleration achieved usually depends on the complexity of the communication between the processes, on the memory necessary to perform the operations, and on the partitioning of the problem among the members of the cluster. We demonstrate a method that takes advantage of a distributed computing environment to efficiently accelerate HYPR reconstructions, achieving a degree of acceleration close to the number of computing nodes included in the cluster.

Methods:

Healthy volunteers were scanned on a clinical 3.0 T system (Signa HDx, GE Healthcare, Waukesha, WI). A hybrid 3D stack-of-stars [3] trajectory was used for acquisition of extremity and head CE-MRA data. An optimized HYPR reconstruction consisted of the following steps: (a) An FFT was applied along the slice direction of the data, then data were partitioned to compute nodes on a slice-by-slice basis. (b) For each slice, an FFT was applied to each partial-echo projection and homodyne correction [4] was applied to the sinogram before transforming the data back to k-space. (c) An efficient gridding algorithm [5] was applied, with anti-Gibbs ringing apodization incorporated directly into the density compensation function for optimal efficiency. (d) The HYPR algorithm [1] was applied in k-space to each slice, with typical reconstruction parameters of 16 new projections per frame and a sliding composite of 256 total projections. Each HYPR dataset was reconstructed using one to eight of the compute nodes of the scanner's reconstruction hardware. Reconstruction times were recorded in all cases and the corresponding images from each reconstruction were compared.

Volume Dimensions	1 node	2 nodes	3 nodes	4 nodes	5 nodes	6 nodes	7 nodes	8 nodes
256x256x52 x 4 rcvrs 80 time frames	37.7 min	19.0 min	13.2 min	10.9 min	8.73 min	7.49 min	6.60 min	5.80 min
512x512x96 x 8 rcvrs 48 time frames	82.0 min	44.2 min	28.7 min	22.0 min	17.8 min	15.9 min	13.5 min	11.4 min
256x256x96 x 8 rcvrs 64 time frames	25.1 min	13.1 min	8.6 min	6.6 min	5.4 min	4.7 min	4.0 min	3.7 min

Table 1. Reconstruction time scales as the inverse of the number of nodes used independently of the acquisition matrix, the number of coils, and the number of time frames reconstructed.

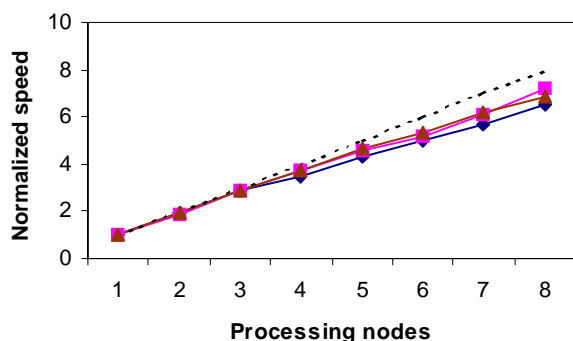


Figure 1. Normalized reconstruction speed scales with the number of processing nodes, indicating the low level of synchronization overhead and optimal memory management. The blue line corresponds to the first volume described in Table 1, the pink line to the second volume and the brown line to the third volume. The dashed line represents the case where the speed scales exactly with the number of processors.

Results:

The reconstruction times with the acquisition parameters are presented in Table 1. Figure 1 shows that normalized reconstruction time scales as the inverse of the number of nodes used during the reconstruction, independently of the acquisition's characteristics such as size of the coil array and matrix size. Figure 2 shows representative images of several of the reconstructed datasets.

Discussion and Conclusions:

HYPR MRA can produce temporal resolution up to a 100 times greater than traditional CE-MRA methods [6, 7]. However, the large data volumes and increased computational complexity prolong reconstruction times and increase data management and storage requirements, making routine use challenging in clinical practice. The proposed distributed HYPR reconstruction reduces the computation time by a factor close to the number of compute nodes available for processing. The hybrid 3D stack-of-stars acquisition is well suited for distributed processing. Each slice can be processed separately and there is minimal communication necessary for the synchronization of the processes. The addition of techniques to accelerate the acquisition such as parallel imaging or the use of different trajectories, such as VIPR [8], will increase the level of complexity of the reconstruction algorithm. An increase in the number of channels used for acquisition might also add to the complexity if the memory associated with a single processor is unable to hold all the required data. Further investigation is necessary to determine the performance of the algorithm under these conditions in a distributed computing environment. While the reconstruction times monotonically decrease with number of nodes (Fig. 1), the marginal benefit of adding compute nodes diminishes as the number of nodes increases. The optimal number of nodes would be dependent on specific acquisition parameters.

An optimized and distributed HYPR reconstruction enables the clinical application of the technique. Adding compute nodes to a cluster, it should be possible to further reduce reconstruction times without any modifications to the algorithm. This should enable clinical use, and might also enable the clinical evaluation of iterative reconstruction algorithms.

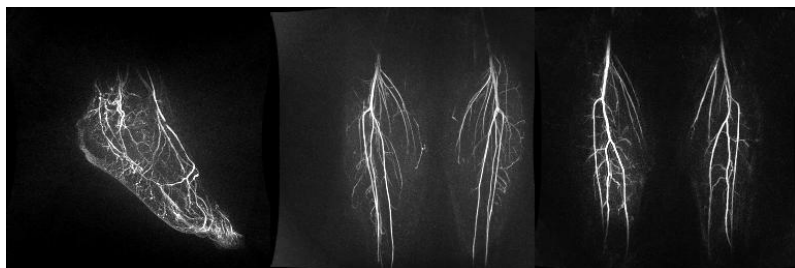


Figure 2: Representative HYPR MIPS of the data described in Table 1.

References:

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