Accelerated reconstruction using parallel computing for spiral spectroscopic imaging

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Introduction

Over the years, the development of fast spectroscopic imaging techniques has found applications in full coverage CSI (chemical shift imaging) and/or high resolution CSI. Recently, the interest has continued with usage in areas such as real time metabolite imaging [1] and temperature mapping, which can be used in interventional procedures [2]. Of these fast spectroscopic imaging procedures, spiral CSI has a special feature in that while spectral information is gained (kf), temporal information from two domains can be obtained simultaneously (e.g. kx and ky) [3]. This feature gives the potential to collect spectroscopic data with high temporal resolution. However, as with all non-cartesian sampling patterns, a lengthened reconstruction time accompanies. Most non-cartesian sampling sequences therefore use the fast gridding algorithm to reduce the reconstruction time [4]. For spiral CSI also, gridding is conventionally used. To extract the spectral information, gridding in spectroscopic imaging has an additional domain (kf), which will prolong the reconstruction. To alleviate this problem, we demonstrate here the usage of parallel computing to reduce the reconstruction time necessary for spiral CSI. We show that reconstruction times can be significantly reduced using this approach.

Theory and Methods

In spiral spectroscopic imaging, data is simultaneously collected in kx, ky, and kf (Fig.1). For volumetric spiral CSI, an additional kz domain will be collected using phase encoded gradients. In the reconstruction, gridding is performed in kx, ky, and kz. For each spiral lobe of the readout, the gridding in kx and ky can be thought to be an independent process, which enables its parallelization (Fig. 1). An alternative method is to parallelize k-space interleaved data collected (not shown).

We have collected various spiral CSI data and performed this parallelization. Spiral CSI data were set to collect 500~1000Hz spectral bandwidth over a 2D or 3D region. For the parallelization, a multi-thread process was used with an Intel CPU (XEON E5440, 2.83 GHz, quad core*2, eight CPU cores total, OS: Linux Fedora9 64bit, RAM: 16GB). Various numbers of multithread was used (1,2,4, and 8) to compare the reconstruction time performance. The execution time was measured and the speedup time was calculated.



Table 1 and Figs. 2, 3 shows the execution time and speedup of the gridding process for the various imaging parameters used. It shows that increasing the number of threads results in nearly proportional increase in the speed up factor. The small deviation from the theoretical increase can be overcome by further optimizing the algorithm [5]. The resulting outputs of the parallel computation showed maximum difference compared to conventional reconstruction of only the least significant bit. For the case of a 32x32x16x256 (kx, ky, kz, kf) acquisition, the gridding algorithm time was

reduced from 15.8 to 2.64 seconds. Table 2 shows the total reconstruction time for the imaging parameters when using a single thread. The total reconstruction time for using other number of threads can be deduced from this table. As seen, gridding accounts for almost 30% of the total reconstruction time. For the 32x32x16x256 case, using 8 threads can reduce the total reconstruction time to be dominated by FFT and other routines such as file input/output, windowing, etc. Increasing imaging parameter settings for other spiral CSI applications will likely benefit more with

CPUs will correspond to proportional increase in performance.

Conclusion

For 'real' real-time spectroscopic imaging, not only is the fast data collection component important, but a means for reconstructing the collected data promptly can be as important. Fast imaging techniques such as spiral CSI have been continuously developed. Here, we have shown that by using parallel computing, the reconstruction time of spiral CSI can be reduced to as small as those of Cartesian sampled FFT based approaches. The recon time can be further reduced when the recon algorithm is ported to a GPGPU (general purpose GPU) and further optimization. We believe that this work will can be an important initial step for applying this to hyperpolarized 13C metabolite imaging, or for intervention RF thermal ablation procedures using real time temperature mapping.



<u>References</u>: [1] Golman K., et al, PNAS, 103:11270-5 (2006). [2] Kuroda D., et al, MRM 43:220-225 (2000). [3] Adalsteinsson E., et al, MRM 39:889-898 (1998). [4] Jackson J., et al, IEEE Med Imaging 10:473-8 (1991) [5] Sorensen T., et al, IEEE Med Imaging 27:538 (2008).



Figure 2. Gridding algorithm processing time as a function of thread number for various imaging parameters.



Figure 1. Spiral CSI sequence k-space sampling diagram. Multi threading can be performed for each spiral lobe or for k-space interleaved data.

recon size	1thread	2threads	4threads	8thread
16*16*1*256	0.30	0.17	0.08	-
32*32*1*256	1.30	0.73	0.38	0.21
32*32*16*256	15.80	9.77	4.83	2.64

Table 1.	Gridding	algorithm	processing	time	for	various
imaging	paramete	rs and mu	lti-thread le	vels.		





recon size	total	gridding	FFT	other
16*16*1*256	1.0	0.3	0.3	0.4
32*32*1*256	3.9	1.3	1.3	1.2
32*32*16*256	41.6	15.9	19.8	5.9

Table 2. Total reconstruction time for various imaging parameters (one thread).