Advancing the clinical utility of MRI with online quantitative analysis: application to brain tissue classification in multiple sclerosis

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Purpose: Recent advances in MRI and image processing have significantly increased the data size and computation time. The constant increase in the computing power still cannot cope with the pace of data generation in MRI. With the big data size and the sophisticated neuroimaging analysis techniques, generation of quantitative measures from MRI can take several minutes to hours, hence the analysis is typically done off-line. Consequently, access to the quantitative information is delayed until after the patient had already left the scanner. A framework for fast online image analysis is needed to provide quantitative information immediately after the scan while the patient is still in the scanner

Methods: We have developed a fast online analysis pipeline executed on a high-performance computer. The pipeline is seamlessly integrated into a clinical MRI system, and is utilized for brain tissue classification and lesion detection from multi-contrast data in patients with multiple sclerosis (MS). Imaging sessions for 16 MS patients scanned with an IRB-approved protocol were included. Experiments were performed on a Philips Achieva 3.0 T system (Philips Healthcare). The MRI protocol included the acquisition of multi-slice fat-saturated dual-echo fast spin-echo (FSE) and fluid-attenuated inversion recovery (FLAIR) sequences (FOV = 256×256×132 mm^3, matrix= 256×256×44; FSE: TR/TE1/TE2 = 6800/8.2/90 msec, scan time 3:24; FLAIR: TR/TI/TE = 10000/2600/80 msec, scan time 4:20). Data analysis was performed on a dedicated workstation (3.2-GHz 8-core Intel Core i7, 12 GB of memory running Windows 7) connected to the scanner through a fast network link. The workstation was equipped with a Tesla C2050 graphical processing unit (GPU; NVIDIA, Santa Clara, CA). Software modules were added to the scanner to automatically read in and write back the data from and to the patient database, to and from specific directory locations. The scanner software was modified to automatically launch a remote application with these directories as input and output locations upon completion of the data acquisition. Image analysis was performed using an in-house custom software package written in C, IDL, Matlab and CUDA programming platforms.

The pipeline for MS was designed to work in synchrony with MRI data acquisition (Fig. 1). As soon as the dual-echo FSE data were acquired and acquisition proceeded to the FLAIR sequence, the FSE data were transferred to the workstation for initial pre-processing including brain extraction[1] and nonuniformity correction[2]. Once the FLAIR acquisition completed, the FLAIR dataset was immediately transferred to the workstation for co-registration using a GPU-accelerated method[3,4]. The registered FLAIR was then processed for brain extraction and nonuniformity correction. Brain tissue was segmented as described previously[5,6] to generate white matter (WM), grey matter, cerebrospinal fluid, and WM lesion maps. The maps were automatically imported back into the MRI scanner and added to the patient database. Processing times of the pipeline were recorded including database access and network transfer times.

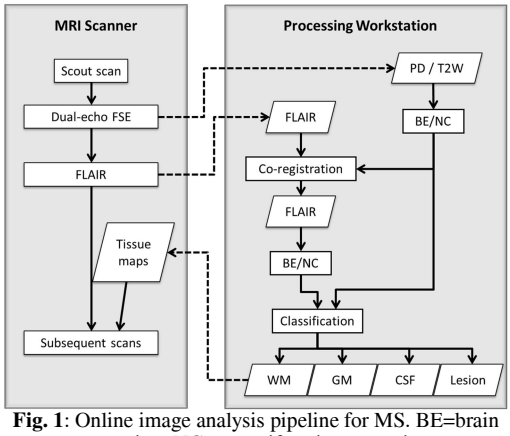

Fig. 1: Online image analysis pipeline for MS. BE=brain extraction; NC=nonuniformity correction.

Results: Table 1 reports the average processing times. Nonuniformity correction was the most time consuming operation. The time for database access and network transfer was ~10 sec/datasets. Note that the pipelined implementation in this work achieves faster turn-around times by performing the preprocessing of the dual-echo FSE data while the scanner is actively acquiring FLAIR. The time taken for database access, network transfer, and preprocessing of the dual-echo FSE dataset is not perceived as a delay, and does not count towards the wait time. Delay between the acquisition of FLAIR and the availability of the tissue maps is only 50 sec, making the results available in almost real-time to the care giver. Fig. 2 shows a representative tissue and lesion segmentation in one MS patient.

Discussion: Previewing the quantitative analysis immediately after the scan may reveal certain results which if not acted upon could result in recalling the patient for another study. In addition, prescription or optimization of the following scans based on the quantitative information, e.g. location of the MRS voxel, can improve the diagnostic value of the study. We have developed a scanner-integrated online pipeline for fast MRI image analysis and demonstrated its application for brain tissue classification in MS patients. We expect the proposed framework to have an impact on patient management, bringing isolated research activities to be part of the general imaging practice.

References: [1] Datta S and Narayana PA, JMRI, 2011. [2] Tustison NJ et al., IEE TMI, 2010. [3] Collignon A et al., Information processing in medical imaging, 1995. [4] Huang T et al., MRI 2011. [5] Sajja et al., Annals of biomedical engineering, 2006. [6] Datta et al., Neuroimage, 2006.

Table 1: Average execution times in the image analysis pipeline.

Processing phase	Operations	Processing time (sec) Mean ± SD
Dual-echo data processing	Brain extraction	1.5 ± 0.0
	Nonuniformity correction	40.6 ± 10
	Total-processing	42. 0± 10
	Total-pipeline	68.4 ± 38
FLAIR processing and tissue classification	Registration	8.9 ± 0.5
	Brain extraction	0.6 ± 0.0
	Nonuniformity correction	10.0 ± 1.7
	Segmentation	16.2 ± 1.4
	Post-processing	8.0 ± 0.6
	Total-processing	43.8 ± .2
	Total-pipeline	49.9 ± 3.3

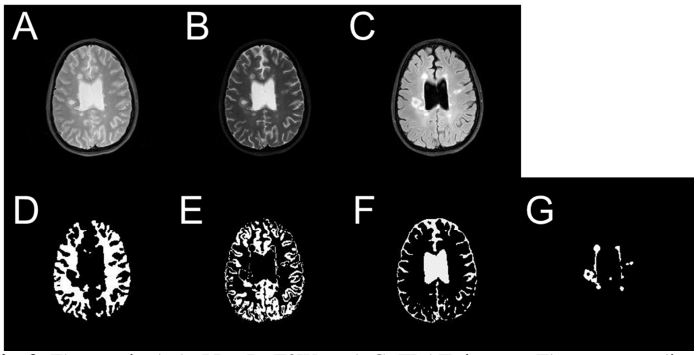

Fig. 2: The acquired (A) PD, (B) T2W, and (C) FLAIR images. The corresponding segmentation is shown for the (D) WM, (E) GM, (F) CSF, and (G) WM lesion.