Improvement of Thigh Muscle MRI Image Processing Efficiency using a Batch-Scripted N4ITK Intensity Normalization Algorithm Implemented in 3D Slicer

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Introduction: T$_1$-weighted (T$_1$w) magnetic resonance imaging is a common technique for morphological muscle assessments in the thigh using magnetic resonance techniques[1]. In T$_1$w MRI, image contrast between muscle and fat is high which can lead to efficient

segmentation of muscle and fat voxels via automated and semi-automated image segmentation algorithms. However, factors such as signal inhomogeneity confound image quality and can hinder automated and semi-automated image segmentation techniques. When applied to images with inhomogeneous signal distribution, a variant of the nonparametric nonuniform intensity normalization algorithm (N4ITK) corrects the images by use of a calculated bias field[2]. Open-source image processing software such as 3DSlicer (www.slicer.org) includes an implementation of the N4ITK algorithm which can be accessed via graphical user-interface (GUI). However, for large data sets overall image processing time via the native GUI would be prohibitive. Therefore, we sought to reduce the overall image processing time by creating a custom GUI which would facilitate batch processing of the N4ITK algorithm within 3D slicer and would allow for efficient segmentation of thigh muscle T1w MRI datasets. Herein, we demonstrate that use of a batch-scripted N4ITK algorithm leads to an efficient workflow for thigh muscle MR image processing.
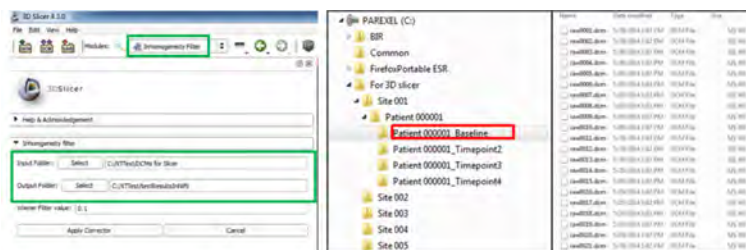

Figure 1: Screenshot of the batch processing GUI (left) and a schematic of a typical root folder with subfolders containing DICOM images (right).

Batch Scripting Methods: Following the batch-scripting examples from the 3DSlicer website we created a GUI to facilitate batch processing of thigh MR images. The GUI allows the user to specify the root folder of all DICOM images which need to be processed, and the location of the output folder to which processed images will be saved (Figure 1). The batch process starts by examining all subfolders and files in the root folder in order to create a list of the paths of all DICOM images under the root folder. DICOM images are then processed one-by-one using the N4ITK algorithm and are then stored in the user-specified output folder. A log file recording the filtering status of each DICOM image is subsequently created and stored within the
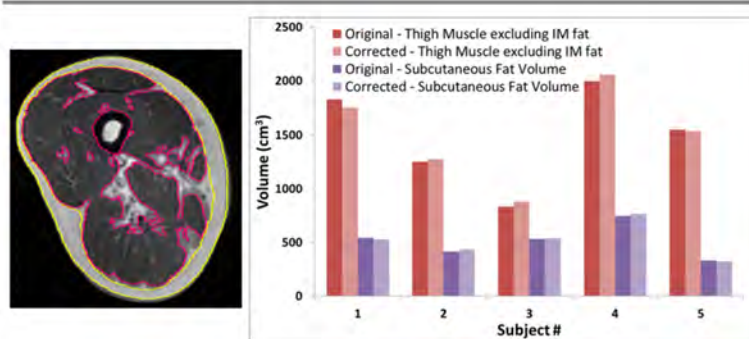

Figure 2: (left) Representative image showing ROIs for the thigh muscle (pink) and the subcutaneous fat (yellow); (right) comparison between volume measurements generated using the original uncorrected images and the same images corrected with the batch-scripted N4ITK algorithm. The batch-scripted N4ITK correction algorithm did not significantly affect volume measurements made on corresponding images (P > 0.9).
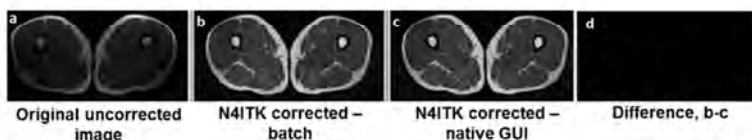

Figure 3 (a-c): Qualitative visualization of T$_1$w axial thigh MRI images pre- and post-N4ITK corrections. (d) subtraction image computed by subtracting the image generated using the native GUI (c) from the image generated using the batch processing GUI (b).

parent input folder. A screenshot of the batch processing GUI and a schematic of a typical root folder with subfolders containing DICOM images is shown in Figure 1. DICOM images are corrected for signal inhomogeneity during batch processing according to the following steps: 1) load DICOM images into 3DSlicer using the custom GUI, 2) retrieve the image data object from the scene model, create an output buffer, and add the output buffer back to the scene, 3) create a dictionary object with all of the input parameters and make a synchronous call to the N4ITK algorithm for signal inhomogeneity correction, and 4) save the corrected image into the output folder, and reset the scene object data.

MRI Methods: T1w MRI was acquired via a fast spin-echo sequence with TR/TE = 500-700/minimum ms, ETL=3-4, slice thickness = 5 mm (no gap), # of slices = 21 (mid-thigh), FOV = 38 – 46 cm x 38 – 46 cm, slice interleaving, NEX=2, imaging matrix = 512x256, and no fat suppression.

Results: Figure 2 (right) shows the comparison between volume metrics (volume of thigh muscle excluding intra-muscular fat and volume of subcutaneous fat) generated using the original "uncorrected images" and the same images corrected using the batch-processed N4ITK correction algorithm. A one-way ANOVA showed that there was no statistical difference between the volume analyses conducted on the original uncorrected images and the volume analyses conducted on the batch-processed N4ITK-corrected images (P > 0.9). Figure 3 allows qualitative visualization of the T$_1$w axial thigh MR images pre- and post-N4ITK corrections (a, b and c) and in Figure 3(d) we demonstrate that there is no difference in the output from the native N4ITK GUI implementation and our batch-processed N4ITK GUI implementation.

Conclusions: Customized automation and N4ITK batch processing of MR images through 3DSlicer is possible for efficient signal inhomogeneity correction in large data sets common to clinical multi-site imaging trials. In addition, the N4ITK intensity inhomogeneity correction step results in quicker turnaround and efficient implementation of automated and semi-automated segmentation tools resulting in reliable & faster segmentation in thigh muscle MRI data sets (several hours vs. <1 hour per image set for segmenting both legs on 10 slices).

References: 1. Mercuri et al. J Magn Reson Imaging 25:4332 (2007), 2. Tustison et al. IEEE Trans Med Imaging 29:1310 (2010)