Accurate assessment of muscle/fat distribution on MR images of the thigh

V. Positano¹, T. Christiansen², M. Santarelli¹, A. Gastaldelli¹, S. Ringgaard³, and L. Landini⁴

¹Institute of Clinical Physiology, Pisa, Italy, ²Department of Medicine and Endocrinology C, Aarhus University Hospital, Aarhus, Denmark, ³MR Research Center, Aarhus University Hospital, Aarhus, Denmark, ⁴University of Pisa, Pisa, Italy

Introduction: Accurate assessment of subcutaneous adipose tissue (SAT), inter-muscular adipose tissue (IMAT), and muscle mass in legs is important in monitoring the effect of nutrition and exercise and in other applications. MRI is able to perform these measurements safely and accurately. In this study we propose a method for robust and effective quantification of muscle/fat tissues.

<u>Materials and methods</u>: Twenty subjects (10 male, age 37 ± 7 yr, weight 94 ± 11 Kg, BMI 31 ± 3) underwent MR imaging. Informed consent was obtained from all. Subjects were imaged on a Philips Achieva 1.5T scanner using a Q-body coil with a FSE pulse sequence (TR=210 ms, TE=18 ms, NEX=3, matrix 288x202, FOV 530x530, slice thickness 6 mm). For each subject, from 22 to 35 axial slices covering the thigh region were acquired and analyzed by a custom-made software (HIPPO FAT 3.0). The software extends a validated approach [1,2,3] used in abdominal fat assessment to thigh images analysis. Briefly, the software computed three masks (background/bone, fat, and muscle tissues) using a fuzzy clustering segmentation. The background map is used to identify the two legs. For each leg, external and internal SAT boundaries were defined by means of an active contour algorithm that exploited the previously computed fat mask as external force map. The internal SAT contour converged to the fascial planes separating IMAT from SAT. A third contour was computed to identify the bone region using background/bone mask. Muscle volume and IMAT was assessed by processing the signal histogram in of the region between the second and the third contour, by identifying the two peak of the signal histogram by an expectation maximization (EM) algorithm. The whole analysis was performed in unsupervised manner without the need of any user interaction. The figure shows a typical example of detected contours and histogram fitting.



All subjects were analyzed with the fully-automatic procedure. The results were reviewed by two independent observers, which modified the contours and the histogram fitting if needed. The coefficient of variation (CoV) was defined as the standard deviation of the differences between two separated measurements, divided by their means, and expressed as percentage.

<u>Results:</u> 513 slices were processed. Automatic segmentation of four slices (0.8%) completely failed due to the incorrect separation of the two legs. These slices were reprocessed manually tracing the external SAT contours and running again the automatic segmentation. 3078 contours (513x6) were defined by the automatic procedure. A total of 294 (9.5%) contours were considered wrong by the observers and corrected. Most of the corrected contours (80%) were related to definition of bones. The table shows the inter-observer variability (difference between the two manual observers) and the human observer vs. the automatic procedure variability for six different measurements. A strong correlation exists between all measurements on right and left leg (p<0.001, CoV<4%).

CoV	L. VOLUME	R VOLUME	L SAT	R SAT	L MUSCLE	R MUSCLE	L IMAT	R IMAT
Inter-observer	0.39	0.38	1.13	1.11	2.78	0.54	1.17	1.95
Auto vs. manual	0.29	0.60	0.87	1.08	0.52	0.38	1.58	5.25

Discussion: In intra-observer variability analysis, CoV was very low for all measurements, suggesting that the developed software allows performing robust measurements of muscle/fat distribution. Variability between the manual observer and the fully-automatic procedure was low for all measurements, suggesting that the developed software is able to perform automatic measurements of muscle/fat distribution with good accuracy, if obviously wrong segmented slices are reprocessed. Wrong bone segmentation does not significantly affect the muscle but may leads to IMAT overestimation due to erroneously inclusion of marrow signal. In conclusion, the proposed approach allows effective unsupervised analysis of high-quality MR images. The proposed methodology showed also a good robustness when employed as a tool for semi-automatic, computer-assisted image processing.

<u>References:</u> [1] Positano V et al. JMRI 2004;23(5):662-668. [2] Demerath EW et al. Int J Obes 2006; 31(2):285-91 31(2):285-91. [3] Arif A et al. Obesity 2007;15(9):2240-2244