FAST INTERACTIVE SEGMENTATION OF SKELETAL MUSCLES IN MRI

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Target audience: Researchers involved in image processing or in clinical protocols in the muscle field.

Introduction

In the study of neuromuscular pathologies, NMR imaging is a powerful and non-invasive method for the monitoring of disease progression and for the comparison of populations using biomarkers such as: muscle volume, muscle atrophy, proportion of adipose tissues within muscle, etc. In order to perform such analysis on a per-muscle basis (or group of muscles), it is necessary to segment the acquired volumes. While such task is easily achieved manually, segmenting entire muscles this way is extremely timely and rather tedious for the operator. As a result, it often happens that studies are delayed or cancelled due to the amount of work that segmenting dozens of volume represents. Automatic segmentation would be an obvious solution to this problem. However, certain visual properties of the muscles in NMR imaging, such as fuzzy boundaries, different regions with similar texture make the development of automatic methods complicated. Typically, the obtained results of a fully automatic segmentation (without user interaction) are unsatisfactory. Therefore, in this context, a semi-automatic image segmentation approach looks very promising, since an appropriate graphical interface can improve, accelerate and facilitate such a work. A lot of software for manual segmentation routines has already been developed and available under free licenses. Based on this, we present a user-friendly interactive segmentation tool that is handy and suitable for clinicians and incorporates a robust semi-automatic segmentation algorithm. This software allows us to significantly reduce segmentation time while still having accurate results, comparable with fully manual segmentation.

Material and Methods

Taking into account the performance, effectiveness and speed of correction of the results by adding additional markers, the random walker algorithm [1] was selected as a basis for our interactive segmentation tool. This algorithm usually requires to be used with *seeds*, that are small pre-segmented regions. Typically, a user draws seeds on the non-segmented image, and then runs the calculation to obtain the full segmentation. Corrections can be dealt with by adding more seeds and re-launching the computation. Our version of the random walker algorithm was implemented in C++ programming language with pure C inclusions (for low-level memory operations: allocation, copying and moving) and can be compiled for Windows and Linux systems. For sparse matrix manipulations a compressed sparse row (CSR) format was used, that is efficient for arithmetic operations, row slicing, and matrix-vector products. The system of linear equations of the random walker method was solved using the conjugate gradient method with algebraic multigrid preconditioning, implemented by means of Hypre linear algebra package [2]. For execution on a multicore processor the OpenMP interface was used. Some usability testing with clinicians was performed to find a graphical user interface to be the basis for a new segmentation tool. The ITK-SNAP software [3] was selected as it provides a set of tools to make manual segmentation of volumetric data easy and fast. They are mainly used for segmentation with hand contouring, for segmentation correction and statistics calculation. A new segmentation tool using random walker algorithm was integrated into ITK-SNAP software. It is a special brush, that places new seeds of a selected color using the computer mouse, then a segmentation area around the newly drawn seeds is automatically computed. Close to real-time re-segmentation can be achieved thanks to the locality of the segmentation and to the efficient algorithm implementation. The proposed tool is very intuitive and allows building a muscle by muscle progressive segmentation as well as an effective local correction. Process of quadriceps muscles segmentation is shown in Figure 1.

Results

A set of 10 human thigh muscle volumes was used for comparison tests. The volumes were acquired on 3T whole body scanner (Tim Trio, Siemens Healthcare) and consists of out-of-phase Dixon images, (TE/TR = 3.95/10ms) with spatial resolution = $1x1x5mm^3$ and grid size = 224x224x116 voxels. The four muscles of the quadriceps were manually segmented for a previous study [4]. Segmentation time was reported to be more than 3 hours. The same volumes were blindly segmented by two users. Segmentation time was fixed to be less than 10 min. The resulting segmentations were compared to the manual segmentation for measuring the accuracy in a given time (inter-technique variability), and compared with respect to the users, for reproducibility results (inter-user variability). The criteria that were used were relative volume differences and Dice coefficients (Table 1). The results showed that interactive segmentations were very close to the manual ones, which was confirmed by visual inspection. Inter-operator variability was also extremely small. The majority of the observed differences are due to operator choices in places where fasciae are not visible. This was confirmed by the decrease in relative difference when one considered the entire quadriceps.

Conclusions

It was shown that it is possible under 10 min to accurately segment the four muscles of the quadriceps with little difference from the fully manual segmentation which takes more than 3 hours. This made an acceleration factor larger than 18 at the minimum, where the gain in time was not compromised by a loss in segmentation quality.

Inter-technique variability					
	R. Femoris	V. Lateralis	V. Intermedius	V. Medialis	Whole Quadriceps
Relative volume difference	7,61	5,98	4,68	6,21	4,49
Dice coefficient	0,926	0,919	0,867	0,934	0,956

Inter-user variability					
	R. Femoris	V. Lateralis	V. Intermedius	V. Medialis	Whole Quadriceps
Relative volume difference	2,98	6,26	14,43	6,12	1,45
Dice coefficient	0,956	0,937	0,88	0,951	0,983

Table 1. Muscle segmentation comparison results

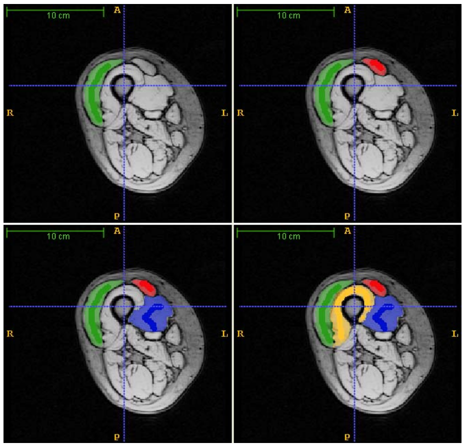

Figure 1. Example of different steps of the progressive muscle interactive segmentation

References

1. L. Grady. Random walks for image segmentation. Pattern Analysis and Machine Intelligence. 2006;28(11):1768–1783.
2. Hypre library, Lawrence Livermore National Laboratory, USA. http://acts.nersc.gov/hypre/. Accessed November 12, 2013.
3. ITK-SNAP, Penn Image Computing and Science Laboratory, University of Pennsylvania, USA. http://www.itksnap.org/. Accessed November 12, 2013.
4. Y. Barnouin et al. MRI biomarkers of muscle volume and intramuscular fat infiltration in the thigh muscles: variations with gender, age and physical activity // Journal of Magnetic Resonance Imaging, submitted.