

Towards the definition of a patient-specific rehabilitation program for TKA: A new MRI-based approach for the easy volumetric analysis of thigh muscles*

M. Azimbagirad, G. Dardenne, D. Ben Salem, O. Rémy-Néris and V. Burdin

Abstract— After Total Knee Arthroplasty (TKA), a global post-operative rehabilitation programme is commonly performed. However, this current program is not always adapted to every patient and it could be improved by deeply reinforcing weaker thigh muscles. To do this, a muscle volume estimation coupled with force evaluation is required to therefore adapt the rehabilitation as a specific patient exercise plan. In this paper, we presented an MRI protocol allowing the acquisition of the whole thigh as well as a semi-automated pipeline to segment two main groups of thigh muscles, i.e., the quadriceps femoris and the hamstrings muscles. The pipeline is based on a few cross-sections manually labelled and a 3D-spline interpolation using directed graphs corresponding points. The seven muscles of ten thighs (70 muscles in total) were segmented and reconstructed in 3D. To assess this pipeline, three types of metrics (volumetric similarity, surface distance, and classical measures) were employed. Furthermore, the inter-muscle overlapping was calculated as an additional metric. The results showed mean DICE was 99.6% (± 0.1), Hausdorff Distance was 4.9 mm (± 1.8) and Absolute Volume Difference was 2.97 cm³ (± 1.94) in comparison to the manual ground truth. The average overlap was 2.05% (± 0.54).

Clinical Relevance— The proposed segmentation method is fast, accurate and possible to integrate in the clinical workflow of TKA.

I. INTRODUCTION

Total knee arthroplasty (TKA) is one of the most cost-effective and steadily successful surgery in orthopedics [1]. Today, only a post-surgical rehabilitation is performed after TKA surgery [2]. However, a pre-surgical training programme may also be used to improve patients' post-surgical functional status. To be successful, these pre- and post-surgical training programmes should focus on postural control, functional lower limb exercises and bilateral lower extremity strengthening exercises [3]. In order to define an effective patient specific training programmes, probably targeting the reinforcement of weaker muscles may help. But to do this, an accurate analysis to detect them is required.

Estimation of thigh muscle volume, fat proportion and strength are important clinical parameters used to assess and monitor muscle disease [4]. It is therefore necessary to have an accurate and easy-to-use tool that allows the physician to measure these parameters specifically on each muscle in the

clinical routine. Several tools have been developed and used to extract this muscle information such as, cross-sectional segmentation [5], anthropometric assessment [6] and bioelectrical impedance analysis [7]. However, the most reliable technique and gold-standard method for extracting these clinical muscle data remains MRI. But, to be accurate, it is still today necessary to make manual segmentation which is time-consuming [8]. In order to reduce the manual segmentation time, several effective strategies have been introduced to decrease the number of cross-sections or their position, although the accuracy decreases accordingly [9, 10]. In addition to manual segmentation, automatic and semi-automatic approaches are two other categories of muscle volume estimation. Automatic approaches are still in progress with concepts such as graph cut [11], atlas-based segmentation [12] or more recently deep-learning methods [13]. Up to now, these fully automatic methods have not yet achieved sufficient accuracy to robustly detect changes in muscle volumes of less than 5% error which is the target of this paper.

Semi-automatic approaches may be a relevant alternative. These methods typically use a few manually labelled cross-sections and then estimate or reconstruct the entire volume of each muscle with high accuracy. For instance, Albu et al. [14] proposed a morphological contour interpolation to fill the space between segmented cross-sections of the same anatomical structure. The proposed interpolation process is iterative such that at each iteration it computes a transition sequence between a pair of corresponding input slices and selects the element located at equal distance from the two input slices. This algorithmic design allows for a smooth and gradual change in shape throughout the volume object. Another example of semi-automatic approach is a model-based method introduced by Jolivet et al. [15]. In this method, the muscles are reconstructed based on a few selected MRI slices by fast rough contouring using polygons. These polygons were matched to the muscle shape by an optimisation method using an original cost function. However, the aforementioned methods, i.e., morphological contour interpolation and the model-based reached an accuracy (e.g., DICE and volume similarity) lower than 95% comparing to manual segmentation. This accuracy might be insufficient when comparing the muscle volumes of two groups which are close to each other. That means, if the difference between two

*Research supported by ANR-17- RHUS-0005.

M. Azimbagirad, University of Western Brittany (UBO), INSERM UMR 1101 LaTIM, Brest, France (corresponding author phone: 33-06767-78898; e-mail: mehran.azimbagirad@univ-brest.fr)

G. Dardenne, University Hospital of Brest, INSERM UMR1101 LaTIM, Brest, France; e-mail: guillaume.dardenne@univ-brest.fr

D. Ben Salem, UBO, University Hospital of Brest, INSERM UMR 1101 LaTIM, Brest, France; e-mail: douraid.bensalem@chu-brest.fr

O. Rémy Néris, UBO, University Hospital of Brest, INSERM UMR 1101 LaTIM Brest, France; e-mail: olivier.remy-neris@univ-brest.fr

V. Burdin, IMT Atlantique, INSERM UMR 1101 LaTIM, Brest, France; e-mail: valerie.burdin@imt-atlantique.fr

groups is lower than 5%, the results are not reliable since the accuracy of estimation was higher than 5%. Particularly, in the follow-up studies this situation might happen.

This paper proposes a quantitative and accurate estimation of thigh muscles volume using MRI. Our semi-automated muscle reconstruction was based on a few hand-labelled cross-sections and a 3D-spline interpolation of corresponding points using directed graphs. We evaluated and compared the proposed pipeline to manual ground truth and a well-known tool respectively. We also defined a new metric as overlaps which might take place between the thigh muscles after volumetric reconstruction.

Section II describes the overall processing pipeline in four main steps: MRI protocols for muscles (A), manual contours registration and mapping (B), 3D-spline interpolation (C), and 3D reconstruction of each muscle (D). Section III is dedicated to the experiments (70 muscles from 10 thighs). A discussion section and a conclusion conclude the paper.

II. METHODS

A. Subjects and MRI protocols

According to the Declaration of Helsinki with ethical approval protocol (n° 2019-A01703-54), 10 entire thighs from 5 healthy volunteers with an average age of 48 years (± 10) were acquired using a 3.0 Tesla scanner (Elition X, Philips Medical System, Best, The Netherlands) with modified Dixon three-dimensional (3D) T1-weighted (T1W) gradient echo technique (mDixon-3D-GRE), allowing fat (F)-water (W) separation and a voxel resolution of $0.5 \times 0.5 \times 1.0 \text{ mm}^3$. In addition to F and W, two other images were extracted, namely input phase (IP= W + F) and output phase (OP= W-F). We chose the OP image for manual segmentation because the intermuscular septum is more visible in OP. We used the 3D Slicer software to manually segment axial slices, spaced 30 mm apart for the proposed method and adjacent for ground truth. Two groups of thigh muscles were selected to evaluate the pipeline: the quadriceps Femoris muscles (Rectus Femoris (RF), Vastus Lateralis (VL), Vastus Intermedius (VI), Vastus Medialis (VM)), and the Hamstrings muscles (Biceps Short Head (BSH), Semitendinosus (ST), Semimembranosus (SM)).

B. Registration and matching of annotated contours

For each selected slice in each thigh muscle, an expert (10 years' experience) performed a manual annotation on axial slices. In order to find the corresponding points between the annotated contours of each muscle (and to be able to calculate an accurate interpolation between them), a registration of each successive pair annotated contours (smaller to larger) is performed sequentially.

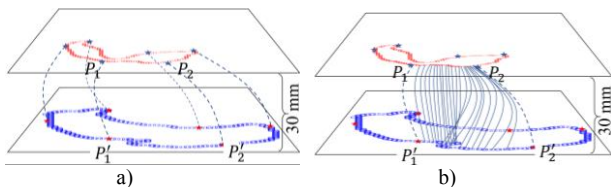


Figure 1. a) finding the accurate corresponding points (e.g., P_1 from upper to P'_1 from lower contour points) using registration technique and minimum distances, b) association of the inter points between P_1 to P_2 and P'_1 to P'_2 using a unique distribution.

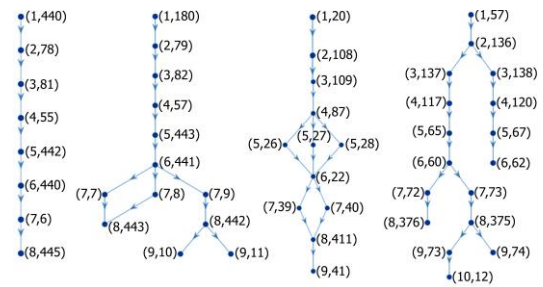


Figure 2. Four real examples of trees (directed graphs) for 10 successive contours. The first digits are the number of contour (slice) and the second digits are the label of points in that contour.

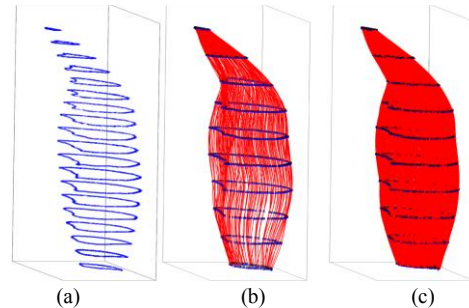


Figure 3. a) extracted contours from a manual delineation of Biceps short head, b) Vertical 3D spline curve for interpolating the corresponding points between two contours, c) 2D horizontal spline interpolation of b) for creating new contours.

After this registration, we proposed to use only a few accurately matched points (separated by Euclidean distance of less than 1 mm). Then, between every two points selected for matching, on the same slice, and on both contours, we selected the same number of equidistant points and we one-to-one linked them, providing all the matched points in a stepwise fashion (Fig. 1).

C. 3D Spline interpolation

We provided the corresponding points lists in a tree structure (directed graphs, e.g., see Fig. 2) and all paths from the roots to the leaves were interpolated using spline curves. The interpolation is carried out in two phases. The first phase aims to perform the interpolation using 3D splines according to the longitudinal direction, i.e., between each corresponding point along all contours (Fig. 3.b). The second phase aims to interpolate the 3D splines points located on the same z-plane (indeed 2D splines) in order to create new continuous contours to bridge the gap (Fig. 3.c).

D. Reconstruction

In order to reconstruct the volume of each thigh muscle, we filled in all created horizontal contours (fill function from Scipy package [16]) and we used the marching cubes algorithm [17] to extract each muscle volume as a mesh. We refer to our method as “Spline” in the results section. The proposed pipeline for 3D reconstruction of the thigh muscle was compared with Albu’s method, namely “SDF” which is a tool proposed by ITKSnap [14].

Then, both methods (spline and SDF) were used to 3D reconstruct the volume from the same few manually segmented slices, and both results are compared to a fully manual segmentation of all adjacent contours.

We used 3 types of metrics in order to quantitatively evaluate the accuracy of the methods (Spline and SDF) compared to the fully manual method: I) volume similarity (Dice Coefficient (DICE), Volumetric Similarity Coefficient (VOLSMTY)), II) surface distance (Hausdorff distance (HDRFDST), average distance (AVGDIST)), III) classical measures (Sensitivity or true positive rate (SNSVTY), Specificity or true negative rate (SPCFTY) and absolute volume distance (AVD)) [18].

For each pair successive manual corresponding points, the borders of each muscle are fully connected. We expected the spline interpolation to correctly connect each corresponding point in the same path of the intermuscular septum. Indeed, the curvature of each spline curve might path through other spline curves. This perturbation may result in an overlap between adjacent muscles (see dashed boxes in Fig. 4). One reason for this overlap is associated to the wrong corresponding points that might increase the curvature of the 3D spline curves. As a new metric, we assessed the overlap between adjacent muscles to see the impact of independent reconstruction of each muscle.

III. RESULTS

A. MRI protocols and manual labeling

We optimised the MRI protocol parameters to increase the contours visibility of each muscle, and we set TE=1.96/3.3 msec, TR=5.6 msec, Flip Angle=10 deg in coronal direction acquisition. Using the 3D slicer software, 7 muscles of 10 thighs were segmented from top to bottom in original resolution. Fig. 5 shows an example of each muscle: segmented cross-sections and the associated rendered volume.

B. evaluation using manual reference

In the first evaluation scheme, the reconstructed volumes and meshes of the thigh muscles provided by the proposed method (spline) were compared to those obtained by manual

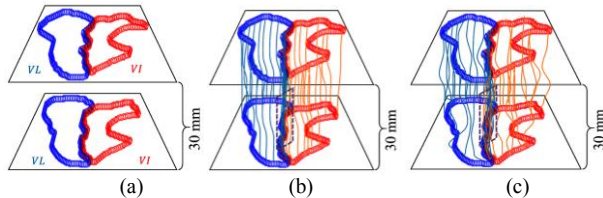


Figure 4. Overlap metric to evaluate 3D spline curves for corresponding points. a) Two manually labeled adjacent thigh muscle VL and VI b) correct 3D spline curves to link corresponding points, c) incorrect 3D spline curves which make overlaps with other interpolating curves can be seen in the dashed box.

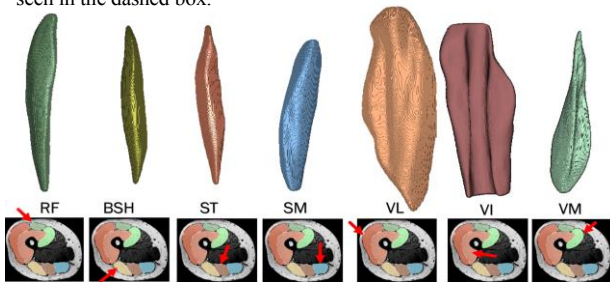


Figure 5. Volume reconstruction/segmentation of thigh muscles using manual labelling, RF=Rectus Femoris, VL=Vastus Lateralis, VI=Vastus Intermedius, VM=Vastus Medialis, BSH=Biceps Short Head, ST=Semitendinosus, SM=Semimembranosus.

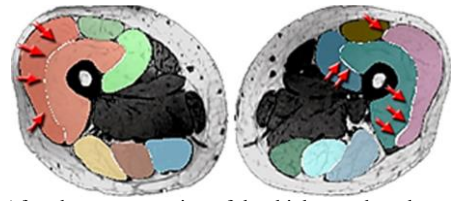


Figure 6. After the reconstruction of the thigh muscle volumes using our "spline" method, an overlap (white voxels) may take place in the borders between adjacent muscles (~2%).

TABLE I. EXTRACTED SIMILARITY METRICS BETWEEN THE PROPOSED METHOD "SPLINE" OR MORPHOLOGICAL CONTOUR INTERPOLATION METHOD "SDF", AND THE MANUAL SEGMENTATION

Metrics	Method	Mean	STD	Min	Max
DICE +	Spline	0.996	0.001	0.994	0.998
	SDF	0.958	0.007	0.926	0.969
VOLSMTY +	Spline	0.996	0.001	0.994	0.998
	SDF	0.991	0.005	0.979	1.000
HDRFDST* -	Spline	4.868	1.830	3.464	7.488
	SDF	6.094	2.179	2.828	15.167
AVGDIST -	Spline	0.006	0.002	0.003	0.009
	SDF	0.051	0.008	0.040	0.094
SNSVTY +	Spline	0.999	0.001	0.999	1.000
	SDF	0.966	0.011	0.911	0.979
SPCFTY +	Spline	0.999	0.001	0.999	1.000
	SDF	0.999	0.001	0.999	1.000
AVD** -	Spline	2.975	1.938	0.959	7.313
	SDF	4.984	5.219	0.370	20.072

* unit is mm + best if high value
 ** unit is cm³ - best if low value

TABLE II. OVERLAP ERRORS BETWEEN RECONSTRUCTED THIGH MUSCLE VOLUMES USING THE PROPOSED METHOD "SPLINE"

N*	Joint Thigh muscles overlaps (%)							Sum
	RF-VL	RF-VI	RF-VM	VL-VI	VI-VM	BSH-ST	ST-SM	
1	0.25	0.08	0.12	0.84	0.25	0.23	0.28	2.04
2	0.17	0.05	0.08	0.70	0.32	0.41	0.25	1.99
3	0.01	0.02	0.08	0.26	0.27	0.21	0.28	1.13
4	0.07	0.00	0.07	0.63	0.22	0.21	0.20	1.41
5	0.06	0.26	0.10	1.27	0.41	0.30	0.32	2.73
6	0.08	0.26	0.08	0.75	0.12	0.46	0.67	2.41
7	0.15	0.04	0.03	0.99	0.32	0.64	0.33	2.50
8	0.22	0.06	0.01	0.95	0.35	0.77	0.50	2.85
9	0.13	0.02	0.22	0.68	0.27	0.21	0.19	1.70
10	0.20	0.07	0.09	0.73	0.22	0.18	0.26	1.75
Mean	0.13	0.09	0.09	0.78	0.27	0.36	0.33	2.05
STD	0.07	0.09	0.05	0.25	0.07	0.19	0.14	0.54

* Number of each thigh in the inclusion
 RF=Rectus Femoris, VL=Vastus Lateralis, VI=Vastus Intermedius, VM=Vastus Medialis, BSH=Biceps Short Head, ST=Semitendinosus, SM=Semimembranosus.

labelling. In addition, we challenged our pipeline with the morphological contour interpolation method (SDF) which is also evaluated using the manual labelling. The results are presented in Tab. I showing the mean, standard deviation, minimum and maximum of the extracted similarity metrics for 70 muscles in total.

C. Overlapping estimation

We defined another metric to measure the accuracy of our method for thigh muscle segmentation as overlap (Fig. 6). The average overlap taking place in volume reconstruction was 2.05% (std 0.54) of the total muscle volume. Tab. II presents the detailed results for each adjacent muscle overlapping.

IV. DISCUSSION

For the proposed method, an inter-slice distance of 30 mm was selected, based on a systematic analysis of the position

and distance between slices to be manually segmented (from 1 mm to 100 mm). A spacing greater than 30 mm can decrease the accuracy by about 1% and a spacing less than 30 mm has no effect on the accuracy. As this study is the first step in a follow up project for TKA patients, the accuracy is crucial and takes precedence over calculation time.

For the 10 thighs, the results showed a mean DICE and volumetric similarity of 99.6% (std 0.1), Hausdorff Distance 0.49 cm (std 0.2) and AVD 2.97 cm³ (std 1.94) in comparison to manual ground truth (Tab. I). Furthermore, the proposed method “Spline” averagely improved 2.2% the similarity metrics in comparison to the “SDF” method. In addition, the average overlap taking place in volume reconstruction was 2.05% (std 0.54) which is negligible.

The running time for volume segmentation using Jolivet’s method [15] averagely took 21 minutes to perform and the volume error was inferior to 5 %. The running time of our method averagely takes about 15 minutes which is under the limitation for our TKA study which implements the results in the following next training day.

Overlap metrics can be assumed as new metrics in segmentation method for multi-connected regions scheme which might not be considered in other metrics such as DICE, Volume similarity, or Hausdorff since they only measure similarity between two muscles.

To the best of our knowledge, our method reached the highest accuracy among the reviewed thigh muscle segmentation methods in aforementioned references. This method is parametrized and geometric, no need for training data such as deep learning approaches, and guarantees the gradual smoothing of the muscle change. Much is left to be assessed on pathological data, and provide a module based on the proposed algorithm for 3D Slicer platform targeting larger community.

V. CONCLUSION

In this study, we introduced an accurate semi-automatic segmentation method for thigh muscles based on manual annotation of few slices, contours registration, directed graphs corresponding points and a two-phases spline interpolation. The accuracy of the method is sufficient to be used in follow up studies aiming to monitor changing the muscles shape and other quantitative MRI protocols such as T2, T1 and DTI. The running time to segment manually few slices, automatically reconstruct the 3D muscle and evaluate its volume is compatible to integrate our method in the clinical workflow of TKA. This method needs to be evaluated on pathological data and it will be extended to other longitudinal muscles such as leg muscles.

ACKNOWLEDGMENT

This work has benefited from a French grant managed by the National Research Agency under the “programme d’investissements d’avenir” bearing the reference ANR-17-RHUS-0005, and the financial support of the Brittany Region. The Institution’s Ethical Review Board approved all experimental procedures involving human subjects.

REFERENCES

- [1] M. Varacallo, T. D. Luo, and N. A. Johanson, "Total knee arthroplasty (TKA) techniques," *StatPearls [Internet]*, 2020.
- [2] S. Lassche *et al.*, "Correlation Between Quantitative MRI and Muscle Histopathology in Muscle Biopsies from Healthy Controls and Patients with IBM, FSHD and OPMD," *J. Neuromuscul. Dis.*, vol. 7, no. 4, 2020, pp. 495-504.
- [3] J. Warman Chardon *et al.*, "MYO-MRI diagnostic protocols in genetic myopathies," (in eng), *Neuromuscul. Disord.*, vol. 29, no. 11, Nov 2019, pp. 827-841.
- [4] Y. X. Yang *et al.*, "Validity of estimating muscle and fat volume from a single MRI section in older adults with sarcopenia and sarcopenic obesity," *Clin. Radiol.*, vol. 72, no. 5, 2017, pp. 427.e9-427.e14.
- [5] A. Nordez, E. Jolivet, I. Südhoff, D. Bonneau, J. A. de Guise, and W. Skalli, "Comparison of methods to assess quadriceps muscle volume using magnetic resonance imaging," *Journal of Magnetic Resonance Imaging*, vol. 30, no. 5, 2009, pp. 1116-1123.
- [6] M. A. S. Carneiro, L. C. Barcelos, P. R. P. Nunes, L. R. M. F. de Souza, E. P. de Oliveira, and F. L. Orsatti, "Anthropometric equations to estimate the thigh muscle cross-sectional area by magnetic resonance imaging in young men," *Science & Sports*, vol. 34, no. 6, 2019, pp. 418-421.
- [7] Y. Yamada *et al.*, "Estimation of thigh muscle cross-sectional area by single- and multifrequency segmental bioelectrical impedance analysis in the elderly," *J. Appl. Physiol.*, vol. 116, no. 2, 2014, pp. 176-182.
- [8] C. Pons *et al.*, "Quantifying skeletal muscle volume and shape in humans using MRI: A systematic review of validity and reliability," *PLOS ONE*, vol. 13, no. 11, 2018, p. e0207847
- [9] H. Lund, L. Christensen, A. Savnik, J. Boesen, B. Danneskiold-Samsøe, and H. Bliddal, "Volume estimation of extensor muscles of the lower leg based on MR imaging," *European Radiology*, journal article vol. 12, no. 12, Dec 2002, pp. 2982-2987.
- [10] B. L. Tracy *et al.*, "A More Efficient Magnetic Resonance Imaging-Based Strategy for Measuring Quadriceps Muscle Volume," *Medicine & Science in Sports & Exercise*, vol. 35, no. 3, 2003, pp. 425-433.
- [11] P.-Y. Baudin, "Graph- based segmentation of skeletal striated muscles in NMR images. Signal and Image processing," PhD, Ecole Centrale Paris, 2013.
- [12] F. Yokota *et al.*, "Automated muscle segmentation from CT images of the hip and thigh using a hierarchical multi-atlas method," *International Journal of Computer Assisted Radiology and Surgery*, vol. 13, no. 7, 2018, pp. 977-986.
- [13] P.-H. Conze, S. Brochard, V. Burdin, F. T. Sheehan, and C. Pons, "Healthy versus pathological learning transferability in shoulder muscle MRI segmentation using deep convolutional encoder-decoders," *Computerized Medical Imaging and Graphics*, vol. 83, 2020, p. 101733.
- [14] A. B. Albu, T. Beugeling, and D. Laurendeau, "A Morphology-Based Approach for Interslice Interpolation of Anatomical Slices From Volumetric Images," *IEEE Trans. Biomed.*, vol. 55, no. 8, 2008, pp. 2022-2038.
- [15] E. Jolivet *et al.*, "Skeletal muscle segmentation from MRI dataset using a model-based approach," *Comput Methods Biomech Biomed Eng Imaging Vis*, vol. 2, no. 3, 2014, pp. 138-145.
- [16] scipy.org. "Fill the holes in binary objects." https://docs.scipy.org/doc/scipy-0.15.1/reference/generated/scipy.ndimage.morphology.binary_fill_holes.html (accessed 2019).
- [17] W. E. Lorensen and H. E. Cline, "Marching cubes: A high resolution 3D surface construction algorithm," presented at the Proceedings of the 14th annual conference on Computer graphics and interactive techniques, 1987.
- [18] A. A. Taha and A. Hanbury, "Metrics for evaluating 3D medical image segmentation: analysis, selection, and tool," *BMC medical imaging*, vol. 15, no. 1, 2015, p. 29.