A Knowledge-Based Modality-Independent Technique for Concurrent Thigh Muscle Segmentation: Applicable to CT and MR Images

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Abstract

The mass of the lower extremity muscles is a clinically significant metric. Manual segmentation of these muscles is a time-consuming task. Most of the segmentation methods for the thigh muscles are based on statistical models and atlases which need manually segmented datasets. The goal of this work is an automatic segmentation of the thigh muscles with only one initial segmented slice. A new automatic method is proposed for concurrent individual thigh muscles segmentation using a hybrid level set method and anatomical information of the muscles. In the proposed method, the muscle regions are extracted by the Fast and Robust Fuzzy C-Means Clustering (FRFCM) method, and then a contour is determined for each muscle which changes according to the muscle shape variation through its length. The anatomical information is used to control the contours variations and to refine the final boundaries. The method was validated by 22 CT datasets. The average dice similarity coefficient (DSC) of the method for individual muscle segmentation with one and two initial slices were 89.29 ± 2.59 (%) and 91.77 ± 1.87 (%), respectively. Also, the average symmetric surface distances (ASSDs) were 0.93 ± 0.29 mm and 0.64 ± 0.18 mm. Furthermore, applying to ten MRI datasets, the average DSC and ASSD for muscles were 90.9 ± 2.61 (%) and 0.71 ± 0.33 mm, respectively. The quantitative and intuitive results of the proposed method show the effectiveness of this method in segmentation of large and small muscles in CT and MR images. The consumed computation time is lower than the previous works, and this method does not need any training datasets.

Keywords Thigh muscle segmentation · Knowledge-based level set · FRFCM · MRI · Multi-slice CT images

Introduction

The mass of thigh muscles is affected by some diseases such as peripheral arterial disease [1], chronic obstructive pulmonary disease [2], and muscular dystrophies [3]. Therefore, thigh muscle quantification plays an important role in diagnosing and treatment of these diseases. Besides, it is a critical step in surgical planning and postoperative assessment in orthopedic surgery [4]. Segmentation of different muscles in the thigh region is an open-research subject and a challenging task, as they have a similar intensity in computed tomography (CT) and magnetic resonance (MR) images. Uemura et al.

evaluated the changes in the gluteal and thigh muscles volumes after total hip arthroplasty in CT images, but they segmented these muscles manually in a few slices [5]. So far, several studies have been devoted to the automatic segmentation of thigh muscles, individually, in three dimensions (3D). Most of the previous works used MR images [6–12], and only one recent study segmented the pelvic and hip muscles in CT scan datasets [4] which is an extension of their previous work [13]. In some previous works [14–16], thigh muscles were extracted in CT and MR images as one object and have not been segmented individually. Recently, some studies have used deep learning methods to segment thigh muscles [17–19]. These methods did not segment all the muscles, individually. Since the deep learning-based methods need a high number of manually segmented images for training, these methods have not been investigated in this research, and the proposed method is adjusted to work in a situation where segmented datasets are not available. MRI potentially provides higher contrast in comparison with CT for the soft tissues, but it suffers from long acquisition time and needs fine-tuned protocol design for each study [4]. Furthermore, both slice thickness and space between slices are larger in clinical

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MRI of the thigh region. Therefore, the number of MR slices is obviously much less than those of CT slices, in common clinical practice. Consequently, CT images are more appropriate not only in muscle quantification but also in corresponding 3D surface visualizations. In addition, these images are commonly used in orthopedic surgery. Therefore, this research concentrates on CT scan datasets for thigh muscles quantification.

Yokota et al. [4] employed a hierarchical multi-atlas method for the individual muscle segmentation in the hip and thigh regions. Although it has very good accuracy in the large muscles segmentation, its resolution is lower for the smaller muscles. This method needs manually segmented muscles in three dimensions to create multi-atlas, and this process is time-consuming. While a powerful system was used by Yokota et al. [4], the consumed computation time for this method was relatively high (41 min on Intel Xeon processors (2.8 GHz, 60 cores)). Furthermore, the method only applied to the female subjects which generally have more fat between the muscle tissue in the thigh region [20, 21]. Therefore, the muscles' boundaries are more discernible. In this study, we propose a level set-based method with low computation time for individual muscle segmentation. This method does not need 3D manual segmented muscles a priority and only requires one initial segmented slice. Then, the method segments muscles, automatically, in three dimensions. This method was applied to male and female subjects. The active contour-based methods were used in [22, 23] to segment thigh muscles. These methods segmented some of the thigh muscles only in one slice of MR images and did not extract muscles in 3D. The proposed method in [22] was extended to 3D [24]. This method has been only performed between 25 and 65% of the thigh and needs manual interaction in the segmentation process. Also, the muscles have been segmented in 4 groups. In the current research, the level set method based on anatomical information of the thigh muscles for 3D segmentation is used. This method is applicable for both CT and MR datasets, and it segments thigh muscles individually. Furthermore, the consumed computation time for the proposed method is less than the previous works [4, 6, 24].

The main goal of this paper is to segment thigh muscles by a novel knowledge-based level set. At first, noise of the images is reduced, and then, muscles regions are extracted by FRFCM algorithm after improving the image intensity. Finally, muscles are segmented using the proposed level set method based on the anatomical information.

Material and Methods

Dataset

Figure 1 shows a sample axial slice of CT and MR images from the thigh region. As shown in Fig. 1, muscles are more

distinctive in MR than CT images, and therefore, muscle segmentation is a more challenging task in CT images. So this research concentrates on these images. Furthermore, the method is performed for MRI datasets.

In this research, 22 CT datasets, taken from reference [25], were used to verify the proposed method effectiveness. There were ten males and twelve females datasets with a mean age of 50.55 ± 12.6 years. The slice thickness was 1.25 mm, and the image size was 512×512 . The X-ray tube voltage was 110 or 130 kVp, and tube current was between 80 and 136 mA.

In addition, the proposed method was applied to 10 T1-weighted MRI datasets with a mean age of 35.5 ± 13.28 years. These datasets have been acquired with a 1.5T Siemens scanner and using a spin-echo (SE) scanning sequence with the following parameters: the slice thickness, 4.5–6.6 mm; the space between slices, 6.21–9.72 mm; the echo time, 11–12 ms; the repetition time, 450–515 ms; and the in-plane sizes, 320×320 or 636×896 .

CT datasets completely include femur bone, and MRI datasets include femur bone from the knee to the insertion of gluteus maximus muscle. Muscles have been segmented from the top of the patella in the distal femur to the insertion of gluteus maximus muscle in MRI images and to the top end of the femur shaft in CT datasets.

The Proposed Method

In the proposed method, the segmentation of the muscles starts from an initial segmented slice. Each slice including all muscles can be considered as the initial slice. It was heuristically found that all of the thigh muscles segmented in this research exist in the slices approximately located in a distance between 25 and 45% of the distal to proximal femur length. The boundaries of the muscles in the initial slice are given a priori. These boundaries are propagated to the upper and lower slices as the initial contours of each muscle; the final contour of the muscles in these slices is determined by the proposed level set method. The algorithm is repeated until the final slice. Generally, the proposed method consists of three steps: preprocessing, segmentation of muscles from other tissues using FRFCM method, and concurrent individual muscle segmentation using a new knowledge-based level set method. Figure 2 shows the block diagram of the proposed method along with its steps which are explained as follows.

Preprocessing

As CT images are often degraded by noise, in the first step, noise of the images is reduced by the optimized anisotropic diffusion filter proposed by Kroon [26]. This scheme has better results in comparison with the other diffusion filtering with

Fig. 1 Sample axial slice of CT (a) and MR (b) images from the thigh region

standard and rotation invariant schemes for low-dose CT images as shown in [27]. In MRI datasets the preprocessing is different from CT images. In these images, N4ITK method [28] is applied to correct the bias field distortion. Then, thigh region in each axial slice is extracted, and the skin is removed by morphological erosion. The extraction of the thigh is performed by selecting an appropriate threshold value that distinguishes the thigh from the background. This threshold value is identified using the Fuzzy C-Means (FCM) algorithm [29].

Segmentation of Thigh Muscles from Other Tissues Using FRFCM Method

In CT scan images, the bone region has a higher intensity than the other tissues. After that, the muscle and fat tissues have higher intensities, respectively. In this step, at first, the region corresponding to the bone is extracted by thresholding and morphological operators and removed from the image. Then, the FRFCM method [30] is used to extract muscle, fat, and background classes.

There are three main intensity classes in MR images: “dark” (background, cortical bone), “gray” (muscle), and “light” (fat, bone marrow) [6]. Therefore, the FRFCM algorithm is applied to classify these three classes and extract muscles regions.

FRFCM algorithm is an improved FCM method by employing the morphological reconstruction and membership filtering that is significantly faster and more robust than FCM. The objective function of this algorithm is defined as

$$J_m = \sum_{l=1}^q \sum_{k=1}^c \gamma_l u_{kl}^m \|\xi_l - v_k\|^2, \quad (1)$$

where γ_l is the number of pixels with gray value equal to l . u_{kl} represents the fuzzy membership of gray value l with respect to cluster k , and m denotes the fuzzy weighted factor. v_k is the center of the k th cluster, and c defines the number of clusters. ξ is the filtered image by the bi-directional morphological filter, and ξ_l is a gray level; $1 \leq l \leq q$, q denotes the number of the gray levels contained in ξ .

Lagrange multiplier technique is employed to minimize the objective function as follows:

$$\tilde{J}_m = \sum_{l=1}^q \sum_{k=1}^c \gamma_l u_{kl}^m \|\xi_l - v_k\|^2 - \lambda (\sum_{k=1}^c u_{kl} - 1), \quad (2)$$

where λ is a Lagrange multiplier. By computing $\frac{\partial \tilde{J}_m}{\partial u_{kl}} = 0$ and $\frac{\partial \tilde{J}_m}{\partial v_k} = 0$, u_{kl} and v_k are obtained as follows:

$$u_{kl} = \frac{\|\xi_l - v_k\|^{-2/(m-1)}}{\sum_{j=1}^c \|\xi_l - v_j\|^{-2/(m-1)}}, \quad (3)$$

$$v_k = \frac{\sum_{l=1}^q \gamma_l u_{kl}^m \xi_l}{\sum_{l=1}^q \gamma_l u_{kl}^m}. \quad (4)$$

Optimal solution of u_{kl} is obtained iteratively. Equations (3) and (4) are repeatedly implemented until their variations will be lower than a threshold.

The muscles regions are extracted by clustering the images using the mentioned FRFCM method. To this aim, three classes are extracted by this method. The class with the highest intensity in CT images and with the middle intensity in MR images is corresponding to the muscle regions. In order to better visualize and to find the muscle weak boundaries in CT images, other tissues which have lower intensities than the muscle are replaced by the mean of the fat tissue class intensity. The pixels corresponding to the muscle class still remain unchanged. This approach is employed due to the intermuscular adipose tissue between muscles. This mask of the muscles is used as the input image in the next step. Figure 3 shows applying the steps of preprocessing and segmentation of muscles regions in a sample CT image.

The Proposed Concurrent Individual Muscles Segmentation Using a New Knowledge-Based Level Set

There are twelve muscles in the middle slices of the thigh: three vastus muscles, three adductor muscles, gracilis, rectus femoris, sartorius, biceps femoris, semitendinosus, and

Fig. 2 The block diagram of the proposed method

semimembranosus. The cross-sectional area (CSA) of these muscles varies in the different parts of the femur, but their shapes are correlated in the adjacent slices. Changes in the CSA along with the muscle length are similar in the different subjects.

After extracting the muscle regions, a contour is considered for each muscle in axial slices in order to segment muscles individually. These contours change simultaneously between slices according to the muscle CSA variations. There are false boundaries within muscles because of the presence of the intramuscular adipose tissue. As the slice thickness in clinical CT images is low, the muscle shapes and their CSA changes are very low in the adjacent slices, and the boundaries in the initial slice are close to the true boundaries of the muscles in the upper and lower slices. So the boundaries of the muscles in the initial slice are propagated to the upper and lower slices and considered the initial contours of the muscle in the next slice. On the other hand, in the active contour-based methods, faster and more accurate results are obtained when the initial contour position is close to the desired object boundary. Therefore, an active contour model (ACM) is used to find the primitive boundary of each muscle in the upper and lower

slices using the propagated boundaries from the previous slice as the initial condition.

In each slice before applying the ACM, the initial boundaries from the previous slice are geometrically aligned for some muscles such as sartorius and gracilis, which are moving between slices. As the slice thickness and the space between slices are high in clinical MRI datasets, firstly, the previous segmented slice is registered to the current slice using a non-rigid registration method performed by Kroon et al.[31]. The energy function of the Chan-Vese (CV) model [32] is used for each muscle such as follows:

$$E_i(c_1, c_2, \varphi_i) = \mu_i \cdot \text{Length}(\varphi_i) + v_i \cdot \text{Area}(\text{inside}(\varphi_i)) + \lambda_{1i} \int_{\text{inside}(\varphi_i)} |u_0(x, y) - c_1|^2 dx dy + \lambda_{2i} \int_{\text{outside}(\varphi_i)} |u_0(x, y) - c_2|^2 dx dy, \quad i = 1, 2, \dots, M \quad (5)$$

where M is the number of muscles, $\lambda_1, \lambda_2 > 0, v \geq 0$ and $\mu \geq 0$ are constant parameters, φ is the evolving contour, and c_1 and c_2 are the averages of intensity inside and outside the contour, respectively. The parameters of these models are determined according to the shape of the CSA and its variations between

Fig. 3 Preprocessing and muscles regions extraction in a sample CT image: original image (a), filtered image (b), and muscle mask (c)

Fig. 4 Propagation of the muscles boundaries to the upper and lower slices from the initial slice and 3D segmentation of the muscles

slices for each muscle. Since the muscles areas change slowly between the adjacent slices, the iteration number of the ACMs is low, and before applying them in each slice, the initial contours are eroded to be within the muscles. Then, the contours are allowed to expand during the ACM employing. The ACMs of all muscles are applied simultaneously, and a mask is achieved for each muscle: $A_1, A_2, \dots, A_M$. Due to the partial volume effect, some of the true edges between muscles are not discernible. In these situations, the contour of one muscle

would exceed to the adjacent muscle's region. Therefore, the anatomical information of the muscles and their adjacency information are used to modify the obtained muscle masks. The final muscles areas are determined as follows:

$$(A_{1f}, A_{2f}, \dots, A_{Mf}) = E_{\text{knowledge}}(A_1, A_2, \dots, A_M) \quad (6)$$

$$E_{\text{knowledge}}(A_1, A_2, \dots, A_M) = \left(\left(\sum_{i=1}^{M-1} \sum_{j=i+1}^M (A_i \cap A_j) \right) = 0 | B \right) \quad (7)$$

$$B = \begin{cases} A_i \cap A_j \subset A_i, & \text{if } A_i \cap A_j \text{ is allocated to } A_i \text{ in the previous slice or } A_i \text{ is growing or moving to } A_j \\ A_i \cap A_j \subset A_j, & \text{if } A_i \cap A_j \text{ is allocated to } A_j \text{ in the previous slice or } A_j \text{ is growing or moving to } A_i \end{cases} \quad (8)$$

where A_{if} is the final mask of the muscle i in each slice. According to Eqs. (6), (7), and (8), after applying ACMs, if adjacent muscles have overlapped area, this area would be allocated to the muscle that belongs to it in the previous slice. If the overlapped area is not in the muscle regions in the previous slice, using the anatomical knowledge, it is allocated to the muscle which is going to have a bigger area in that direction (downward or upward from the initial slice) or to the muscle which is moving toward the other muscle. Finally, these masks are propagated to the next

slice as the initial conditions, and the algorithm is repeated. Figure 4 shows an overview of the proposed method for individual muscle segmentation in 3D from one initial segmented slice.

Since different muscles have similar intensity and texture, the traditional level set method cannot correctly segment individual muscles. Figure 5 shows the results of the proposed method and traditional C_V model in one slice lower than the initial slice in a sample CT dataset. As shown in this figure, if the anatomical

Fig. 5 Comparing the results of the conventional CV model (a) and the proposed level set method (b) in concurrent individual muscle segmentation. As shown in this figure, the proposed method has segmented thigh muscles correctly

information is not used, the contours of the muscles would exceed to the other muscles region, where the edges of the muscles are not visible.

Some of the anatomical information used to obtain the final boundaries of the muscles in each slice is as follows: The muscle's CSA changes are very low in the adjacent slices; therefore, the iteration number of the algorithm is low. The adductor muscles area decreases from the initial slice in the downward direction (to the knee) and increases in upward direction. Their changes are faster than the other muscles. Therefore, for these muscles, the iteration number is higher than the others.

The CSA of gracilis and sartorius muscles does not significantly change. Vastus muscles area does not change much in the middle slices and decreases slowly in the upper and lower slices. The area of the rectus femoris muscle slowly decreases downward and increases upward. The CSA of the biceps femoris muscle increases firstly and then decreases in the downward direction. Its CSA decreases upward, but it changes slowly. Semimembranosus muscle's area increases in the downward direction and decreases upward. The area of the

semitendinosus muscle increases upward and decreases downward. As these muscles areas change slowly, the iteration numbers of ACMs are low for them. The ACMs for all muscles are applied simultaneously, and their variations are affected by the other ones.

Experimental Results

In this research, among 24 CT datasets, taken from reference [25], 2 male's datasets were very muscular, and due to partial volume effect and noise, their boundaries are not visible in many slices. So, their segmentation was not possible even manually, and they have been discarded. Then, the proposed method has been applied to 22 CT scan datasets. Furthermore, the performance of the method has been evaluated for 10 T1-weighted MRI datasets. The proposed algorithm was implemented on MATLAB 9.1 environment, and to visualize the results of the segmentation, Slicer 4.8.1 was applied. Manual segmentation of the muscles which were used as ground truth was done on

Table 1 The DSC (%) of the proposed method with one initial slice for the individual muscles for a subset of datasets

Muscle/dataset	#1	#2	#3	#4	#5	#6	#7
Gracilis muscle	89.67	87.20	94.12	90.36	89.25	85.56	92.57
Sartorius muscle	89.84	88.76	89.09	88.39	84.61	86.23	91.78
Biceps femoris muscle	89.19	89.53	90.63	90.28	86.98	90.31	88.69
Rectus femoris muscle	93.19	92.98	84.51	94.52	92.80	87.13	93.15
Adductor muscles	91.6	93.07	93.78	93.29	90.15	91.91	92.48
Semimembranosus muscle	91.26	92.63	91.64	90.35	83.96	85.99	92.11
Semitendinosus muscle	90.46	77.68	79.48	79.69	83.95	87.59	84.24
Vastus lateralis and vastus intermedius muscles	91.77	92.96	93.32	95.03	89.61	91.55	91.00
Vastus medialis muscle	86.82	88.01	85.18	89.80	91.66	84.06	84.33
Mean±SD	90.42 ± 1.84	89.20 ± 4.92	89.08 ± 5.03	90.19 ± 4.55	88.11 ± 3.36	87.81 ± 2.79	90.04 ± 3.51

Fig. 6 The boxplots for the DSCs (%) and ASSDs (mm) of the individual muscles over the 22 CT datasets using the proposed method with one (blue) and two initial slices (red)

ITK_SNAP 3.6.0. The average computation time was about 12 min for about 400 CT slices per case on Intel® processors (Corei7, 2.4 GHz, 16GB RAM). We can reduce the computation time by decreasing the number of slices (downsampling).

Evaluation of the method was performed by computing precision, sensitivity, specificity, dice similarity coefficient (DSC) [33], Hausdorff distance (HD), and average symmetric surface distances (ASSD) [34] metrics defined in Eqs. (9), (10), (11), (12), (13), and (14).

Fig. 7 Boxplots of the average DSC (a) and ASSD (b) for all individual muscles over 22 CT datasets

Table 2 Mean and standard deviation of HD for the proposed method with one and two initial slices for the individual muscles over the 22 CT datasets

Muscle\method	The proposed method with one initial slice Mean $\pm$ SD (mm)	The proposed method with two initial slices Mean $\pm$ SD (mm)
Gracilis muscle	4.70 $\pm$ 2.28	3.53 $\pm$ 0.99
Sartorius muscle	6.85 $\pm$ 2.41	5.01 $\pm$ 2.49
Biceps femoris muscle	10.83 $\pm$ 3.50	6.97 $\pm$ 2.76
Rectus femoris muscle	6.50 $\pm$ 3.78	6.19 $\pm$ 3.83
Adductor muscles	7.99 $\pm$ 2.10	6.53 $\pm$ 0.59
Semimembranosus muscle	10.62 $\pm$ 3.93	5.36 $\pm$ 1.29
Semitendinosus muscle	8.15 $\pm$ 3.08	6.62 $\pm$ 2.37
Vastus lateralis and vastus intermedius muscles	11.60 $\pm$ 3.24	9.84 $\pm$ 1.70
Vastus medialis muscle	17.53 $\pm$ 5.34	13.95 $\pm$ 2.32
Mean $\pm$ SD	9.34 $\pm$ 3.46	7.81 $\pm$ 2.18

$$\text{Precision} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Positive}} \quad (9)$$

$$\text{Sensitivity} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}} \quad (10)$$

$$\text{Specificity} = \frac{\text{True Negative}}{\text{False Positive} + \text{True Negative}} \quad (11)$$

$$\text{DSC} = \frac{2|A \cap B|}{|A| + |B|} \quad (12)$$

$$\text{HD}(A, B) = \max \left(\max_{s_A \in S(A)} d(s_A, S(B)), \max_{s_B \in S(B)} d(s_B, S(A)) \right) \quad (13)$$

$$\text{ASSD}(A, B) = \frac{1}{|S(A)| + |S(B)|} \left(\sum_{s_A \in S(A)} d(s_A, S(B)) + \sum_{s_B \in S(B)} d(s_B, S(A)) \right) \quad (14)$$

In Eqs. (12), (13), and (14), A and B are the segmentation results of the method and manual segmentation. $S(A)$ indicates

the set of surface voxels of A. $d(v, S(A))$ is the shortest Euclidean distance of an arbitrary voxel v to $S(A)$.

Results of the Proposed Method for CT Datasets

The DSCs for each individual muscle for a subset of the dataset are given in Table 1.

According to Table 1, the proposed method has good accuracy for small and large muscles. The slice located at 35% of the distal to proximal femur length was selected as the initial slice. If we use more than one initial slice, the proposed method would be more accurate. Therefore, we also performed our method using two initial slices. The results of the method with one and two initial slices have been compared together. The boxplots for DSC and ASSD of each individual muscle have been shown in Fig. 6.

Figure 7 shows the boxplot of the method with one and two initial slices for overall average DSC and ASSD of the muscles.

The average DSCs of all individual muscles from 22 CT datasets were 89.29 ± 2.59 (%) and 91.77 ± 1.87 (%) for the

Table 3 Mean and standard deviation of precision, sensitivity, and specificity metrics for the proposed method with one initial slice for the individual muscles over the 22 CT datasets

Muscle\metric	Precision Mean $\pm$ SD	Sensitivity Mean $\pm$ SD	Specificity Mean $\pm$ SD
Gracilis muscle	0.9276 $\pm$ 0.0616	0.8705 $\pm$ 0.0283	0.9997 $\pm$ 0.0003
Sartorius muscle	0.9368 $\pm$ 0.0471	0.8505 $\pm$ 0.0198	0.9997 $\pm$ 0.0003
Biceps femoris muscle	0.9037 $\pm$ 0.0365	0.8940 $\pm$ 0.0225	0.9985 $\pm$ 0.0011
Rectus femoris muscle	0.8981 $\pm$ 0.0618	0.9105 $\pm$ 0.0321	0.9992 $\pm$ 0.0006
Adductor muscles	0.9402 $\pm$ 0.0158	0.9080 $\pm$ 0.0341	0.9982 $\pm$ 0.0005
Semimembranosus muscle	0.9064 $\pm$ 0.0610	0.9002 $\pm$ 0.0400	0.9990 $\pm$ 0.0010
Semitendinosus muscle	0.8866 $\pm$ 0.0449	0.8011 $\pm$ 0.0752	0.9992 $\pm$ 0.0004
Vastus lateralis and vastus intermedius muscles	0.9345 $\pm$ 0.0273	0.9188 $\pm$ 0.0288	0.9954 $\pm$ 0.0048
Vastus medialis muscle	0.8723 $\pm$ 0.0293	0.8549 $\pm$ 0.0529	0.9973 $\pm$ 0.0007
Mean $\pm$ SD	0.9118 $\pm$ 0.0428	0.8787 $\pm$ 0.0371	0.9985 $\pm$ 0.0011

Table 4 Mean and standard deviation of precision, sensitivity, and specificity metrics for the proposed method with two initial slices for the individual muscles over the 22 CT datasets

Muscle/metric	Precision Mean $\pm$ SD	Sensitivity Mean $\pm$ SD	Specificity Mean $\pm$ SD
Gracilis muscle	0.9607 $\pm$ 0.0332	0.8731 $\pm$ 0.0346	0.9998 $\pm$ 0.0002
Sartorius muscle	0.9586 $\pm$ 0.0300	0.8605 $\pm$ 0.0201	0.9998 $\pm$ 0.0002
Biceps femoris muscle	0.9377 $\pm$ 0.0231	0.9055 $\pm$ 0.0308	0.9991 $\pm$ 0.0006
Rectus femoris muscle	0.9204 $\pm$ 0.0323	0.9207 $\pm$ 0.0249	0.9994 $\pm$ 0.0003
Adductor muscles	0.9530 $\pm$ 0.0230	0.9222 $\pm$ 0.0234	0.9985 $\pm$ 0.0010
Semimembranosus muscle	0.9212 $\pm$ 0.0669	0.9210 $\pm$ 0.0307	0.9991 $\pm$ 0.0011
Semitendinosus muscle	0.9135 $\pm$ 0.0190	0.8741 $\pm$ 0.0424	0.9994 $\pm$ 0.0002
Vastus lateralis and vastus intermedius muscles	0.9532 $\pm$ 0.0167	0.9281 $\pm$ 0.0223	0.9978 $\pm$ 0.0015
Vastus medialis muscle	0.9127 $\pm$ 0.0203	0.9046 $\pm$ 0.0386	0.9982 $\pm$ 0.0005
Mean $\pm$ SD	0.9368 $\pm$ 0.0294	0.9011 $\pm$ 0.0298	0.9990 $\pm$ 6.2424e-04

proposed method with one and two initial slices, respectively. Therefore, the method with two initial slices has better accuracy in comparison with the method with one initial slice ($p < 0.01$). Also, the average ASSD was 0.93 ± 0.29 mm for the method with one initial slice and 0.64 ± 0.18 mm for the method with two initial slices. According to ASSDs, the accuracy of the method was improved for all individual muscles by using two initial slices with a significance level of 0.01 ($p < 0.01$).

Fig. 8 The 3D visualization of the anterior (top) and posterior (down) views. Manual segmentation (a) and the results of the proposed method with one (b) and two (c) initial slices

Hausdorff distance (HD) metric which measures the maximum distance between the results of the method, and manual segmentation has been reported in Table 2.

According to Table 2, the maximum Hausdorff distance is corresponding to the vastus medialis muscle. It is due to this fact that its boundaries with vastus lateralis and vastus intermedius muscles are not discernible in many slices. Also, this metric shows a better performance of the method with two initial slices than one initial slice. Means and standard deviations of precision, sensitivity, and specificity of the method with one and two initial slices for each individual muscle are presented in Tables 3 and 4, respectively.

The average precision, sensitivity, and specificity of the method with one initial slice were 0.9118 ± 0.0428 , 0.8787 ± 0.0371 , and 0.9985 ± 0.0011 , respectively. The average of these metrics for the method with two initial slices were 0.9368 ± 0.0294 , 0.9011 ± 0.0298 , and $0.9990 \pm 6.2424\text{e-}04$, respectively. The precision of the proposed method with two initial slices is higher than the method with one initial slice with a significance level of 0.001.

The 3D and 2D visualization of the manual segmentation and the results of the method with one and two initial slices are presented in Figs. 8 and 9 for a typical subject. Anterior and posterior views of the segmented muscles are shown in Fig. 8. Three axial cross sections of the upper, middle, and lower thigh are shown in Fig. 9.

As shown in these figures, the intuitive results show improved accuracy of the method with two initial slices.

Results of the Proposed Method for MRI Datasets

Figure 10 shows the boxplots for ASSD and DSC of each individual muscle from 10 MRI datasets, respectively.

The mean DSC and ASSD for all individual muscles from 10 MRI datasets were 90.9 ± 2.61 (%) and 0.71 ± 0.33 mm, respectively. The average HD of the method with one initial

Fig. 9 Three axial slices of the manual segmentation (a) and the results of the proposed method with one (b) and two (c) initial slices from the upper (top), middle (middle), and lower (down) sections of the thigh

Fig. 10 The boxplots for the ASSDs (mm) and DSCs (%) of the individual muscles from the 10 MRI datasets using the proposed method with one initial slice

Table 5 Mean and standard deviation of precision, sensitivity, and specificity metrics for the proposed method with one initial slice for the individual muscles over the 10 MR datasets

Muscle/metric	Precision Mean $\pm$ SD	Sensitivity Mean $\pm$ SD	Specificity Mean $\pm$ SD
Gracilis muscle	0.9321 $\pm$ 0.0310	0.8984 $\pm$ 0.0649	0.9998 $\pm$ 0.0001
Sartorius muscle	0.8907 $\pm$ 0.0484	0.8972 $\pm$ 0.0644	0.9996 $\pm$ 0.0003
Biceps femoris muscle	0.9173 $\pm$ 0.0285	0.8884 $\pm$ 0.0484	0.9990 $\pm$ 0.0006
Rectus femoris muscle	0.8840 $\pm$ 0.0313	0.9424 $\pm$ 0.0331	0.9993 $\pm$ 0.0004
Adductor muscles	0.9064 $\pm$ 0.0378	0.9073 $\pm$ 0.0464	0.9982 $\pm$ 0.0008
Semimembranosus muscle	0.9124 $\pm$ 0.0404	0.9213 $\pm$ 0.0389	0.9992 $\pm$ 0.0006
Semitendinosus muscle	0.9101 $\pm$ 0.0375	0.8895 $\pm$ 0.0883	0.9994 $\pm$ 0.0003
Vastus lateralis and vastus intermedius muscles	0.9203 $\pm$ 0.0296	0.9706 $\pm$ 0.0116	0.9960 $\pm$ 0.0012
Vastus medialis muscle	0.9049 $\pm$ 0.0235	0.8993 $\pm$ 0.0333	0.9986 $\pm$ 0.0006
Mean $\pm$ SD	0.9087 $\pm$ 0.0342	0.9127 $\pm$ 0.0477	0.9988 $\pm$ 5.5599e-04

slice for MRI datasets was 8.1 ± 3.94 mm. Means and standard deviations of precision, sensitivity, and specificity of the method with one initial slice for each individual muscle are given in Table 5.

The average precision, sensitivity, and specificity of the method for MRI datasets are 0.9087 ± 0.0342 , 0.9127 ± 0.0477 and $0.9988 \pm 5.5599\text{e-}04$, respectively. Figure 11 shows the results of the proposed method with one initial slice and manual segmentation in three axial slices of a sample MR dataset.

Discussion

As mentioned earlier, segmentation of the thigh muscles is a time-consuming and challenging task. For example, fully manual segmentation of the thigh muscles requires about 800 min for one case with about 400 slices. Most of the previous researches have segmented these muscles in MR

images. Only one recent study segmented individual muscles in the thigh and hip regions in CT images using a hierarchical multi-atlas method [4]. This method had very good accuracy in segmentation of large muscles, but its precision was lower for the small muscles such as gracilis, sartorius, rectus femoris, and semitendinosus. Furthermore, Atlas-based methods will not perform well for very different data from the atlases, and this method is computationally expensive. In the current study, a knowledge-based level set method has been proposed to segment thigh muscles individually in CT and MR images. Although the proposed method is application-oriented, with regard to the importance of the problem and clinical daily need in applying this method in health centers, existing methods are not efficient enough; the clinical application of this method is very important. The proposed method only needs one initial segmented slice. To manually segment the first slice, it required about 2 min. To improve the performance of the method, more than one initial slice could be used. As shown in Fig. 7 and Tables 3 and 4, the

Fig. 11 Results of the manual segmentation (top) and the proposed method (down) in a sample MR dataset. Three axial slices from the upper (a), middle (b), and lower (c) sections of the thigh

Table 6 Overall comparison of the proposed method and the hierarchical multi-atlas method proposed in [4]

Method	Consumed computation time	DSC (%)	ASSD (mm)
		Mean $\pm$ SD	Mean $\pm$ SD
The hierarchical multi-atlas method proposed in [4] ¹	41 min on Intel Xeon processors (2.8 GHz, 60 cores)	84.82 $\pm$ 4.53	1.75 $\pm$ 0.42
The proposed method with one initial slice	12 min on Intel® processors (2.4 GHz, Corei7, 16GB memory)	89.29 $\pm$ 1.08	0.93 $\pm$ 0.16
The proposed method with two initial slice	12 min on Intel® processors (2.4 GHz, Corei7, 16GB memory)	91.77 $\pm$ 0.8	0.64 $\pm$ 0.10

¹ Dataset of Osaka University Medical School was applied

performance of the method in terms of DSC, ASSD, and precision was improved using two initial slices ($p < 0.01$). The computation time of this method is lower than the previous study [4]. Overall comparison of the proposed method and hierarchical multi-atlas method is reported in Table 6 which shows the high performance of the presented method in terms of DCS, ASSD, and time consumption.

The segmentation results of these methods for each muscle are compared in Table 7.

In the proposed method, while only a single segmented slice is used, the accuracy of this method is desirable. High performance of the proposed method is due to using of the high correlation of the muscle shapes in the adjacent slices, considering the variations of the muscles shapes along with their length, and applying these variations to determine the parameters of the level set method.

As shown in Fig. 6, the performance of the proposed method for the semitendinosus muscle was lower than the others in CT images. It is due to this fact that the semitendinosus and semimembranosus muscles are adjacent in many slices and due to the partial volume effect, their boundary is invisible in some slices. On the other hand, when the proposed method fails to identify the boundary between two muscles in one slice, it maintains the boundary in the previous slice whereas the muscles move together. As the semitendinosus muscle is

smaller in the lower slices than the semimembranosus muscle and it moves in these slices, the accuracy of the method for it is lower than the other muscles. The vastus medialis muscle is adjacent with the vastus lateralis and vastus intermedius muscles, and their boundaries for some cases are not visible in most slices in CT images. Therefore, the DSC of the method for this muscle is lower than the other muscles, and the Hausdorff distance for this muscle is higher than the others. If we consider three vastus muscles as one object, the DSC for them will be 94.71 ± 0.74 (%) and 95.33 ± 0.76 (%) for the method with one and two initial slices, respectively.

Most of the boundaries between muscles are not discernible in very muscular cases, and the proposed method is not very successful in segmentation of these cases. Furthermore, manually segmentation of the muscles is not possible in these datasets. The sample slice of two muscular cases discarded from datasets is shown in Fig. 12.

The proposed method is highly accurate for MRI datasets with only one initial segmented slice due to more distinct boundaries between muscles in MRI datasets. The method could be more accurate by reducing the space between slices.

The previous work, which has used the generalized log-ratio representation to 3D segment thigh muscles in MRI datasets [6], has an average DSC of 0.808 ± 0.074 which is lower than the DSC obtained with the proposed method in this

Table 7 Overall results of the proposed method and the hierarchical multi-atlas method proposed in [4] for each muscle

Method	The hierarchical multi-atlas method proposed in [4]		The proposed method with one initial slice		The proposed method with two initial slice	
	DSC (%)	ASSD (mm)	DSC (%)	ASSD (mm)	DSC (%)	ASSD (mm)
Gracilis muscle	78.1	1.61	89.66	0.4654	91.38	0.3642
Sartorius muscle	81.12	1.39	89.09	0.4554	90.63	0.3728
Biceps femoris muscle	87.39	1.55	89.81	0.8309	92.07	0.6020
Rectus femoris muscle	82.15	2.28	90.29	0.9282	92.02	0.6394
Adductor muscles	89.62	1.89	92.34	0.8082	93.70	0.6630
Semimembranosus muscle	84.64	1.75	90.13	0.7683	91.97	0.6537
Semitendinosus muscle	81.86	2.51	83.91	1.3378	89.30	0.8071
Vastus lateralis and vastus intermedius muscles	92.49	1.15	92.11	1.1514	94.02	0.7184
Vastus medialis muscle	86.06	1.69	86.24	1.6330	90.81	0.9616

Fig. 12 Sample axial slice of two muscular cases. As shown most of the boundaries are not visible in these samples

study. Furthermore, the segmented area in this research is more than the previous research introduced in reference [6]. In the proposed method, segmentation starts from the top of the patella and is extended to the insertion of the gluteus maximus muscle in MRI datasets (about 400 mm in the available datasets). However, segmentation of the muscles in reference [6] started just above the knee and extended 200 mm to the upper thigh [6].

Although the method introduced in reference [24] has higher DSC than the proposed method, muscles have been segmented in 4 groups and not individually. Also, manual interaction was needed in the segmentation process, and the segmentation was performed between 25 and 65% of the thigh. Furthermore, the consumed computation time is higher than the proposed method in this study.

The quantitative and intuitive results reveal that the proposed method is efficient for both CT and MR datasets. The limitation of the proposed method is the requirement of one initial segmented slice. Whereas the segmentation of this slice is propagated to upper and lower slices, each error in the segmentation of this initial slice would propagate to other slices. Therefore, since there is no automatic method to segment the muscles in this slice without error, the segmentation was done manually in this initial slice.

Conclusion

Thigh muscle quantification has an important role in postoperative assessment in orthopedic surgery. Besides, it is useful in the diagnosis of some diseases which change these muscles' volume. This research focused on CT images since this imaging modality is commonly used to diagnose the bones in orthopedic surgery. Furthermore, the proposed method has been evaluated on MRI datasets. A new knowledge-based level set method has been applied to the thigh muscles segmentation. The proposed method is based on thigh muscles' anatomical information, correlation of this information in the adjacent slices, and level set method. In this method, a contour

is assumed for each muscle in the axial slices which changes according to the muscle shape changes with its length. All muscles are segmented simultaneously, and their contours are affected by each other. Unlike the hierarchical multi-atlas method, which had less accuracy in the small muscle segmentation, the efficiency of the proposed method was similar for the small and large muscles. In order to improve the performance of the method, more than one initial slice could be employed. The method has been evaluated with two initial slices, and its improvement was confirmed by the DSC, ASSD, and precision evaluation. As shown in the results, this method works for both CT and MR datasets regardless of the modalities.

In future works, we are going to segment the muscles in the pelvic region, too. To fully automate the method, the next step of this research is to automatically segment the boundaries of the muscles in the initial slice. The ultimate goal of this research is to visualize muscle fiber in the muscles whose fibers are distinctive in CT images. To this aim, the muscle attachment regions to the bones are needed. Therefore, in the future works, bone-muscle attachment regions will be estimated.

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