Automated muscle segmentation from 3D CT data of the hip using hierarchical multi-atlas method

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Introduction: Patient-specific biomechanical simulations using image-based musculoskeletal modeling have been proved to be useful [1]. However, time-consuming nature in image segmentation of muscles is an obstacle to their clinical application. Although previous works tried to automate muscle segmentation, they still involved considerable manual interactions [2] or just approximated muscles as strings instead of segmenting their regions [3]. In this paper, we propose a fully-automated method for segmentation of muscles from hip CT data whose FOV covers the entire pelvis and femur. The feature of the proposed method is hierarchical strategy using hierarchical nature inherent in the musculoskeletal anatomy. We validate that the hierarchy embedded in the proposed method significantly improves the segmentation accuracy.

Method: Our targets were 17 muscles of the hip and thigh. We utilize hierarchical relations among structures in the hip CT images during multi-stage segmentation processes. Easier segmentable regions are extracted at earlier stages while more difficult ones at later stages using the constraints derived from regions extracted at earlier stages. Based on the above strategy, we firstly segment the body, pelvis, and femur regions, and then a novel hierarchical multi-atlas method is applied to segment the muscle tissue and 17 individual muscle regions.

Hierarchical multi-atlas segmentation: The multi-atlas method [4] assumes that multiple atlas datasets consisting of original CT images and their pre-segmented label images of target structures, which we call "target label images" hereafter, are prepared beforehand. Given an input CT image, intensity-based nonrigid registration is performed between the input CT image and that of each atlas dataset to estimate the deformation field, and then the corresponding target label image is deformed using the estimated deformation field to obtain a segmentation result. The different segmentation results for different atlases are fused by their weighted sum whose weights are based on similarity in registration. The fused segmentation result is thresholded to obtain a final segmentation result.

We apply the multi-atlas method hierarchically. Our hierarchical multi-atlas method assumes that the pre-segmented label images of reference structures, which we call "reference label images", are prepared in the atlas datasets in addition to the target label images. We also assume that the regions of the reference structures (which we call "reference regions") have already been segmented from an input CT image at the previous stage of segmentation processes. That is, the input dataset consists of the original CT image and its reference label image. Before the registration of original CT images, nonrigid registration of the reference label images between the input dataset and each atlas is performed to deform each original CT image of the atlas so that the reference structures are registered. This registration is quite stable because the segmented regions are used. It normalizes inter-subject variations of the reference structures, and thus subsequent intensity-based nonrigid registration for multi-atlas segmentation is stabilized because it only deals with remaining reduced variations mainly originated from the target structures. The segmented target structures are added to the reference label image at the next stage of segmentation processes. This procedure is iterated until the target structures at the final stage are segmented

Application to muscle segmentation: In order to apply the hierarchical multi-atlas method to muscle segmentation, we firstly segment the regions of the body, pelvis, and femur to use them as the initial reference label image (Fig. 1(a)) for the subsequent hierarchical multi-atlas segmentation. The body is segmented by a simple binarization using a fixed threshold value. The pelvis and femur are segmented using our previous method based on hierarchical statistical shape models [5].

Given the input dataset of an original CT image and its initial reference label image (body, pelvis, and femur), the hierarchical multi-atlas method is applied. At the first stage, the target structure is the muscle tissue (Fig. 1(b)), which is added to the reference structures of the second stage to segment out 17 individual muscles, which are the final target structures.

Results: 20 patient datasets used for the atlas datasets for muscle tissue segmentation at the first stage while one patient dataset for 17 individual muscle segmentation at the second stage. Because one-side of the hip was diseased in our datasets, there was considerable difference between left and right hemi-hips. 40 and two atlas datasets of the left and mirror-transformed right hemi-hips were used for the first and second stages, respectively.

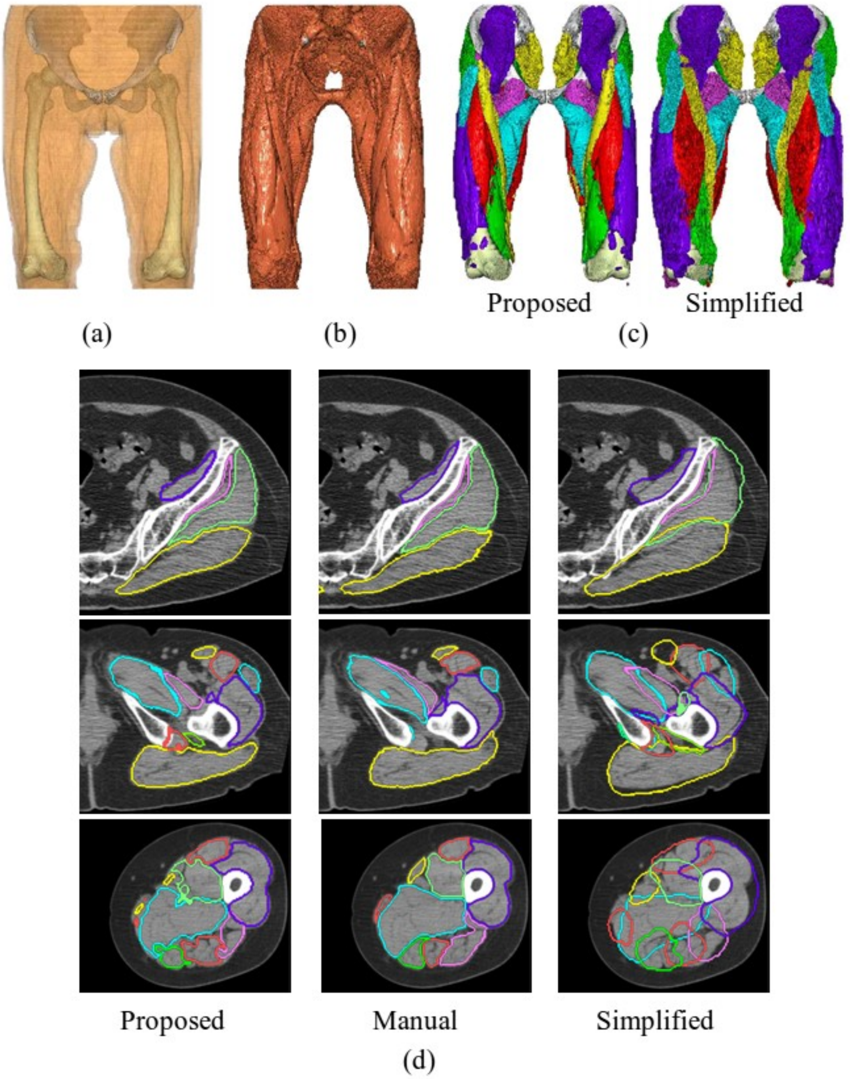

Figure 1 Typical case of muscle segmentation. (a) Body (skin), pelvis, and femur. (b) Muscle tissues. (c) 17 individual muscles. Left: Proposed method. Right: Simplified method. (d) Axial slices of segmentation results of individual muscles. Left: Proposed method. Middle: Manual traces. Right: Simplified method.

The evaluation was performed using the ground truth on three representative 2D axial slices of 10 CT datasets in a leave-one-out manner. We compared the proposed two-stage method with a simplified single-stage method without muscle tissue segmentation. These methods were fully-automated. Fig. 1(c) and (d) show typical results of individual muscle segmentation. The average absolute distance error of segmented 17 muscles was 3.1 mm for the proposed and 4.0 mm for the simplified methods, respectively. In 9 out of 17 muscles, the proposed method was significantly accurate ($p<0.01$) (no significance in 8 muscles). These results show that the hierarchy embedded in the proposed method was quite effective.

Discussion & Conclusion: We have described a method for muscle segmentation from CT data. By adding intermediate muscle tissue segmentation in the proposed hierarchical method, segmentation accuracy was significantly improved. This addition was also effective with respect to the amount of labor, which was much less in preparing the atlas datasets of muscle tissues for 20 cases than 17 individual muscles for only one case because the interactive graph-cut editing is possible in the former while full manual traces are inevitable in the latter. As future work, we will add another intermediate stage of segmenting a few individual muscles using 20 patient atlas datasets so as to improve the accuracy.

References

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