Muscle Boundary Estimation Using Interpolated Image Masks

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Introduction

The use of imaging data to compute muscle volumes is essential for studies of muscle atrophy. Hand digitization of muscle cross-sections is time-consuming, but the work associated with this can be reduced by measuring a subset of slices and using regression approaches to predict the total muscle volume. However, techniques such as diffusion-tensor MRI-based muscle fiber tracking (1) and the generation of anatomy-based musculoskeletal models (2) require knowledge of a muscle's boundaries in each imaging slice, not just total muscle volume. For these applications, it may be feasible to hand digitize the (x,y) coordinates of a muscle's boundaries in a subset of the slices and to interpolate those positions to predict the (x,y) coordinates of the muscle borders in the intervening slices. Thus the purposes of this study were: 1) to investigate the potential for polynomial fitting of uniformly sampled muscle boundary positions to predict the whole muscle's boundaries and 2) to investigate the sensitivity of the predictions to the number of slices sampled.

Methods

Data Acquisition Nine healthy adults (aged 23 ± 2 years; mean ± SD) participated in this study. A Philips 3T Intera Achieva MR Imager/Spectrometer was used, and a phased array torso coil and a pair of flexible 10×14 surface coils were placed around the distal right lower extremity. Proton density (PD) weighted images were obtained from the distal thigh to the ankle with slice thickness=6 mm, field of view=20×20 cm, and reconstructed matrix=512×512.

Image Analysis All analysis was performed in Matlab v2010a. To create a complete model, regions of interest (ROI's) defining the borders of the soleus and lateral and medial heads of the gastrocnemius were hand-digitized and then interpolated to 100 points (Figure 1). The points were ordered in clockwise order, with the most anterior point labeled as the first point in the ROI. Following this, the data from slices spaced at 10% and 20% distance increments between the first and last slice were sampled. A piecewise cubic hermite interpolating polynomial (pchip) was fitted to the x coordinate of point #1 in the sampled slices and used to interpolate the x coordinates in the intervening slices. This was repeated for each point in the ROI; the whole procedure was repeated for the y coordinates. Finally, image masks were created for each of the interpolated ROI's.

Data Analysis and Statistics To assess the goodness of the interpolated masks, the hand-digitized original mask was subtracted from the corresponding interpolated ROIs. The absolute differences in pixel count between the original and interpolated masks were calculated. Also, the root-mean square (*rms*) differences between the original (x, y) positions and the interpolated (x, y) positions were calculated. A 2-factor ANOVA (method×slice) was conducted to determine whether or not the *rms* differences were greater for the 20% sampling interval. Also, 2-factor ANOVA (method×slice) tests were conducted separately for each subject to check for significant differences between the (x, y) positions determined by the three methods.

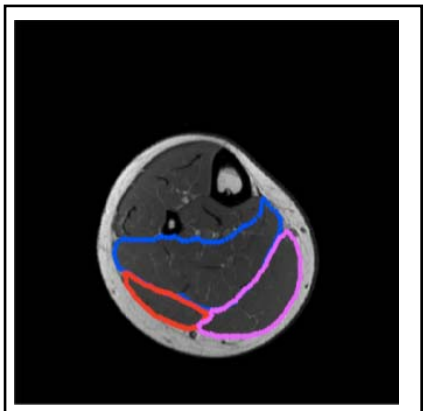

Figure 1. Sample image of the right leg with the muscles of interest outlined in blue (soleus), magenta (medial gastrocnemius), and red (lateral gastrocnemius).

Results and Discussion

Figure 2 shows sample data from the soleus muscle for the hand-digitized points and the pchip interpolation of the sampled points. The within-subject, 2-way ANOVA for differences between the x and y coordinates for the original model, 20% distribution and 10% distribution revealed no significant differences in the (x,y) positions of the 100 points defining the muscle border in any of the subjects. Figure 3 shows the *rms* error and absolute difference in mask size for each individual slice, averaged over all 9 subjects, for the 20% distance increment sampling condition. The largest *rms* errors occur 1) where the mask reaches its largest cross-sectional area and 2) at the superior extent of the muscle, where the cross-sectional area changes rapidly. The ANOVA conducted to compare the 20% sampling interval and the 10% sampling interval showed that there were no differences in either *rms* error or absolute difference in mask size between the two sampling methods.

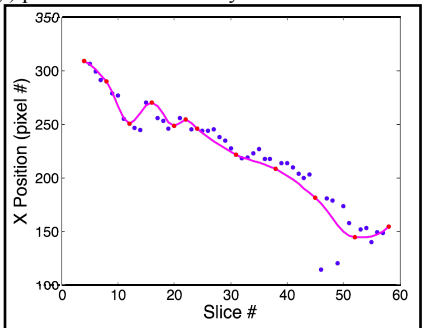

Figure 2. Graphical representation of the pchip function for point 25. Sampled points for curve fitting (red), hand defined points on intervening slices (blue) and line of best fit (magenta).

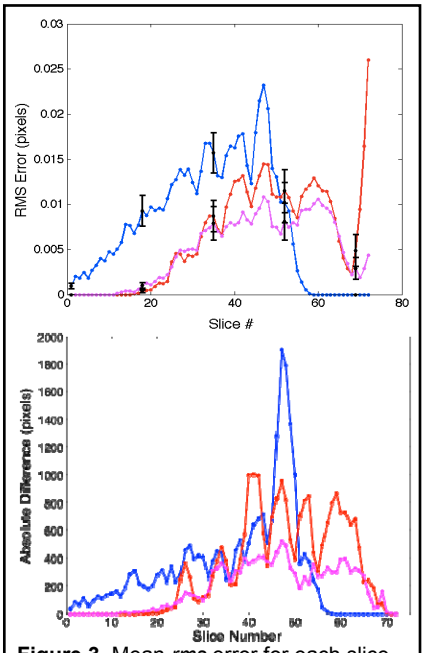

Figure 3. Mean *rms* error for each slice for 20% distribution (top panel) and mean absolute difference in mask size (bottom panel). For each analysis, n=9. Error bars indicate the SD. The color scheme corresponds to that for Figure 2.

Conclusions

Polynomial curve fitting and interpolation of muscle shape data can greatly decrease the amount of time required for determining muscle volumes from MRI data. This reduction does not introduce significant differences between the original data and the interpolated data. This is true for interpolations based on both the 10% and 20% distance increments.

References

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