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Evaluation of a morphing based method to estimate muscle attachment sites of the lower extremity

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ABSTRACT

To generate subject-specific musculoskeletal models for clinical use, the location of muscle attachment sites needs to be estimated with accurate, fast and preferably automated tools. For this purpose, an automatic method was used to estimate the muscle attachment sites of the lower extremity, based on the assumption of a relation between the bone geometry and the location of muscle attachment sites. The aim of this study was to evaluate the accuracy of this morphing based method. Two cadaver dissections were performed to measure the contours of 72 muscle attachment sites on the pelvis, femur, tibia and calcaneus. The geometry of the bones including the muscle attachment sites was morphed from one cadaver to the other and vice versa. For 69% of the muscle attachment sites, the mean distance between the measured and morphed muscle attachment sites was smaller than 15 mm. Furthermore, the muscle attachment sites that had relatively large distances had shown low sensitivity to these deviations. Therefore, this morphing based method is a promising tool for estimating subject-specific muscle attachment sites in the lower extremity in a fast and automated manner.

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1. Introduction

Musculoskeletal models are used to predict muscle and joint reaction forces in order to analyze complex biomechanical problems, such as the functional outcome after surgery (Delp et al., 1994; Piazza and Delp , 2001; Reinbolt et al., 2009). Furthermore, musculoskeletal models have been used to model the effects of a stroke (Higginson et al., 2006), spinal cord injuries (Paul et al., 2005; To et al., 2005) and sport injuries (McLean et al., 2003; Manal and Buchanan, 2005).

In general, musculoskeletal models are based on one or more cadaver studies to represent the anatomy of an average adult person (Delp et al., 1990; Klein Horsman et al., 2007). To represent different subjects, relatively simple geometrical scaling methods, based on the subject′s size and weight, are commonly used (Damsgaard et al., 2006; Delp et al., 2007). These methods may be sufficient when analyzing generic musculoskeletal problems without the need of detailed musculoskeletal models (Rasmussen et al., 2002). However, they do not incorporate the inter-individual differences present in musculoskeletal anatomy (White et al., 1989; Duda et al., 1996), which may, amongst other parameters, influence model force predictions at the subject-specific level. In addition, geometrical scaling methods rely on the identification of bony landmarks to estimate the subject′s segment lengths. It is known that there is an uncertainty in locating these landmarks (Brand et al., 1982; White et al., 1989), leading to errors in the scaling procedure. These potential errors and assumptions may result in inaccurate and unreliable model force predictions.

When exploring complex biomechanical problems, such as representing pathologies in the musculoskeletal anatomy, subject-specific models are expected to be more suitable than generally scaled models (van der Krogt et al., 2008; Lenaerts et al., 2009; Scheys et al., 2009). Several recent studies have indeed focused on developing such subject-specific models based on imaging or functional measurements (Blemker et al., 2007; Scheys et al., 2011; Hainisch et al., 2012; Hausselle et al., 2012). To generate subject-specific musculoskeletal models, inter-individual anatomical variations should be estimated accurately. Small differences in muscle attachment sites, which may considerably affect muscle moment-arms, have been shown to often affect muscle force predictions to a great extent (Carbone et al., 2012).

To use subject-specific musculoskeletal models in a clinical setting, methods used to individualize the model need to be

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accurate, fast and preferably automated. A semi-automatic method, based on a magnetic resonance (MR) atlas, was introduced by Scheys et al. (2009) to determine subject-specific muscle attachment sites from muscle paths. However, this method showed limited accuracy, since only 31% of the attachment sites were in the correct position. The remaining attachment sites had to be corrected manually. Kaptein and van der Helm (2004) applied a combination of a rigid transformation and local deformations to different cadaveric bone models of the shoulder joint, so that their surfaces would be morphed on top of each other. Using these techniques, 45% of the muscle attachment contours were predicted with high accuracy. They concluded that most muscle attachment contours in the shoulder can be predicted using only the geometry of the bone, but also that their results were influenced by measurement errors and possible inter-individual differences.

The purpose of this study was to evaluate the accuracy of estimating muscle attachment sites of the lower extremity by applying morphing techniques on the meshes of segmented bones, under the assumption of a direct relationship between the bone geometry and the location of muscle attachment sites. We used advanced morphing techniques to deform bone geometries including the muscle attachment sites of the lower extremity from one cadaver to the other and vice versa. After morphing, we compared the morphed muscle attachment sites with the actual measured attachment sites.

2. Methods

The method section is divided in four major sections; data collection, registration, data evaluation and morphing, which represents the workflow of the study (Fig. 1). For each section, the applied method will be explained and the possible errors (i.e. measurement errors, registration errors, fitting errors and morphing errors) will be calculated.

2.1. Data collection

Two fresh, randomly selected cadavers identified as C1 and C2 (C1: 80 year old male and C2: 85 year old male) with no clear pathologies affecting the musculoskeletal system were used. The leg length, measured from the anterior superior iliac spine (ASIS) to the medial malleolus, was 913 mm and 801 mm for C1 and C2 respectively. CT scans of the lower extremity of the two cadavers were made at the department of Radiology of the University Medical Centre Nijmegen (UMCN) using a Siemens Somatom Sensation 64 CT scanner. The resulting CT images consisted of about 1900 slices for C1 and 2600 slices for C2 with a resolution of 512 × 512 pixels. The dimension of one voxel was $0.828 \times 0.828 \times 0.600\ \text{mm}^3$ for C1 and $0.977 \times 0.977 \times 0.750\ \text{mm}^3$ for C2. The CT images were used to segment the bones of the lower extremity (pelvis, femur, patella, tibia, fibula and calcaneus) into STL-files using Mimics 15.01 software and remeshed to obtain a higher resolution in regions with a high curvature.

A complete dissection of the two lower extremity specimens was performed at the Anatomy department of the UMCN. The order of dissection was defined by a detailed dissection protocol. First, skin and fat were removed. Subsequently, reference frames with retro-reflective markers were attached to the pelvis, femur, tibia, calcaneus and patella. The Brainlab Kolibri™ image-guided surgery platform was used to measure 3-D points with respect to the corresponding reference frame fixed in the bones. The 3-D navigation system had a spatial accuracy of 0.231 ± 0.137 mm (RMS ± SD) and an average orientation error of 0.383° (Wiles et al., 2004). During the dissection, the leg could be moved freely due to the use of local reference frames fixed to the bone segment, facilitating measurements of muscle attachment sites. During the dissection, the contours of 72 muscle attachment sites were measured. Each muscle was identified with the help of two anatomical textbooks (Sobotta, 2006; Agur and Dalley, 2008) and experts opinion. Each muscle was dissected and its origin and insertion were measured. The number of points measured to define each muscle attachment site depended on its shape and size. In total, 1440 muscle attachment points were measured for C1 and 1539 muscle attachment points for C2. After all muscles had been removed, for each bone at least 100 additional registration points were collected from the surface of the bone.

2.2. Registration

To register the cadaver measurements to the segmented STL files, previously obtained from the CT scans, the iterative closest point (ICP) method (Besl and Mckay, 1992) was used to minimize the sum of the squared errors (SSE) between the registration points and the closest points on the faces of the STL:

$$SSE = \sum_{i=1}^{n} (y_i - \hat{y}_i)^2 \qquad (1)$$

where y_i represents the registration points, $\hat{y}_i$ represent the closest point on the face of the STL to y_i, and n represents the number of registration points. To improve results, 5% of the worst registration points were rejected after the first 50 iterations. After registration, the measured muscle attachment points were projected to the closest point on the face of the STL.

2.3. Data evaluation

The measured muscle attachment sites for both cadavers were divided into three types: a point, line and area attachment site with an equal and sufficient number of muscle elements according to the TLEM dataset of Klein Horsman et al. (2007).

- Point attachment sites (*P*) were described as the mean of the measured muscle attachment points, P_{C1} (Fig. 2A).
- Line attachment sites (*L*) were described by *e* equidistant points, $L_{C1,1} \ldots L_{C1,e}$, (e=2,3,4 or 6), on a polynomial curve, l_{C1}, with order 1,2 or 3, that fitted the measured muscle attachment points, based on the method proposed by Van der Helm and Veenbaas (1991) (Fig. 2B).
- For area attachment sites (*A*), a planar surface was fitted through the measured muscle attachment points by orthogonal regression using the principal component analysis (PCA) method (Joliffe and Morgan, 1992) (Fig. 2C). The measured muscle attachment sites were projected to the fitted plane. Then, a surface area was interpolated through the projected points using a method based on Delaunay triangulation and rotated to its principal axis (Berg, 2008). Finally, the area attachment sites were calculated as the centroid of 6 equi-areal parts, called $A_{C1,1} \ldots A_{C1,6}$, based on the method of Van der Helm et al. (1992), and projected back to surface of the STL (Fig. 2C).

Afterwards, all the calculated muscle attachment elements were projected to the closest node point of the STL. The same methods were applied for the measured muscle attachment sites of C2.

2.4. Morphing

An advanced method, based on Redert et al. (1999), was developed and used by Materialise N.V. for morphing the bone geometries of the lower extremity of one cadaver to another and vice versa. The accuracy of the morphing was determined by calculating the distance between the vertex of the morphed and the corresponding point on the surface of the originally segmented mesh. To obtain an indication of the mesh correspondence the vertex to vertex distance for all muscle attachment sites was calculated after morphing the segments of C2 to C1 and back to C2. The morphing errors were acceptable if the maximal vertex to vertex distance of the mesh correspondence was smaller than 10 mm given by the sensitivity study of Carbone et al. (2012).

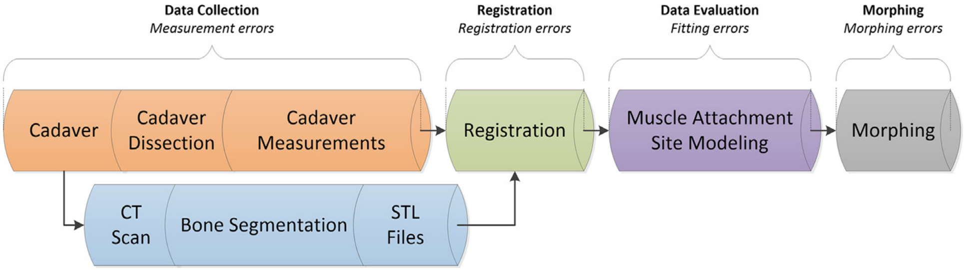

Fig. 1. Overview of the different method sections with additional sources of error representing the workflow of the study.

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