FISEVIER

Contents lists available at ScienceDirect

# **Journal of Biomechanics**

journal homepage: www.elsevier.com/locate/jbiomech www.JBiomech.com



Short communication

# Non-linear scaling of a musculoskeletal model of the lower limb using statistical shape models



Daniel Nolte\*, Chui Kit Tsang, Kai Yu Zhang, Ziyun Ding, Angela E. Kedgley, Anthony M.J. Bull

Department of Bioengineering, Imperial College London, London SW7 2AZ, United Kingdom

#### ARTICLE INFO

Article history:
Accepted 7 September 2016

Keywords: Lower extremity Musculoskeletal model Scaling methods Subject-specific modelling Statistical shape modelling

#### ABSTRACT

Accurate muscle geometry for musculoskeletal models is important to enable accurate subject-specific simulations. Commonly, linear scaling is used to obtain individualised muscle geometry. More advanced methods include non-linear scaling using segmented bone surfaces and manual or semi-automatic digitisation of muscle paths from medical images. In this study, a new scaling method combining nonlinear scaling with reconstructions of bone surfaces using statistical shape modelling is presented. Statistical Shape Models (SSMs) of femur and tibia/fibula were used to reconstruct bone surfaces of nine subjects. Reference models were created by morphing manually digitised muscle paths to mean shapes of the SSMs using non-linear transformations and inter-subject variability was calculated. Subjectspecific models of muscle attachment and via points were created from three reference models. The accuracy was evaluated by calculating the differences between the scaled and manually digitised models. The points defining the muscle paths showed large inter-subject variability at the thigh and shank – up to 26 mm; this was found to limit the accuracy of all studied scaling methods. Errors for the subject-specific muscle point reconstructions of the thigh could be decreased by 9% to 20% by using the non-linear scaling compared to a typical linear scaling method. We conclude that the proposed non-linear scaling method is more accurate than linear scaling methods. Thus, when combined with the ability to reconstruct bone surfaces from incomplete or scattered geometry data using statistical shape models our proposed method is an alternative to linear scaling methods.

© 2016 The Author. Published by Elsevier Ltd. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

#### 1. Introduction

Knowledge of the distribution and magnitude of forces in the musculoskeletal system relies on accurate quantification of muscle forces. This knowledge can be used to investigate all mechanically-mediated conditions and interventions in the musculoskeletal system, including, osteoarthritis, implants, fracture fixation devices, rehabilitation and athletic performance. Several methods to create subject-specific models of muscle geometries of the lower limb have been published. The methods include linear scaling (Cleather and Bull, 2010; Correa and Pandy, 2011; Lund et al., 2015; Sommer et al., 1982), non-linear scaling based on bone geometries (Kaptein and van der Helm, 2004; Pellikaan et al., 2014) and semi-automatic (Scheys et al., 2005) and manual digitisation (Correa et al., 2011; Ding et al., 2016) of medical images. Kaptein and van der

E-mail addresses: d.nolte@imperial.ac.uk, daniel\_nolte@gmx.de (D. Nolte), chui.k.tsang@gmail.com (C.K. Tsang), zhangkaiyu@gmail.com (K.Y. Zhang), z.ding@imperial.ac.uk (Z. Ding), akedgley@imperial.ac.uk (A.E. Kedgley), a.bull@imperial.ac.uk (A.M.J. Bull).

Helm (2004) found that more than 50% of the scapula muscle paths could be reconstructed with high accuracy using a non-linear scaling method. Pellikaan et al. (2014) found that a non-linear morphing algorithm based on digitised bone geometries was able to morph muscle attachment sites between digitised scans of two cadavers with average errors smaller than 15 mm for almost 70% of the muscle attachment points. A common limitation of non-linear scaling methods is the need for either segmented bone surfaces or medical images of the entire limb. This limits the applicability of these methods for musculoskeletal analysis when image data are not available.

Statistical shape models (SSMs) allow accurate reconstruction of geometries from sparse data obtained with basic clinical imaging techniques. These include reconstruction of a 3D shape from a single X-ray (Zheng and Nolte, 2006) or stereo X-ray (Baka et al., 2011) as well as the prediction of a healthy from a pathological shape from 3D scans of joint regions (Rajamani et al., 2004, 2005). Linking together bone morphing using reconstructions and geometrical models of muscle paths has not been attempted previously.

<sup>\*</sup> Corresponding author.

Nomenclature			Male reference subject
		MS	Small male subject
FFD	Free Form Deformation	MT, MT2	2 Tall male subjects
FM	Medium female subject	OI	Origin and insertion
FS	Small female subject	PMV	Principal mode of variation
FT	Tall female subject	RSME	Root Mean Square Error
IRTK	Image Registration Toolkit	SD	Standard Deviation
ISB	International Society of Biomechanics	SSM	Statistical Shape Model
MM, MM2 Medium male subjects			Statistical Shape Modelling Research Toolkit
MR	Magnetic Resonance		
MR	Magnetic Resonance		

In this study, the accuracy of a non-linear scaling method using bone morphing between shapes of nine different subjects reconstructed using a statistical shape modelling toolkit was investigated. Results of muscle paths and landmarks were compared to linearly scaled models using two methods: a landmark-based scaling method, to represent approaches used in the literature, and an affine scaling method minimising the distance between two bone surfaces, to estimate the lower bound for errors that are obtained from an arbitrary linear scaling law. The hypothesis of the study was that non-linearly scaled models created using statistical shape modelling significantly decrease the error between reconstruction and manual digitisation compared to linearly scaled models.

#### 2. Material and methods

#### 2.1. Subjects

The study was approved by the Imperial College Research Ethics Committee and all subjects provided written informed consent. Magnetic Resonance (MR) imaging scans using a 3.0 T MR scanner (MAGNETROM Verio, Siemens, Germany) with a slice thickness of 1 mm and an in-plane resolution of 1.406 mm  $\times$  1.406 mm were obtained of 35 subjects. Additionally, lower limb Computed Tomography scans of eight subjects were used for bone surface segmentations. Bone surfaces of the femur and tibia/fibula were segmented of all subjects using a semi-automatic procedure. For nine of the MR scanned subjects (Table 1) paths of 38 muscles and the patellar ligament were digitised with 163 polygonal line elements in total with origin/insertion and via points following the topology described in Klein Horsman et al. (2007). Further, tibiofemoral contact points, joint centres of rotation and bony landmarks used to create local reference frames of the segments (Table 2), following the ISB recommendations (Wu et al., 2002), were digitised. The digitisations and segmentations were performed using Mimics (Mimics 17.0, Materialise, Belgium) by one imaging expert.

#### 2.2. SSMs and bone surface reconstructions

SSMs of femur and tibia/fibula were constructed from 68 bone geometries of the right and mirrored left leg of the 34 subjects not used to digitise muscle geometries. The SSMs were created using a construction pipeline which aligns and registers surfaces using rigid-body transformations and calculates modes of variation using principle component analysis (described in Zhang et al., 2012). The morphological variation of femur and tibia were well represented, as illustrated by the high power of the models: 95% of the population was represented with four and eight principal modes of variation (PMVs) for femur and tibia/fibula, respectively; 98.5% was represented by 16 and 27 PMVs.

For each of the other nine subjects, the femur and tibia/fibula bones were reconstructed from random point sets containing 1000 points, which is less than 10% of the number of points representing the SSM mean shapes. Further, subsets containing only points from the proximal and distal 20% of the bones for a comparison to reconstructions from incomplete medical images were created. For registration, sets of corresponding landmarks were digitised on mean shapes and subject bones. The random points were registered to the mean shape of the SSM using a sequence of landmark-based and surface-based rigid body transformations using the Image Registration Toolkit (IRTK) (Rueckert et al., 1999; Schnabel et al., 2001) with manual corrections when necessary to reduce errors (see Supplementary Material). For the reconstruction, a morphing algorithm adding weighted PMVs to the mean shape of an SSM to minimise the Mahalanobis distance to a point cloud was used (Rajamani et al., 2005; Yang et al., 2008). Non-linear B-spline Free-Form Deformations (FFDs) with a node spacing of 20 mm using the IRTK for the mappings between mean shapes and

**Table 1**Detailed information of nine subjects used for manual digitisations of muscle geometries. Subject labels describe the gender (M/F) and an attribute (S: small, M: medium, T: tall, ref: reference).

Subject	Gender	Height (cm)	Mass (kg)	Femur length (mm)	Tibia/ Fibula length (mm)	Pelvis width (mm)	Age (years)
MT2	Male	183	96	428.3	441.6	227.9	42
MS	Male	168	64	377.1	384.6	229.4	21
FM	Female	168	70	418.2	414.6	220.8	45
FS	Female	155	45	345.9	366.2	230.8	27
MT	Male	192	85	460.9	465.8	245.0	27
Mref	Male	172	70	407.4	410.4	235.4	35
FT	Female	184	78	446.5	455.4	246.9	43
MM	Male	180	70	418.4	425.5	218.6	25
MM2	Male	175	76	443.7	450.7	219.5	25

**Table 2**List of landmarks digitised on the bone geometry with descriptions of their location

Pelvis	RASIS/LASIS RPSIS/LPSIS	Right/left anterior superior iliac spine Right/left posterior superior iliac spine
Thigh	RLFE/LLFE RMFE/LMFE	Right/left lateral femoral epicondyle Right/left medial femoral epicondyle
Shank	RMM/LMM RLM/LLM	Right/left medial malleolus Right/left lateral malleolus
Foot	RFCC/LFCC RMF2/LFM2 RFMT/LFMT	Right/left calcaneus (heel) Right/left head of second metatarsal Right/left tuberosity of fifth metatarsal

reconstructed surfaces were calculated. All algorithms for creating and morphing SSMs together with the SSM are available as Statistical Shape Modelling Research Toolkit (SSMRT) at <a href="http://www.msksoftware.org.uk">http://www.msksoftware.org.uk</a>. The reconstruction quality of the bones was evaluated by calculating the RMSE between the manually segmented and the reconstructed bone surfaces using Geomagic Studio 12 (Geomagic, Inc., USA).

### 2.3. Reference and subject-specific muscle models

To create reference muscle paths from all nine subjects, FFDs from subject to mean shape were applied to the muscle paths and landmarks. For comparison, muscle paths, bone surfaces and landmarks were scaled to the mean surfaces of the SSM using a two-parameter linear and an affine scaling method. The linear scaling method used segment lengths and pelvis width as scaling factors (Table 3). The affine scaling method minimised the least-squares distance between two surfaces using an affine transformation. Since this method used information of the complete bone surface, it is considered as a lower bound for the error of linear scaling methods using bony landmarks or other bone dimensions. The accuracy of the transformations was evaluated by calculating the root mean square error (RMSE) between mean shapes and the transformed subject. The variances of muscle geometries were calculated using the FFD transformed geometries of all subjects transformed to the mean shapes.

Subject-specific landmarks and muscle paths, origin and insertion points were reconstructed from reference models of three different subjects chosen to represent the breadth of morphological differences of the population: a male subject

## Download English Version:

# https://daneshyari.com/en/article/5032574

Download Persian Version:

https://daneshyari.com/article/5032574

<u>Daneshyari.com</u>