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Lower limb estimation from sparse landmarks using an articulated shape model

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ABSTRACT

Rapid generation of lower limb musculoskeletal models is essential for clinically applicable patient-specific gait modeling. Estimation of muscle and joint contact forces requires accurate representation of bone geometry and pose, as well as their muscle attachment sites, which define muscle moment arms. Motion-capture is a routine part of gait assessment but contains relatively sparse geometric information. Standard methods for creating customized models from motion-capture data scale a reference model without considering natural shape variations. We present an articulated statistical shape model of the left lower limb with embedded anatomical landmarks and muscle attachment regions. This model is used in an automatic workflow, implemented in an easy-to-use software application, that robustly and accurately estimates realistic lower limb bone geometry, pose, and muscle attachment regions from seven commonly used motion-capture landmarks. Estimated bone models were validated on noise-free marker positions to have a lower ($p=0.001$) surface-to-surface root-mean-squared error of 4.28 mm, compared to 5.22 mm using standard isotropic scaling. Errors at a variety of anatomical landmarks were also lower (8.6 mm versus 10.8 mm, $p=0.001$). We improve upon standard lower limb model scaling methods with shape model-constrained realistic bone geometries, regional muscle attachment sites, and higher accuracy.

1. Introduction

Musculoskeletal modeling is required to estimate muscle and joint function, often with a long-term goal of understanding the form-function relationship of the musculoskeletal system (Erdemir et al., 2007). The clinical impact of musculoskeletal models is currently limited, due to the difficulty in generating patient-specific parameters, such as bone and joint geometry. The predicted muscle and joint contact forces are dependent on the accurate estimation of bone geometry and subsequent paths and lines-of-action of muscle-tendon units (Gerus et al., 2013). Estimating bone shape and pose from motion-capture landmarks is an essential part of patient-specific biomechanical simulation.

Simple length scaling of template models to landmarks cannot account for variations in bone shape (Blemker et al., 2007). Musculoskeletal software, such as OpenSim (Delp et al., 2007), typically scale a generic model (e.g. Delp et al., 1990) linearly and often isotropically according to experimental markers or anthropometric measurements. In the Anybody software (Aalborg, Denmark) the anatomy from a single cadaveric specimen (Horsman et al., 2007) is scaled nonlinearly using radial basis functions (Lund et al., 2015; Marra et al., 2015). Other non-linear scaling methods, such as host-mesh fitting (Fernandez et al., 2004), and the elastic registration method of Redert et al. (1999) applied to muscle morphing (Pellikaan et al., 2014) deform a template model to match experimental data. While providing additional degrees of freedom for shape morphing, these methods do not guarantee an anatomically realistic shape and often require extra smoothing constraints, which are chosen arbitrarily.

Statistical shape models are efficient and accurate in capturing realistic variations in anatomy (Allen et al., 2003; Bryan et al., 2009; Styner et al., 2003). In a typical shape model based on

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principal component analysis, realistic shapes can be generated as linear combinations of principal components. In musculoskeletal model generation, non-rigid registration using statistical shape models so far have been restricted to one or two bones. Kainmueller et al. (2009) presented a shape model of the hip joint for estimating full pelvis and femur geometry from limited field-of-view images. Yang et al. (2008) presented a shape model of the scapula and humerus, showing the correlation in shape between the two bones. The shape of the knee joint, in terms of the distal femur, patella, and proximal tibia, have been modelled by Fripp et al. (2007) and Rao et al. (2013), demonstrating the ability to model the shape variations of multiple articulated bodies. However, to the best of the authors' knowledge, shape modeling has not been used to customize a lower limb musculoskeletal model from motion-capture landmarks.

We present an articulated shape model of the left lower limb, including the pelvis, femur, patella, tibia and fibula, with embedded muscle attachment regions. We use this articulated shape model to estimate bone geometry, pose, and muscle attachment locations from a sparse set of 7 common motion-capture landmarks. The output is a unified set of geometries that can be used for both rigid-body and continuum musculoskeletal analysis modelling. The method is validated using clinical computed tomography (CT) data to show improved accuracy compared to the standard isotropic linear scaling method.

2. Methods

The lower limb anatomy model is composed of a statistical shape model, model articulation, and embedded muscle attachment sites. A shape and pose optimization process fits the model to patient specific bony landmarks. We validate the accuracy of the optimization in a leave-one-out experiment and compare the results to conventional isotropic scaling.

2.1. Statistical shape model

A combined statistical shape model of the pelvis, femur, patella, tibia, and fibula was created from a training set of 26 left lower limb bones manually segmented from post-mortem, de-identified CT images collected from the Victorian Institute of Forensic Medicine (Melbourne, Australia) with ethical approval (applications EC9/2007 and EC10/2007). The image set did not include the full foot in most subjects, and so the foot was omitted from our model. The training set was composed of 14 males and 12 females, with age ranging from 15 to 92 years old, height from 154 cm to 174 cm, and weight from 39 kg to 105 kg.

For each bone, a manually designed piece-wise parametric reference mesh was fitted to each of the 26 segmented surfaces (Fig. 1a). The fitting procedure (Zhang et al., 2014a) was compose of a rigid-body iterative-closest point registration, a shape-model fit optimizing rigid-body and principal-component shape transformations, and finally a local fit optimizing the coordinates of each mesh control point individually. Each step minimized the least-squares distance between each segmented data point and its closest point on the mesh surface. The fitting procedure ensured correspondent surface topologies across the training set, which was necessary for creating a statistical shape model. For each bone, all 26 fitted meshes were aligned to a target bone (one of the 26) using rigid-body iterative closest point registration (Besl et al., 1992), i.e. all pelvis meshes were aligned to a target pelvis mesh, all femur meshes were aligned to a target femur mesh, and so on. The target mesh for each bone came from an individual of average stature picked from the training set. The relative position between the bone meshes of a subject was not preserved during alignment and in the shape model. This was intentional since relative position and pose was handled separately by joint articulation independent of shape variations.

A single principal component analysis (PCA) was performed on the control point coordinates of all aligned meshes of all bones to produce a statistical shape model of the whole lower limb. The control point coordinates of all the aligned bone meshes of an individual i were concatenated into a vector $\boldsymbol{x}_i = [\boldsymbol{x}_i^{pelvis}, \boldsymbol{x}_i^{femur}, \boldsymbol{x}_i^{patella}, \boldsymbol{x}_i^{tibiafibula}]$, such that $\boldsymbol{X} = [\boldsymbol{x}_1, \boldsymbol{x}_2, \ldots, \boldsymbol{x}_{26}]^{\mathrm{T}}$ was the PCA data matrix. The PCA resulted in a set of mean mesh control point coordinates (for the mean meshes of each bone) and principal components of their variation (principal components of bone mesh shape and size variation).

2.2. Model articulation

Standard anatomical landmarks were embedded in each bone's mesh as fixed points in mesh parametric coordinates. Each landmark was defined by its mesh patch number and the 2-D patch coordinates within that patch. This meant that a landmark's 3-D position could be evaluated on a subject's mesh or shape model-generated mesh automatically by evaluating the 3-D coordinates of the landmark's parametric coordinates. Using the anatomical landmarks, segmental (Fig. 1c) and joint (Fig. 1d) coordinate systems described in Cappozzo et al. (1995) were established on all bones to define articulation. When the shapes of the bones were updated by the shape model, segmental and joint coordinate systems were recalculated on the new bone meshes, then the bone meshes were placed relative to each other according to their joint angles based on the updated joint coordinate systems.

The pelvis had three translational and three rotational degrees of freedom about its anatomical coordinate system origin (mid-point of the ASISs). The hip joint was a ball-and-socket joint with 3 degrees of rotational freedom at the center of a sphere fitted to the acetabulum regions of the pelvis mesh. The center of the femoral head (center of a sphere fitted to the femoral head region of the femur mesh) was locked to the hip joint center. The knee joint had two degrees of rotational freedom (flexion and abduction). After knee joint rotation, the tibia was translated along the longitudinal tibial Y (axial) axis to maintain a distance of 5mm between the closest pair of points between the tibia

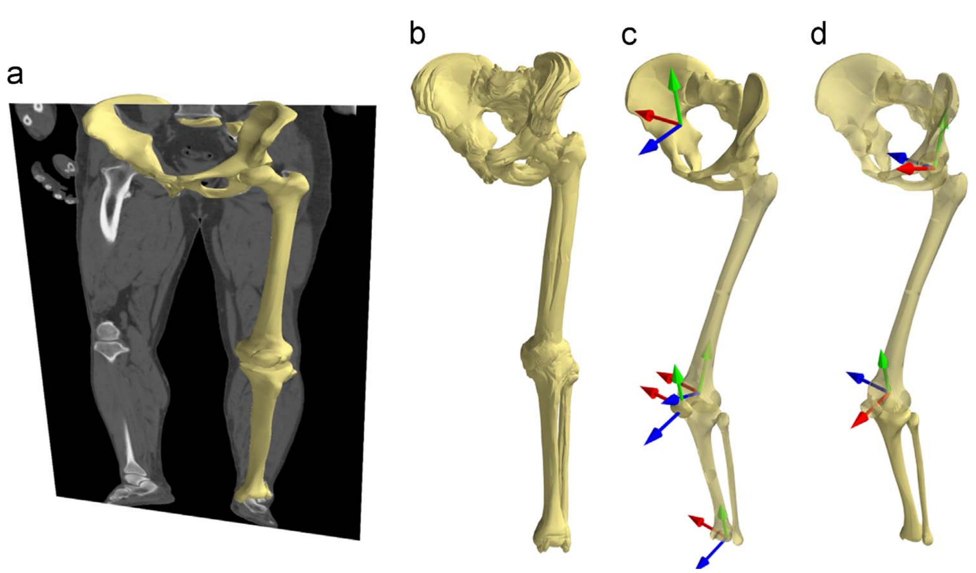

Fig. 1. Constructing the articulated shape model. Twenty-six sets of bones were segmented from CT images, meshed (a), aligned (b), and decomposed using principal component analysis. Using mesh-embedded anatomical landmarks, segmental (c) and joint (d) coordinate systems were established on each bone to allow articulation defined by joint angles.

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