



Automatic reconstruction of the muscle architecture from the superficial layer fibres data



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ABSTRACT

Background and objective: Physiological cross-sectional area (PCSA) of a muscle plays a significant role in determining the force contribution of muscle fascicles to skeletal movement. This parameter is typically calculated from the lengths of muscle fibres selectively sampled from the superficial layer of the muscle. However, recent studies have found that the length of fibres in the superficial layer often differs significantly ($p < 0.5$) from the length of fibres in the deep layer. As a result, PCSA estimation is inaccurate. In this paper, we propose a method to automatically reconstruct fibres in the whole volume of a muscle from those selectively sampled on the superficial layer.

Methods: The method performs a centripetal Catmull–Rom interpolation of the input fibres within the volume of a muscle represented by its 3D surface model, automatically distributing the fibres among multiple heads of the muscle and shortening the deep fibres to support large attachment areas with extremely acute angles.

Results: Our C++ implementation runs in a couple of seconds on commodity hardware providing realistic results for both artificial and real data sets we tested.

Conclusions: The fibres produced by the method can be used directly to determine the personalised mechanical muscle functioning. Our implementation is publicly available for the researchers at <https://mi.kiv.zcu.cz/>.

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1. Introduction

Musculoskeletal modelling plays an essential role in the medicine of 21st century because it allows to assess, for each individual, functioning of their muscles in the simulated environment, e.g., during walking, step climbing, and other motion activities, and thus maximize the effectiveness of the prevention, diagnosis, and treatment of diseases of the musculoskeletal system and connective tissue (Chapter XII in ICD-10), such as osteoporosis or neuromuscular disorders. Muscle moment arms during skeletal motion are the most prominent determinants of the muscles functioning. For their calculation, both physiological and mechanical parameters of each muscle are required, among which the most important are: muscle fibre length, pennation angle (PA), which is usually measured as the acute angle between the muscle fibre and its attachment site on bone, tendon or aponeurosis, and muscle volume [1].

Most models assume a uniform distribution of fibres length and PA within the muscle [2,3], taking their mean values, which are re-

ported in the literature, to represent the whole muscle despite the fact that it has been repeatedly shown [1,3–5] that non-uniformity occur in the architecture of many muscles and this approach may lead to muscle moments errors up to 75% in complex muscles such as gluteus medius [6]. Unfortunately, muscle fibre architecture can be accurately measured only through dissection, as described, e.g., in [7], which is not an option for creating subject-specific models of living subjects [2]. Common practice, therefore, is to extract the architectural information from a single ultrasound image, e.g., [8], or video sequence of ultrasound images, e.g., [9], which may lead to errors up to 23% due to obvious limitation of ultrasound technology to assess volumetric geometry [7].

In this paper, we propose an automatic method to reconstruct the shape of fibres in the entire volume of a muscle from the shapes of fibres defined on the superficial layer of the muscle. We represent the muscle by a triangular surface model which can be easily extracted from the segmented medical images of the subject. Note that, in the context of subject-specific musculoskeletal modelling, such images are typically already available because they are for an instance used to calculate the muscle volume [10,11]. It is sufficient to specify just the principal fibres, with the minimum

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of two, thus the effort is minimal, even if their specification requires user interventions. Both the subject-specific data from an ultrasound-based method or cadaver data, e.g., publicly available on the Internet, can be used. The proposed method interpolates the specified fibres using centripetal Catmull–Rom splines to guarantee realistic shapes, providing the user with an arbitrary number of smooth fibres in the volume of a muscle at near-iterative processing times, correctly handling even muscles with multiple heads. As far as we know, this is the very first method of such capabilities.

The remainder of this paper is structured as follows. In the next section, we give the overview of the related work. This is followed by a detailed description of our method. Section 4 presents the experiments that were performed. Discussion of the achieved results is given in Section 5 and Section 6 concludes the paper and provides an overview of possible future work.

2. Related work

Blemker & Delp in [12,13] proposed using an artificial yet anatomically correct fibre templates derived from the observation of fibres arrangement in muscles during dissection. Each template is a unit cube in which the fibres are represented by a set of interpolated rational Bézier spline curves connecting two attachment sites that are defined on the cube boundary. The authors use a proprietary mapping method available in the commercial TrueGRID (XYZ Scientific Applications) software¹ to semi-automatically map the fibre template, chosen to be appropriate for the muscle being modelled, into a subject-specific 3D hexahedral mesh of the muscle.

Kohout & Kukačka in [14] describe a fully automatic method for mapping the Blemker & Delp's fibre template into the interior of a muscle, which is represented by a subject-specific triangular surface mesh, based on a successive non-rigid transformation of planar slices of the template into curved slices of the muscle, whose shapes are determined from a harmonic scalar field computed on the surface of muscle. The transformation exploits mean value coordinates [15]. The method produces muscle fibres of an arbitrary number in a fraction of a second.

Neither approach supports muscles with multiple heads. In order to process such a muscle, each of its heads must be modelled independently, e.g., as it was done for muscles in the shoulder in [16]. Unfortunately, this is not always possible. Our method, proposed in this paper, on the other hand, can handle these muscles correctly.

Recently, Sánchez et al. [2] demonstrated that such simplified templates might not well represent muscle architecture. The authors, therefore, proposed a different approach. Starting with muscle fibres, represented by polylines, created by a digitization of fibres collected during a dissection of a human cadaver throughout the entire muscle, they construct automatically a tight fitting surface mesh to encapsulate them, using the method described in [3], and then perform a successive non-rigid transformation of volumetric space defined by this surface mesh into the volume of a subject-specific muscle represented by surface mesh. The transformation is based on mechanical deformation energy minimization problem.

Again, muscles with multiple heads are not supported. Furthermore, the availability of the input data, i.e., digitized fibres throughout the entire muscle, is rather limited. Our method needs just a few fibres on the superficial layer of the muscle.

A completely different approach is described in [17]. Muscle fibres are considered to be streamlines resulting from the vector

field computed from muscle diffusion tensor imaging (DTI) data of a subject. We note that DTI is a magnetic resonance imaging method commonly used in neuroscience to study white matter of brain. For muscles, unfortunately, DTI produces data containing lot of noise that must be removed, or at least significantly diminished, prior to the computation of muscle vector field. For this purpose, the authors propose two similar methods based on the assumption that the resulting vector field is smooth, which is, however, an assumption invalid for many muscles, as the authors themselves admit. Many authors, e.g., [2,3], therefore, question the practical use of this approach.

3. Methods

As input, we take a triangular surface model of a muscle, a set Φ_0^c of n control fibres $F_{1,0}^c, F_{2,0}^c, \dots, F_{n,0}^c$ lying on the surface of this muscle, i.e., these are principal fibres from the superficial layer, and, optionally, triangular surface models of attachment sites. For almost flat muscle surface, only two control fibres must be specified, one at each side of the flat area, otherwise more. If the muscle is composed of multiple heads, at least one control fibre must be specified per a head. Control fibres must be ordered so that fibre $F_{j,0}^c$ is adjacent to fibres $F_{j-1,0}^c$ and $F_{j+1,0}^c$, and must be represented by polylines of the same number of segments, m , and of the consistent direction (e.g., from the origin to insertion).

Due to an obvious effort associated with measurement of real fibres, the number of control fibres (n), which are specified in practice, according to our experience, is rarely larger than six. Such a number is often not sufficient to represent the superficial layer of a muscle realistically and, therefore, the method starts with a cubic spline interpolation of the control fibres ($F_{j,0}^c$) in order to get a set Φ_0 of superficial fibres $F_{1,0} \equiv F_{1,0}^c, F_{2,0}, \dots, F_{s+1,0}, F_{s+2,0} \equiv F_{2,0}^c, \dots, F_{n+(n-1)*s,0} \equiv F_{n,0}^c$, where $s \in N_0$ is the user parameter governing the quality of the output – see Fig. 1.

For each vertex $P_{i,j,0}$ of these fibres,² normal vector $n_{i,j,0}$ of the smooth interpolating surface at that point is estimated and the thickness $h_{i,j,0}$ of the muscle in the direction of this vector is determined. If the muscle is composed of multiple heads, $h_{i,j,0}$ might be zero for some point $P_{i,j,0}$. In this case, all the points $P_{i,k,0}$, $a < k < b$, where a and b are indices of the control fibres closest to fibre $F_{j,0}$, are shifted to split the fibres between both heads appropriately.

Next, sets Φ_k , $k \in \langle 1, v \rangle$ of deep fibres $F_{1,k}, F_{2,k}, \dots, F_{n+(n-1)*s,k}$, where $v \in N_0$ is the user specified parameter, are reconstructed from Φ_0 by linear extrapolation of superficial fibres in the direction of normal vectors $n_{i,j,0}$ up to the distance corresponding to the muscle thickness. To avoid regularity, every fibre $F_{j,k}$ is randomly slightly translated. To avoid flatness at the sides of muscle, this is followed by reconstruction of fibres $F_{0,k}$, whereas, in this case, $k \in \langle 1, v \rangle$, using again a cubic spline interpolation of fibres $F_{2,0}, F_{1,0}, F_{1,v}$, and $F_{2,v}$. Fibres $F_{(n-1)*(s+1)+2,k}$ at the other side are reconstructed similarly.

It is typically useful to prolong the fibres to connect them to their origin and insertion attachment sites on bones or other objects (e.g., aponeuroses). An attachment site is specified as an triangular patch, i.e., as a surface mesh with a boundary. We note that if the site is specified by an ordered set of landmarks identifying the boundary of this site on some associated surface mesh (e.g., of a bone), which, providing that the user has fundamental anatomical knowledge, is not difficult to specify, e.g., in our LH-PBuilder WP10 software,³ one can use the approach described in our paper [14] to automatically extract the required patch from

¹ <http://www.truegrid.com/>.

² We denote $P_{i,j,k}$ to be i th vertex of j th control fibre in k th layer.

³ <https://mi.kiv.zcu.cz/en/research/musculoskeletal.html>.

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