Journal of Biomechanics 43 (2010) 2601–2607

Contents lists available at ScienceDirect

Journal of Biomechanics

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

The convex wrapping algorithm: A method for identifying muscle paths using the underlying bone mesh

Eric Desailly [a,b,*], Philippe Sardain [b], Nejib Khouri [c], Daniel Yepremian [a], Patrick Lacouture [b]

[a] *Fondation Ellen Poidatz, 77310 St. Fargeau-Ponthierry, France*
[b] *UPR 3346 CNRS – Université de Poitiers – ENSMA, Département Génie Mécanique et Systèmes Complexes, Axe RoBioSS "Robotique Biomécanique Sport Santé", SP2MI, BP 30179, 86962 Futuroscope Cedex, France*
[c] *Hopital Armand Trousseau, AP-HP, 75571 Paris Cedex 12, France*

ARTICLE INFO

Article history:
Accepted 10 May 2010

Keywords:
Muscle
Tendon
Path
Modeling
Moment arm
Musculoskeletal
Geometry
Algorithm
Length

ABSTRACT

Associating musculoskeletal models to motion analysis data enables the determination of the muscular lengths, lengthening rates and moment arms of the muscles during the studied movement. Therefore, those models must be anatomically personalized and able to identify realistic muscular paths. Different kinds of algorithms exist to achieve this last issue, such as the wired models and the finite elements ones. After having studied the advantages and drawbacks of each one, we present the convex wrapping algorithm. Its purpose is to identify the shortest path from the origin to the insertion of a muscle wrapping over the underlying skeleton mesh while respecting possible non-sliding constraints. After the presentation of the algorithm, the results obtained are compared to a classically used wrapping surface algorithm (obstacle set method) by measuring the length and moment arm of the semitendinosus muscle during an asymptomatic gait. The convex wrapping algorithm gives an efficient and realistic way of identifying the muscular paths with respect to the underlying bones mesh without the need to define simplified geometric forms. It also enables the identification of the centroid path of the muscles if their thickness evolution function is known. All this presents a particular interest when studying populations presenting noticeable bone deformations, such as those observed in cerebral palsy or rheumatic pathologies.

1. Introduction

Muscle–tendon lengths, their lengthening rates as well as their moment arms, are parameters of great utility for clinical interpretation purposes. These parameters depend on the paths that the muscles follow. It is thus necessary to determine accurately muscular paths during movement. The position of the muscles being inaccessible to direct measurement, various methods were proposed in order to evaluate as well as determine possible paths during the movement studied. They can be split into two categories: the wired models and the finite elements models.

Each of these categories contains different algorithms of variable complexity for determining muscular paths. The objectives common to all of these models are firstly, to respect the anatomy as accurately as possible from the muscle origin to its insertion, as it wraps around the bone, and, secondly, respecting anatomical via-points like trochlea or retinaculi. Respecting these constraints, and considering the muscle as a contractile organ, all these models are driven by the common principle of finding the shortest possible path.

The wired models include "straight line" algorithms, "via-points" algorithms, "wrapping surface" algorithms and "dynamic via-points" algorithms.

The "straight line" algorithms are the simplest and oldest ones (Inman, 1947). They are unsuitable for the modeling of numerous muscles that wrap around diverse anatomical structures. They are nevertheless currently used to generate comparative data to evaluate new algorithms and to model the direct paths of certain mono-articular muscles.

"Via-points" algorithms force the muscles to pass through imposed points (Delp et al., 1990). They are particularly useful for modeling the change of direction of certain muscles on structures such as the retinaculi.

The models characterized as "wrapping surface" algorithms constituted an important step forward in the modeling of muscle paths (Garner and Pandy, 2000; Delp and Loan, 2000; Van der Helm et al., 1992). They allow a realistic modeling of the path of certain muscles over elementary geometrical entities (spheres, cylinders or ellipsoids) during movement. The thickness of the muscle/tendon can be taken into account by expanding the simple geometric form, with the limitation that the transverse

---

* Corresponding author at: Fondation Ellen Poidatz, 77310 St. Fargeau-Ponthierry, France. Tel.: +33 160658282; fax: +33 160658285.
E-mail address: eric.desailly@fondationpoidatz.com (E. Desailly).

0021-9290/$ - see front matter © 2010 Elsevier Ltd. All rights reserved.
doi:10.1016/j.jbiomech.2010.05.005

cross-sectional size of the muscles has to be closely approximated in order to determine accurately the moment arms. This type of algorithm was validated on anatomical specimen for the semitendinosus, semimembranosus, gracilis and psoas muscles.

More recently, "dynamic via-points" algorithms were a generalization of the "via-points" models in three-dimensional (3D) situations, with (or without) consideration of the deflection of the muscles on via-points, according to the position of various skeletal segments (Carman and Milburn, 2005). We can include in these algorithms those proposed for determining the paths of ligaments. In order to identify the path of the carpus triangular ligament, Marai et al. (2004) suggest handling this question as an optimization problem solved by a sequential quadratic programming method. The objective function involves finding the shortest path. The constraints consist in not penetrating the underlying bone mesh.

Algorithms based on finite elements modeling appeared more recently. The "host mesh" (Fernandez et al., 2005) and the "complex mesh" (Blemker and Delp, 2005) models use 3D data collected by magnetic resonance imaging (MRI). They deform the muscles in a bounding box while conserving a quasi-constant volume. These models are very realistic, but, on the other hand, require substantial computing times of about 5–10 h on Silicon Graphics Origin 3800 processors with shared memory (Blemker and Delp, 2005). They also entail access to the personal MRI data of the studied subject.

The "wrapping surface" models do not strictly respect the constraints related to bone geometry. Indeed, they use simple geometrical forms such as spheres, cylinders and ellipsoids to model the wrapping of muscles over the bones. On the other hand, they allow the centroid path of the muscles to be closely approximated by increasing the size of these regular-shaped rigid bodies. The bodies have a certain thickness corresponding to the centroid cross-section which, in turn, is related to the wrapping surface. However, the personalized definition of these regular-shaped rigid bodies is not always coherent with the structural variety of the skeleton, as is observed in the case of cerebral palsy or rheumatic pathologies.

The solution proposed by Marai et al. (2004) is interesting because it uses the bone mesh as a wrapping surface, conferring an anatomical realism on this method.

Most of these muscle path modeling algorithms seek to define the shortest paths in spaces containing obstacles. This is a classical problem in robotics. A survey of the substantial literature on the shortest-path problem can be found in Yap (1987). Solutions proposed in robotics are based on the methods of computational geometry (Sharir and Schorr, 1986; Papadimitriou, 1985; Clarkson, 1987; Balstan and Sharir, 1988), graph search-based algorithms (Kiryati and Székely, 1993), differential geometry and hybrid techniques (Beck et al., 1986; Kimmel and Kiryati, 1996; Marai et al., 2004). The type of technique used depends primarily on the assumed structure of the search space (polyhedral or continuous surfaces).

Taking into account the "wrapping surface" algorithm ellipsoid method, the "dynamic via-points" algorithm and Marai's algorithm which uses skeleton mesh, the present authors thus developed the "convex wrapping algorithm" to determine the muscular paths, with the following objective: "Find the shortest path between the insertion and the origin of a muscle wrapping over the skeleton bone mesh while respecting possible non-sliding constraints". This algorithm directly employs exact bone geometry, not simple geometrical forms, as the object of envelopment. To this end, it is an original application of a method which has the same fundamental objective as algorithms already described for other applications in robotics and computer science, such as those reviewed in Agarwal et al. (2009), Mitchell (2000), Mitchell and Sharir (2004), Cook IV and Wenk (2009), Maheshwari and Wuhrer (2009) and Schreiber and Sharir (2008). This algorithm is detailed in Section 2. It is then compared with the "straight line" method and "wrapping surface" algorithm, by measuring the length and moment arm of the semitendinosus muscle during asymptomatic gait.

2. Methods

The "convex wrapping algorithm" is used on a mesh model of the bones of the skeleton to determine the muscle paths. The bone mesh data used come from CT-Scan data supplied by the European project VAKHUM (Contract #IST-1999-10954) (subject006). Every skeleton segment is scaled to the subject of the study by a homothetic transformation based on the ratio, subject/VAKHUM segment lengths. The morphological adaptation of the axial torsion of thighbones and tibias is based on the data obtained by well-validated clinical evaluations (Staheli et al., 1985; Davids et al., 2002; Jacquemier et al., 2008), using state-of-the-art algorithms (Delp et al., 1990; Schutte et al., 1997; Delp et al., 1990; Arnold and Delp, 2001; Arnold et al., 2000). Each time, after an iterative solidification of segment lengths, the position and the orientation of every bone are determined by the homogeneous matrix of the segments to which they belong. Thanks to the high resolution of the CT-scan data used, the insertion sites were specified manually.

The main stage of the "convex wrapping algorithm" consists in determining the convex envelope gathering the whole range of physiologically acceptable paths. The convex envelope is the smallest surface covering the skeleton from the origin point A to the insertion point B of the muscle (Fig. 1a). The last step is to determine the shortest path between points A and B. To speed up the resolution, while including non-sliding constraints on the surface of the skeleton, a prism containing the space of the possible muscular paths is defined.

The "convex wrapping algorithm" is described as follows, while referring to Fig. 1:

- Firstly, the half-space (H) containing all the possible paths is defined (Eq. (1)) by building a reference frame $\Re_H$ using vector $\vec{V}$:

  $$\Re_H(\vec{u},\vec{v},\vec{w}) \quad \text{with} \quad \vec{u} = \frac{\overrightarrow{AB}}{\|\overrightarrow{AB}\|}, \quad \vec{v} = \frac{\vec{V}\times\vec{u}}{\|\vec{V}\times\vec{u}\|}, \quad \vec{w} = \vec{u}\times\vec{v} \tag{1}$$

  $\vec{V}$ is defined (Eq. 2), during the modeling, in relation to the reference frame $\Re_S(\vec{x_S},\vec{y_S},\vec{z_S})$ of one of the segments (S) crossed by the muscle (Fig. 1 a). $\vec{V}$ forms, in the transverse plane $(\vec{x_S},\vec{y_S})$ a chosen angle α with $\vec{x_S}$, the anterior axis of the segment:

  $$\vec{V} = R_{0,S}\begin{bmatrix} \cos\alpha & 0 & \sin\alpha \\ 0 & 1 & 0 \\ -\sin\alpha & 0 & \cos\alpha \end{bmatrix}\begin{bmatrix} 1 \\ 0 \\ 0 \end{bmatrix} \tag{2}$$

  The solution set (H) is restricted to the half-space defined by the plane $(\vec{u},\vec{v})$ and the normal vector $\vec{w}$.
- The second stage is optional depending on the type of constraint:
  - ○ *Case "2 non-sliding constraints"*: 2 points P_1 and P_2 represent non-sliding lateral constraints. Those points belong to (H) is first ascertained. Any P point has a projection P' on the line AB. Therefore, if $\vec{w}\bullet\overrightarrow{P'P} > 0$, then P belongs to (H). Then:
    - – If P_1 and P_2 belong to (H), then the solution prism is defined by the edge AB and the 2 faces passing through AB and, respectively, through the points P_1 and P_2.
    - – If P_1 or P_2 do not belong to (H), then one moves to the case "1 non-sliding constraint".
    - – If P_1 neither P_2 belong to (H), then one moves to the case "0 non-sliding constraints".
  - ○ *Case "1 non-sliding constraint"*: P_1 is the single lateral non-sliding constraint. The objective is to find out if it belongs to (H): if $\vec{w}\bullet\overrightarrow{P'_1P_1} > 0$, then P_1 belongs to (H). Then:
    - – If P_1 belongs to (H), then the prism solution is defined by the edge AB and the face passing through AB and through the point P_1 on the one hand and, on the other hand, the face whose angle β with vector $\vec{w}$ is arbitrarily defined (usually $\pi/6$).
    - – If P_1 does not belong to (H), then one moves to the case "0 non-sliding constraints".
  - ○ *Case "0 non-sliding constraints"*

    The prism solution is defined by the edge AB and the faces passing through the edge AB, whose angle γ is arbitrarily defined (usually $\pi/3$) and is centered on vector $\vec{w}$ as a bisector.
    - – The set M whose elements are the p_i points of the skeleton mesh that are contained inside the solution prism is defined. Then the convex envelope C of these points, including A and B, is calculated. It is the intersection of all convex sets containing M. For N points $p_1, \ldots, p_N$, the convex hull C is defined by

      $$C = \left\{ \sum_{i=1}^{N} \lambda_i p_i : \lambda_i \ge 0 \quad \text{for all } i \quad \text{and} \quad \sum_{i=1}^{N} \lambda_i = 1 \right\} \tag{3}$$

      This calculation is made using the "Qhull algorithm" (Barber et al., 1996).