A method to evaluate human skeletal models using marker residuals and global optimization

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A B S T R A C T

Different models are proposed in the literature to study the musculo-skeletal system. These models differ in several aspects like the number of segments in which the system is divided or the way to model articular joints. Marker residual analysis is a widely used method to evaluate how well the model fits the experimental measurements. However, the same model can yield different values of marker residuals depending on the PGA (Protocol of Gait Analysis) employed. The goal is to analyse the changes in the marker residuals obtained with different PGAs when a certain mechanical parameter is modified. Two of the most important parameters in the kinematic analysis have been studied: the length of a segment and the mechanical model of a joint. The results show that marker residuals obtained using some PGA do not provide valuable information to decide the best value of the analysed parameter. Values of the residuals computed using a PGA where the position of the markers is treated with the GOM (Global Optimization Method) are proposed to quantify the effect of certain parameters in the model.

1. Introduction

Mathematical models are widely used in Biomechanics to simulate human motion. As the elastic deformation of the bones can usually be neglected and relative motion allowed by articular joints is large, a good choice for modelling the musculo-skeletal system is the multibody system method [13]. Biomechanical models are typically more complicated than technical multibody systems, since they involve a larger variety of joint types and body shapes, complex actuators in the form of muscles, connected groups of bones and neighbouring soft tissues, and specific cases of passive elasto-plastic elements. To model the human body as a multibody system, several assumptions are made: the bones are infinitely rigid, the body articulations are modelled as ideal joints, the musculo-tendon units can be represented as one or several linear actuators and the role of soft tissue can be neglected [25].

The musculo-skeletal system can be modelled in many different ways. The number of segments in which the system is divided varies from one model to another. For example, a simple model of the whole body can include just eight segments (HAT segment, pelvis, thighs, shanks and feet [1]) while a more detailed model of the lower limb can use seventeen segments (phalanges, metatarsals, calcaneus, talus, fibulas, tibias, patellas, femurs and pelvis [5]). The type of ideal joints between segments used for modelling the articular joints also varies between models. For example, the five degree-of-freedom knee joint can be modelled as a revolute joint [1,6], as a simple spherical joint [1], or with a simplified one degree of freedom model, where internal/external

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and varus/valgus rotation angles as well as anterior/posterior and medial/lateral translations are functions of the flexion–extension angle [5].

Once the number of segments and the type of joints are selected, the geometric properties required to perform a kinematic analysis must be defined. The skeletal anatomy of a specific subject can be accurately defined from CT or MRI data, but subject-specific techniques are, not only more time-consuming, but also more difficult to implement due to their problem of availability and the costs of the technical implementations. Usually, the position and orientation of the body segments and the joint centre locations are obtained from stereo-photogrammetry data by means of a BPR method. Depending on the procedure selected the values of these properties can reach significant differences.

The different decisions taken to define the multibody system necessarily introduce errors in the model. Thus, two different models will have different levels of error. In general, it is not possible to know, a priori, which model fits the reality more closely. Therefore, it is necessary to develop a procedure to compare different models. The procedure will define the errors and select the one with the lowest deviation from the experimental data as the best model.

One crucial point is to define and quantify those errors. Marker residuals are widely used in the literature [1,18] to compute how well the model fits the experimental data. The residuals are calculated as the differences between experimental measurements and model computed values. The whole error measured by the marker residual contains not only the model errors mentioned above but also the errors caused by other sources like the noise introduced by the motion capture system, anatomical landmark misplacement or the STA [8,10,20]. The STA is due to skin movements by which the markers displace and rotate relative to the underlying bone. Inertial effects, skin deformation and sliding and deformations caused by muscle contractions contribute independently to STA. This movement represents an artefact, which affects the estimation of the skeletal system kinematics and is regarded as the most critical source of error in human movement analysis. Model errors are generally smaller than those associated with STA, but they may still be significant. There are different methods proposed in the literature to treat the STA errors as the local optimization method [1], the GOM [18], the method proposed by Silva and Ambrosio which is called here KC method [24] or the method proposed by Reinbolt and Schutteb [22]. This procedure is based in a two-level optimization to include the identification of the segment length in the optimization process.

Due to the definition of marker residual its value depends on the PGA employed. The PGA is defined as a procedure which establishes a biomechanical model and the methods for data collection, processing, analysis and reporting the results [4,23]. Thus, the value of the marker residual can be calculated just using a BPR or adding a procedure to treat the STA errors. Therefore, the selection of the PGA to evaluate the errors and, in consequence, the quality of the model is critical.

The goal of this work is to analyse the changes in the marker residuals obtained with different PGA methods when a certain mechanical parameter is modified; in other words, to propose a procedure to select the best value of the analysed parameter. This study is focused on the kinematics of the model. Therefore, two of the most important parameters in the kinematic analysis have been studied: the length of a segment and the mechanical model of a joint.

2. Material and methods

Usually, the estimation of the errors in the model is made using marker residuals. These errors are due, mainly, to the STA and the suitability of the model. Once the experimental measurement is carried out using stereo-photogrammetry techniques, the presence of STA errors is assumed. Therefore, the only way to reduce the values of marker residuals is to improve the mechanical model. In general, the PGA leads, not only to marker residuals, but also to the existence of dislocations at the joints and both, residuals and dislocations, are related. The improvement of the model should be defined as a reduction of both, marker residuals and joint dislocations. As different PGAs yield different values for marker residuals and joint dislocations, even if the same mechanical model is used, some common PGAs are briefly described. First, a PGA where only the BPR is applied and second, two PGAs composed of the BPR and a procedure to treat the STA. The differences in the computed residuals and dislocations will be discussed.

2.1. Definition of marker residuals and joint dislocations

Model-determined marker positions correspond to the positions of the markers estimated under the assumption that they were rigidly attached to the corresponding segment of the model. In the case of a perfectly rigid body segment, the global position of the virtual marker m, associated to body i, is described by the position vector $\mathbf{r}_i^m$ as:

$$\mathbf{r}_i^m = \mathbf{r}_i + \mathbf{A}_i \mathbf{s}_i'^m \tag{1}$$

where $\mathbf{A}_i$ is the rotation matrix of the body segment and $\mathbf{r}_i$ is the position vector of the origin of the body segment, both calculated from the marker positions by means of the selected PGA. In the next subsection the influence of the PGA in the estimation of the vector $\mathbf{r}_i$ and the matrix $\mathbf{A}_i$ is discussed. $\mathbf{s}_i'^m$ is the local position of the marker m in the body segment coordinate frame, obtained from a static trial. A standing static trial is chosen to define subject specific functional parameters like the distance from the centre of mass to the markers, which are taken as constants in the dynamic trials and ensure the absence of skin motion effects in the estimation of the marker position. Therefore, the vector $\mathbf{s}_i'^m$ is calculated just once, whereas the vector $\mathbf{r}_i$ and the matrix $\mathbf{A}_i$ are