THE IMPORTANCE OF CONSISTENT KINEMATIC DATA IN THE INVERSE DYNAMIC ANALYSIS OF BIOMECHANICAL MODELS

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INTRODUCTION: The evaluation of the muscular actions and internal forces of human articular joints is of major importance in different areas of medicine, sports, physical rehabilitation or biomedical engineering. There is no experimental methodology that can directly measure these forces. Among the numerical procedures that can be applied, inverse dynamics based methods are still the most commonly used numerical tools. Their use requires that the kinematics of human motion, i.e., the positions, velocities and accelerations of the anatomical points, be known in advance. This is obtained by standard reconstruction methods based on the DLT technique (Aziz and Karara, 1971). Moreover, the equations of motion for the system must be associated to a biomechanical model (Celigueta, 1996; Silva et al., 1997). The muscle action may be obtained by having each particular group of muscles, defined as those with similar functions and common anatomical insertions, modeled independently and included in the biomechanical model (An et al., 1995). This leads to an indeterminate problem, in terms of the unknown forces, that can be solved using the optimization theory (Pedotti et al., 1978). Alternatively, the actions of the different muscle groups can be lumped as moments about anatomical joints leading to a determinate inverse dynamics problem (Winter, 1991).

Regardless of the biomechanical model used or of the way the muscle actions are described, the results obtained from the inverse dynamic analysis are related to the quality of the kinematic data supplied. The problem of the consistency of this kinematic data with respect to the biomechanical model used is addressed in this work, it being shown that the quality of the inverse dynamics analysis results is highly dependent on the data kinematic consistency.

Inverse Dynamics Problem in Biomechanics: A multibody system is defined as a collection of rigid bodies with a relative motion constrained by kinematic constraints and acted upon by forces. The equations of motion for the system, represented in figure 1a as a biomechanical model, are given by (Silva et al. 1997)

$$\mathbf{M}\ddot{\mathbf{q}} + \boldsymbol{\Phi}_{\mathbf{q}}^{\mathrm{T}}\boldsymbol{\lambda} = \mathbf{g} \tag{1}$$

where $\ddot{\mathbf{q}}$ is the vector with *n* accelerations, **M** is the system mass matrix, **g** is the generalized forces vector, λ is a vector with *m* unknown Lagrange multipliers associated with the kinematic constraints and $\boldsymbol{\Phi}_{\mathbf{q}}$ is the Jacobian matrix. A set of natural coordinates, consisting of points and vectors, is used in what follows to describe the multibody system (Celigueta, 1996). The vector of generalized forces is decomposed into the sum of a vector of known generalized external forces $\mathbf{g}_{ext}$ and a vector of unknown generalized internal forces $\mathbf{g}_{act}$

$$\mathbf{g} = \mathbf{g}_{ext} + \mathbf{g}_{act} \tag{2}$$

The vector of unknown forces $\mathbf{g}_{act}$ is related to the internal motor forces and moments $\mathbf{f}_{act}$ acting in the joints, and represented in figure 1c. Their relation is

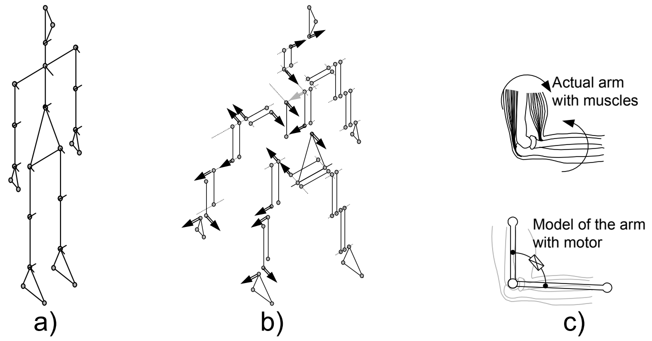

Figure 1 a) Model with 16 biomechanical segments; b) The 33 rigid bodies associated with the model; c) lumped muscle action with a motor

$$\mathbf{g}_{act} = \mathbf{C}^T \mathbf{f}_{act} \tag{3}$$

where matrix $\mathbf{C}^T$ describes the projection of the unknown forces and moments $\mathbf{f}_{act}$ in the coordinates space. In the inverse dynamics problem the accelerations and external forces acting over the system are known and the objective is to evaluate the Lagrange multipliers and generalized motor forces. Then, equations (1) through (3) are substituted into equation (1), which rearranging leads to

$$\begin{bmatrix} \boldsymbol{\Phi}_{\mathbf{q}}^{\mathrm{T}} & -\mathbf{C}^{\mathrm{T}} \end{bmatrix} \begin{Bmatrix} \boldsymbol{\lambda} \\ \mathbf{f}_{act} \end{Bmatrix} = \left\{ -\mathbf{M}\ddot{\mathbf{q}} + \mathbf{g}_{ext} \right\} \tag{4}$$

The number of known accelerations describing the system is n and the number of unknown Lagrange multipliers associated with the constraints is m. The number of unknown motor forces must be n-m, which is also the number of the system dofs.

The biomechanical model used here is made of 33 rigid bodies to represent 16 biomechanical segments (Celigueta, 1996). This form of modeling assures that relative dofs between adjacent bodies are defined about either revolute or universal joints, which have the axis fixed to at least one of the adjacent bodies. The reaction forces that develop between the biomechanical segments are

$$\boldsymbol{\Phi}_{\mathbf{q}}^{\mathrm{T}} \boldsymbol{\lambda} - \mathbf{C}^{\mathrm{T}} \mathbf{f}_{act} = -\mathbf{M}\ddot{\mathbf{q}} + \mathbf{g}_{ext} \tag{5}$$

Two forms of representing the motor forces are used. Either the motors are used to evaluate the lumped action of the muscles at the joints, as in equation (4), or driving constraints controlling the relative rotations between adjacent segments are used. If all motors are replaced by constraints, equation (4) reduces to

$$\boldsymbol{\Phi}_{\mathbf{q}}^{\mathrm{T}} \boldsymbol{\lambda} = -\mathbf{M}\ddot{\mathbf{q}} + \mathbf{g}_{ext} \tag{6}$$

Here, the number of constraints is equal to the number of coordinates and, from a mechanical point of view, the system has no degrees-of-freedom. In either case, six driving constraints are associated with a floating base body, generally the lower torso.

Consistent Versus Inconsistent Biomechanical Data: In order to obtain the Lagrange multipliers associated with the articular moments and with the joint reaction forces, it is necessary to know the positions, velocities and accelerations of the system. These are obtained by reconstructing human motion based on photograms resulting from video cameras.

Let it be assumed that the trajectories of the anatomical points have been reconstructed and filtered in order to minimize the errors associated with the digitalization and reconstruction. Due to the use of natural coordinates, the anatomical points are used directly in the model to represent the rigid segments. Before the data can be used in the inverse dynamics, the positions and orientations of the biomechanical model rigid bodies, defined by the anatomical points, must be adjusted in order to assure that the kinematic constraints are not violated, i.e.,

$$\boldsymbol{\Phi}(\mathbf{q}) = \mathbf{0} \tag{7}$$

Assuming that the anatomical points positions are corrected, the velocities and accelerations must be obtained to solve the inverse dynamics problem. For the first alternative, let the corrected positions of the anatomical points be interpolated by by cubic splines, in order to guarantee C^2 continuity and let time be the global parameter. The anatomical points velocities are obtained as the time derivative of the splines, while the point accelerations are the time derivatives of the velocities. As a second alternative, the first and second time derivatives of equation (7) provide the velocity and acceleration equations respectively written as:

$$\dot{\boldsymbol{\Phi}}(\mathbf{q}) \equiv \boldsymbol{\Phi}_{\mathbf{q}}\dot{\mathbf{q}} - \boldsymbol{\nu} = \mathbf{0} \tag{8}$$

$$\ddot{\boldsymbol{\Phi}}(\mathbf{q}) \equiv \boldsymbol{\Phi}_{\mathbf{q}}\ddot{\mathbf{q}} - \boldsymbol{\gamma} = \mathbf{0} \tag{9}$$

The anatomical points velocities are obtained by the solution of these equations. The kinematic data obtained using this method is said to be consistent with the biomechanical model selected.

APPLICATION RESULTS: The methodologies described are applied to the gait analysis of a 77 Kg human subject with a fast cadence walking a complete stride. The motion is recorded with two cameras, as shown in Figure 2, and the spatial position of the anatomical points is reconstructed. The ground reactions are measured by a force platform and introduced into the inverse dynamic problem as external applied forces .

Figure 2 Measurement of fast cadence walking motion

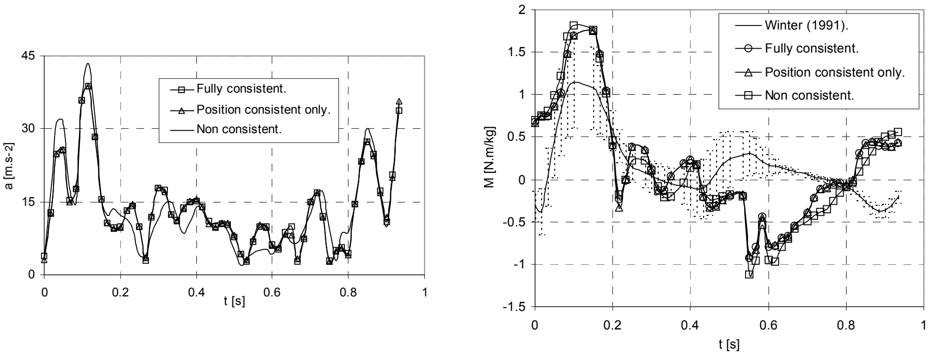

Figure 3 force moments at the knee joint and knee acceleration

Two inverse dynamic analyses are performed in order to obtain the biomechanical moments of force at the joints, using consistent and non-consistent kinematic data. The acceleration of the anatomical point of the right knee and the biomechanical moment of force for this knee are shown in Figure 3. In Figure 3b the results are compared with those presented by Winter (1991).

CONCLUSIONS: It is observed that the predicted moments are similar with both types of kinematic data, and the evolution of the moment in time is within the expected range of variations. It is observed that the differences between the accelerations obtained with the spline derivatives and consistent accelerations are not reflected in the predicted moments of force. However, for motions with a faster cadence, recorded with the same number of frames, the problem of kinematic consistency becomes an issue.

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