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The fundamental problem of myoskeletal inverse dynamics and its implications

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Abstract

The validity of current inverse dynamics models utilized for motion analysis is investigated. It is shown that observables generated by the real biosystem, such as ground reaction forces, are incompatible with comparable responses of skeletodynamical inverse models currently in use. This implies that results obtained with such models are erroneous to varying degrees while a quantification of these errors is difficult or impossible. This phenomenon is termed the fundamental myoskeletal inverse dynamics problem. A model fidelity indicator is proposed which, for a specific inverse dynamics model applied to a particular motion, provides a dimensionless numerical measure for the replicative validity of that model and the fidelity of its input data. A practical example demonstrates the usefulness of this indicator. It is suggested that the development of structurally sufficiently complex and biologically more realistic skeletomechanical models as well as substantial error reductions in data measuring and processing procedures will be necessary to improve the accuracy of inverse dynamics model computations.

Keywords: Motion analysis; External reaction forces; Model fidelity indicator

1. Introduction

Myoskeletal inverse dynamic techniques, that is, biomechanical procedures for the practical implementation of the inverse solution of human skeleto- or myoskeletodynamics are used extensively in orthopaedics, ergonomics, sports and other areas. These techniques are commonly termed human motion analysis. Their purpose is to obtain information about motion characteristics that are either experimentally non-observable by definition such as, for instance, the trajectory of the body center of mass and its time derivatives, or are non-observable for other such as ethical reasons that prevent the application of severly invasive experimental techniques. In either case, abstract finite-dimensional state space analogues (models) of the real biosystem are employed to obtain estimates of the required motion characteristics. The latter comprise kinetic quantities including joint moments, compressive and shear forces in the joints, mechanical energies, powers, linear and angular momenta of the moving segments, muscle power contributions, etc., as well as various kinematic quantities.

There exists, however, a fundamental inconsistency in the practical implementation of current motion analysis methods in that incompatible model input data are used to obtain the desired outputs. More specifically, the observables (histories of configurational coordinates, ground reaction forces, centers of pressure, etc.) result from measurements taken from the *real biosystem* and therefore represent, within certain experimental error bounds, outputs that were generated by the dynamics of the natural (the source) system. These mutually compatible observables are then used as inputs to the *abstract analogue* of the biosystem (i.e., the mathematical model) whose inverse dynamical behavior is profoundly different from that of the source system. This implies that the mutual compatibility of the source observables no longer applies to their destination as input to the model which, in turn, results in substantial and largely unpredictable errors in the computed motion characteristics. This is the fundamental problem of myoskeletal inverse dynamics. Certain aspects of this problem were

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recognized fairly early. In 1981, Hatze (1981a) showed for the first time that, in principle, the external constraint (e.g. ground reaction) forces and moments follow from the dynamical model equations implying that additional measurement of these external forces results in an overdetermined system of equations. Later, Vaughan et al. (1982) used this overdeterminacy to obtain improved estimates of segmental parameter values while, more recently, Kuo (1998) presented a least-squares approach for improving the precision of joint moment computations also based on this overdeterminacy. In both studies, either isolated model properties or measurement and data processing errors were assumed to be responsible for the residuals representing the differences between source system and model responses. A comprehensive treatment of the fundamental inverse dynamics problem does not appear to exist in the literature. It is surprising that textbooks dealing with practical (e.g. Winter, 1990) or fundamental aspects (Andrews, 1995, Winters, 2000) of motion analysis and inverse dynamics hardly pay any attention to the current problem. In the sequel we shall analyse and discuss in detail this problem, its practical implications, and possible solutions both theoretically and by means of a practical example.

2. Biosystem dynamics versus myoskeletal inverse dynamics

Let the real biosystem, i.e. the human subject under consideration, be denoted by $\mathscr{B}$. According to modeling theory (Zeigler et al., 2000, p. 25), $\mathscr{B}$ is called the *source system* because it provides observable data in the form of time-indexed trajectories of specific variables. For the present discussion, the term "model" will be defined to mean "an abstract representation of selected attributes of a real object, event, or process" (Hatze, 2000a). If applied to human body modeling, this definition incorporates both the structural and the functional modeling aspects.

Assume that at some stage an abstract super analogue of $\mathscr{B}$, the *ultimate base model* $\mathscr{S}$ has been created. Such a hyper-complex finite-dimensional state space human body model is conceivable, at least in principle. Structurally it would consist of myriads of tiny mass particles acted upon by a multitude of different-type internal and external forces, while functionally it would be represented by the corresponding super large-scale system of differential equations. If appropriately designed, this super simulation model will, *for a specified experimental frame* (Zeigler et al., 2000, p. 27), mimic the dynamic behavior of $\mathscr{B}$ faithfully to within experimental error bounds. The same argument holds true also for the corresponding inverse dynamics model $\mathscr{I}(\mathscr{S})$. Under these assumptions, the experimental output observables of the source system $\mathscr{B}$ will be mutually compatible inputs for $\mathscr{I}(\mathscr{S})$ because they originate from a real biosystem whose behavior is largely replicated by the super model $\mathscr{S}$.

Obviously, such a super–complex model has only conceptual but no practical value, at least by today's standards. Myoskeletal inverse dynamics models that can be used for practical purposes must be cost-efficient in their execution and therefore much simpler. However, *valid simplification* of a model implies a reduction of model complexity such that *predictive*, *structural* and, most importantly, *replicative validity* is preserved. The stipulation concerning replicative validity means that, for all experiments possible within the given experimental frame, the behavior of model and source system must agree to within acceptable tolerance (Zeigler et al., 2000, p. 31). We are therefore required to devise some measure of replicative validity (or *fidelity*) for a specific myoskeletal inverse dynamics model $\mathscr{I}(\mathscr{H})$, where $\mathscr{H}$ denotes the corresponding myoskeletal (forward) dynamics model. Models $\mathscr{H}$ and $\mathscr{I}(\mathscr{H})$ are mathematically equivalent. We shall restrict our attention to *skeletodynamical models*, i.e. to models of the skeletal subsystem only. The reason is that myoskeletodynamical inverse models require additional specifications and assumptions necessitated by the myodynamic indeterminacy problem (Hatze, 1980a), while the neuromyoskeletal inverse dynamics problem, i.e., the myocybernetic control inverse dynamics problem, cannot be solved in principle, as has been recently demonstrated by Hatze (2000b).

3. A fidelity measure for myoskeletal inverse dynamics models

We shall now derive a dimensionless quantity that permits us to evaluate a combination of input data precision and replicative validity of a specific skeletodynamical inverse model $\mathscr{I}(\mathscr{H})$ in relation to the hypothetical super inverse dynamics model $\mathscr{I}(\mathscr{S})$, i.e., in relation to the responses of the real biosystem $\mathscr{B}$. The equations of motion of a multi-particle system (such as $\mathscr{S}$) or a multi-body system (such as $\mathscr{H}$) subject to external constraints are similar and can be derived by utilizing various formalisms like Newton's method, Kane's method, D'Alembert's principle, or Lagrange's equations. The latter were used (Hatze, 1977) to obtain the second order differential system describing the three-dimensional motion of the model in its explicit vector form (Hatze, 1981a) as

$$C\ddot{q} + B = Q^{\mathrm{M}}(t) + Q^{\mathrm{L}}(q) + Q^{\mathrm{E}}(t) + Q^{\mathrm{C}}(q), \tag{1}$$

where $q := (q_1, q_2, ..., q_f)$ is the f-dimensional vector of configurational coordinates, C denotes the inertia matrix, B is the vector of gravitational and, if applicable,

centrifugal and Coriolis forces or moments, and $Q^{M}, Q^{L}, Q^{E}, Q^{C}$ denote, respectively, the internal muscle forces (or moments for multi-body models using angular coordinates), passive tissue forces (moments), non-gravitational external forces (moments), and the constraint forces (moments) due to environmental contacts such as ground reactions on the feet. It should be noted that, assuming an appropriate interpretation of the various quantities, the differential system (1) describes both the dynamics of the hypothetical multi-particle super model $\mathscr{S}$ and that of a multi-segment model $\mathscr{H}$.

By rearranging terms in Eq. (1), the kth component ($k = 1, \ldots, f$) of the *inverse dynamics vector equation* reads

$$Q_k^{M}(t) + Q_k^{L}(t) + Q_k^{E}(t) = C_{k1}(t)\ddot{q}_1(t) + \cdots + C_{kf}(t)\ddot{q}_f(t) + B_k(t) - Q_{1k}^{C}(t) - \cdots - Q_{sk}^{C}(t), \quad (2)$$

for a number of s active external constraints. Of special interest for the present purpose are those components of system (2) which can be related directly to specific observables of the source system $\mathscr{B}$, namely to the external (e.g. ground) reaction forces. For the multi-particle model $\mathscr{S}$, the number of the respective equations would be very large indeed because they would have to encompass all particles acted upon by fractional external reaction forces. However, by hypothesis, all of these equations are satisfied to within certain error limits and therefore need no longer be considered. Turning now to the multi-segment model $\mathscr{H}$, the three equations of interest correspond to the three linear coordinates q_1, q_2, q_3 that describe the body model's reference point relative to the spatial coordinate system as shown in Fig. 1.

In these three equations which, in effect, define the *external translatory inverse dynamics* of system (2) and therefore the acceleration of the center of mass, the left hand sides must be zero if there are no external forces $Q^{E}(t)$ acting in addition to gravity and the ground reactions. Assuming $Q^{E}(t) \equiv 0$, it is easy to show that these equations have the form

$$O = C_{11}^{*}(t)\ddot{q}_1^{*}(t) + \cdots + C_{1f}^{*}(t)\ddot{q}_f^{*}(t) + B_1^{*}(t) - \sum_{j=1}^{s} F_{xj}^{C}(t) = \eta_1(t), \quad (3)$$

$$O = C_{21}^{*}(t)\ddot{q}_1^{*}(t) + \cdots + C_{2f}^{*}(t)\ddot{q}_f^{*}(t) + B_2^{*}(t) - \sum_{j=1}^{s} F_{yj}^{C}(t) = \eta_2(t),$$

$$O = C_{31}^{*}(t)\ddot{q}_1^{*}(t) + \cdots + C_{3f}^{*}(t)\ddot{q}_f^{*}(t) + B_3^{*}(t) - \sum_{j=1}^{s} F_{zj}^{C}(t) = \eta_3(t),$$

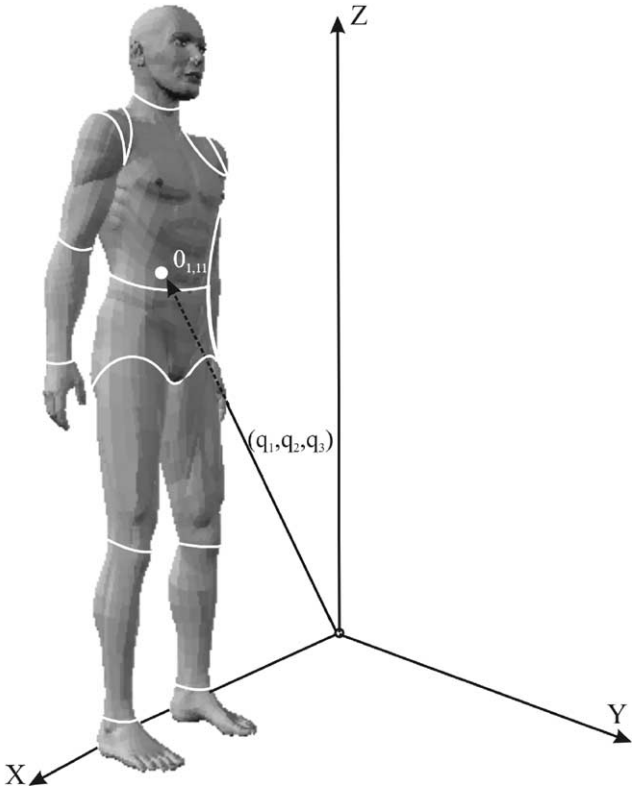

Fig. 1. Graphical representation of the 17-segment body model (hominoid) of Hatze (1980a,b). The hominoid reference point $O_{1,11}$ described by the position vector (q_1, q_2, q_3) relative to the spatial coordinate system XYZ is also shown. Note that the hominoid reference point is not identical with the hominoid center of mass. Figure created with the aid of POSER 3 (MetaCreations).

where $F_{nj}^{C}(t)$, $n = x, y, z$, $j = 1, \ldots, s$ are the *measured* (experimentally with negligible errors observed) histories of the three spatial components of the s external environmental reaction forces; $\ddot{q}_i^{*}(t)$, $i = 1, \ldots, f = f_{\mathscr{H}}$, denote the *computed* second derivatives of the *recorded* (noise-contaminated) coordinate histories $q_i^{*}(t)$, $i = 1, \ldots, f_{\mathscr{H}}$; and $C_{ki}^{*}(t) = C_{ki}^{*}(q^{*}(t), P_s^{*})$ and $B_k^{*}(t) = B_k^{*}(q^{*}(t), \dot{q}^{*}(t), P_s^{*})$ are the elements of the respective matrices computed using the functions $q_i^{*}(t), \dot{q}_i^{*}(t)$. The segmental parameter values P_s^{*} (masses, principal moments of inertia, locations of segmental mass centroids, segment lengths, etc.) were *determined experimentally* for the subject in question. The symbols $\eta_1(t), \eta_2(t), \eta_3(t)$ denote the *translatory inverse dynamics residuals*. It is to be noted that the positive terms in Eqs. (3) are, in fact, the model expressions for the 3 mass-times-acceleration components of the center of mass, with the gravity term added to the third equation.

To be precise, we need to mention that three additional relations similar to Eqs. (3) and defining the *external rotatory inverse dynamics* result from the condition of zero external moments (other than that

produced by gravity and reaction forces) about the body model's reference point. However, the computations of the constraint moment components involve both the measured reaction forces and the moment arms. The latter reflect properties of model $\mathscr{H}$ and are highly error-prone (McCaw and DeVita, 1995). A clear distinction between observables originating solely from the biosystem $\mathscr{B}$ and quantities that are influenced by properties of model $\mathscr{H}$ is therefore not possible. For this reason, these three equations are disregarded in the treatment to follow.

The important point to realize now is that Eqs. (3) constitute an overdetermined system containing implicit statements about the replicative validity of model $\mathscr{H}$ as well as the fidelity of the measured quantities. While the negative terms (the experimentally recorded external reaction forces) represent observables that were generated directly by the complex actions of the real biosystem $\mathscr{B}$ (or equivalently, by the corresponding super model $\mathscr{S}$), all positive terms in Eqs. (3) represent the actions of model $\mathscr{H}$ utilizing as input the observables P_s^* (segment parameter values) and $q_i^*(t), \dot{q}_i^*(t), \ddot{q}_i^*(t)$, the $i = 1, \ldots, f_{\mathscr{H}}$ histories of the (non-exact) configurational coordinates and their first and second time derivatives. For a perfect response of a high fidelity model $\mathscr{H}$ and highly accurate measured quantities, the *residuals* $\eta_1(t), \eta_2(t), \eta_3(t)$ in Eqs. (3) would be almost zero, apart from minimal values $\eta_1^0(t), \eta_2^0(t), \eta_3^0(t)$ that result from unavoídable errors in measurement and data processing. These residuals will serve as the tolerances mentioned in Section 2. In passing it should be noted that Eqs. (3) permit, in principle, the computation of the three sums representing the external (ground) reaction force components from the dynamics of the observed motion if a valid model $\mathscr{H}$ is employed and the measured input quantities are sufficiently accurate. In this case reaction force measurements would be no longer necessary.

We now have to devise an appropriate measure for the model fidelity indicator for evaluating a specific model $\mathscr{H}$ and the quality of its inputs, for a particular motion. To this end one may use the transentropy measure for function deviations (Hatze 1986, 1995). For the present case an adapted version of this measure is defined by

$$\gamma = \sum_{i=1}^{v} \lambda_i / \sum_{i=1}^{v} \lambda_i \varepsilon_i, \tag{4}$$

where λ_i, $0 \leqslant \lambda_i \leqslant 1$, are weighting factors and

$$\varepsilon_i = (1/2\ln 2)\ln\{1 + u_i^2/\sigma_{\omega i}^2\}, \tag{5}$$

with

$$u_i^2 = \frac{1}{\tau}\int_0^{\tau} \eta_i^2(t)\,\mathrm{d}t, \tag{6}$$

and $\sigma_{\omega i}^2$ denoting a reference variance while τ is the motion interval. The value of v is 3 for three-dimensional motion analysis and 2 for two-dimensional analysis. It must, however, be emphasized again that the present model fidelity indicator in its present form expresses both the effects of model inadequacy and those of poor input data quality. In this sense, the evaluation of model validity also encompasses the simultaneous evaluation of the fidelity of its input quantities. However, in many applications reliable estimates of input data errors may be available in which cases a separation of residual components into those that result from input errors and those that originate from model inadequacies is possible. The latter type of residual components are then used in Eqs. (4)–(6) for the computation of the model fidelity indicator.

4. Application to myoskeletal inverse dynamics—an example

The above measure was applied to the analysis of bi-legged vertical maximum effort jumping as illustrated in Fig. 2.

The motion was considered planar, i.e., to take place predominantly in the sagittal plane YZ as indicated in Fig. 2. In addition, left–right symmetry was assumed. The observables were the histories of the horizontal (F_y) and vertical (F_z) ground reaction forces, the center of pressure function $a_y^*(t)$, the histories of the trunk angle q_{15}^*, the hip angle q_{16}^*, the knee angle q_{17}^*, the ankle angle q_{18}^*, and the segmental parameters P_s^* of the subject under consideration. The model used was the 17-segment body model of Hatze (1980a) as illustrated in Fig. 1, together with the associated inverse dynamics equations. The input data sequences and their derivatives were computed by optimally filtered Fourier approximations as described in Hatze (1981b). Because the motion was considered planar, only two of Eqs. (3) (the y- and z-equations) needed to be considered. The segmental parameters P_s^* (masses, moments of inertia, etc.) were determined for each subject with high precision by using the anthropometrico-computational method of Hatze (1980b).

Three male (average age 26.8 years) and three female (average age 24.3 years) physical education students volunteered as subjects. There were altogether 12 trials, the results of which were pooled for the present purpose. In Fig. 3 is shown a typical record (female subject IM) of the residuals $\eta_2(t)$ and $\eta_3(t)$ of the y- and z-Eqs. (3), respectively.

It was noted that the functions $\eta_i(t)$ in Fig. 3 were very similar for different trials of a specific subject but differed considerably between subjects. The average value of the model fidelity indicator γ for the present population and this type of motion was found to be $\bar{\gamma} = 0.277$ with a standard deviation of 0.019 for 12

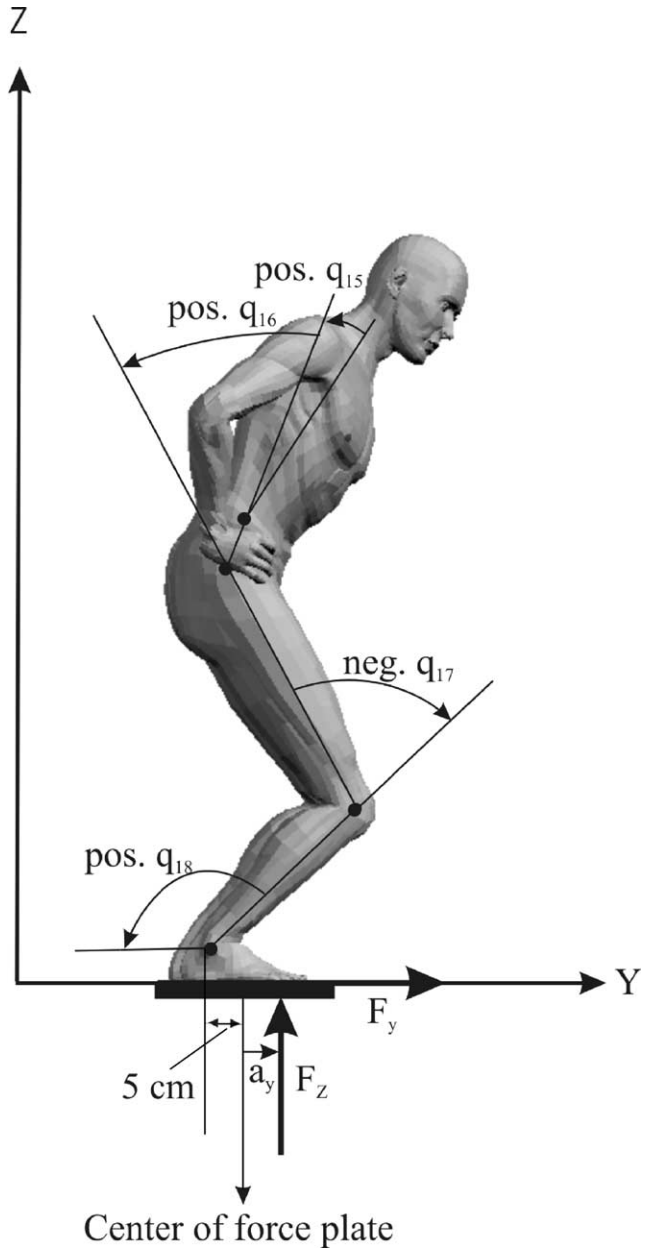

Fig. 2. Diagrammatic representation of the observables (joint angles) $q_{15}, \ldots, q_{18}$, the horizontal and vertical ground reaction force components F_y, F_z, and the center of pressure location a_y in bi-legged vertical maximum effort jumping. Note that the positive and negative directions of the angular excursions are also indicated. Figure generated by using POSER 3 (MetaCreations).

trials. In computing γ from Eq. (4), the reference variance $\sigma^2_{\omega i}$ was put equal to $c^2(Mg)^2$ with $c^2 = 0.000741$. This value corresponds to $\gamma = 1$ for $u_i^2 = 3c^2 \times (Mg)^2$, which is equivalent to saying that the mean residual u_i in expression (6) is about 4.7% of body weight (40 N of 850 N weight) for $\gamma = 1$. It is instructive to plot relation (4) as a function of u_i. More specifically, putting $u_i^2 = p_i^2(Mg)^2$ and setting $v = 1$, relation (4) may be expressed as a function of the normalized mean residual p_i, as depicted in Fig. 4.

From the nonlinear nature of the function $\gamma(p)$ it is obvious that improvements in model validity and (or) input data precision will be noticeable most dramatically near $\gamma = 1$ that is, in the region where a model approaches an acceptable validity level. On the other hand, fidelity indicator values below 0.4 are indicative of poor model validity and (or) imprecise input data, as is the case for the present model ($\gamma = 0.277$) applied to bi-legged vertical maximum effort jumps.

5. Implications of model deficiencies and future perspectives

The problem discussed above is usually not recognized as such because Eqs. (3) are redundant and do not provide any information on motion characteristics, which information is extracted from equations for $k > 6$ in system (2). However, deficient models produce results that are erroneous to varying degrees. A quantification of these errors is difficult or impossible because they affect quantities that cannot be measured directly, such as joint moments or joint loads. A more thorough investigation into the current problem is therefore warranted.

The model fidelity indicator introduced in Section 3 provides an objective means of assessing both the validity of a given inverse dynamics model when applied to a specific motion and its input data quality but it gives no clue as to the origins of model inadequacy and data imprecision. To investigate the probable causes of the inappropriateness of skeletodynamical models, extensive sensitivity studies will be necessary. One of the drawbacks of such studies is that the resulting sensitivity functions will be typical of the investigated motions only as is the case with model fidelity indicator values. A broader indication as to which model components and data processing procedures are most probably responsible for the model deficiencies can be inferred from the comparisons given in Table 1, from which it is obvious that a multitude of factors contribute to the inadequacy of myoskeletal inverse dynamics models currently in use. These factors range from structural oversimplifications to error-prone motion recording and data processing techniques. At this point it should be remarked that, in principle, Eqs. (3) could be used to adjust the model $\mathscr{H}$ more closely to system $\mathscr{B}$ if it would be known precisely which variables or model components are responsible for the deviations of the responses of $\mathscr{H}$ from those of $\mathscr{B}$.

In the near future we will probably see the development of sufficiently complex and biologically more realistic anthropomorphic models, as well as improvements in the accuracy of data processing techniques,

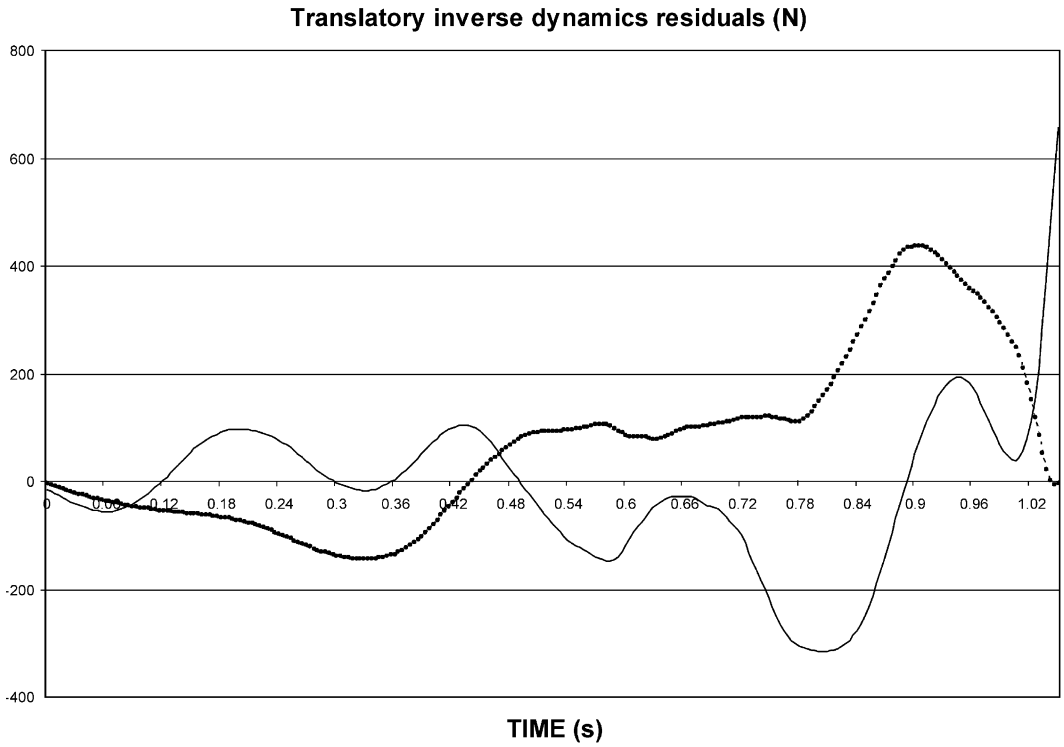

Fig. 3. Translatory inverse dynamics residuals $\eta_2(t)$ (- - - -) and $\eta_3(t)$ (——) representing the mismatch between model prediction and biosystem response for a planar bi-legged vertical maximum effort jump (female subject IM). Notice the fluctuations of the residual functions around the zero value.

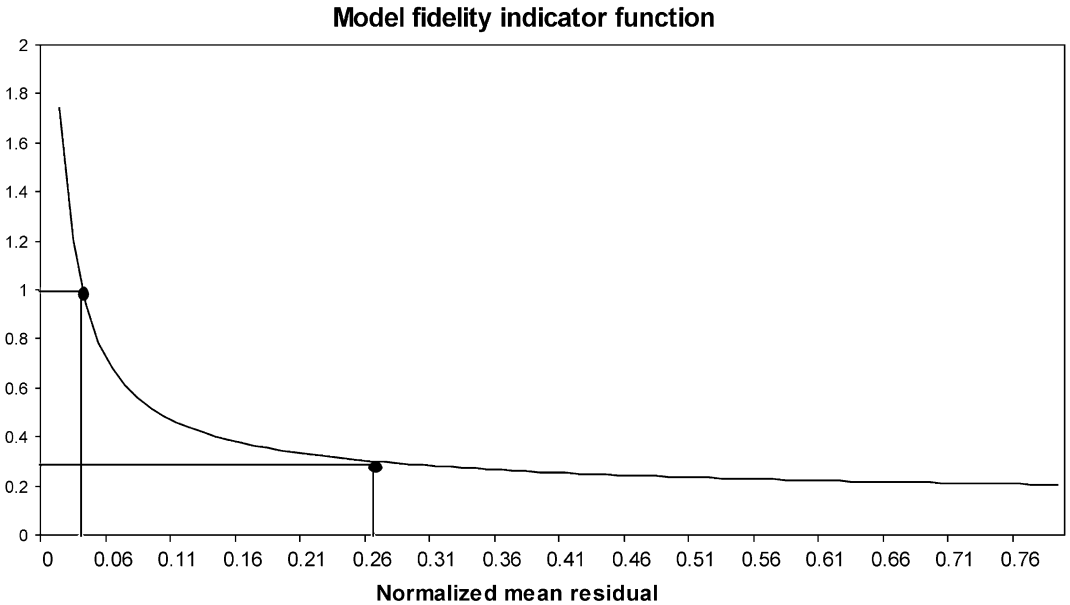

Fig. 4. Model fidelity indicator γ as a function of the normalized mean residual. The value of 0.277 is the mean of the current model evaluation. Detailed explanations in the text.

notably in derivative computation. Efficient hybrid algorithms exist already (Hatze, 2001) for simulating on the computer the forward dynamics version of this new model generation while the validity of these new models could be tested by computing the value of the model fidelity indicator introduced in this paper for a standardized motion such as bi-legged vertical maximum effort jumping.

Table 1
Comparison between skeletostructural properties or descriptive quantities of the real biosystem $\mathscr{B}$ (or super model $\mathscr{S}$) and a multi-segment model $\mathscr{H}$

Property or quantity	Biosystem $\mathscr{B}$ (or Particle Model $\mathscr{S}$)	Model $\mathscr{H}$
Composition of body segments	Limbs composed of particles, soft tissue properties preserved	Rigidity of segments assumed
Number of body segments	No actual segments in particle assemblage	>26
Segment boundaries and local segment coordinate systems	Non-existent owing to overlapping structures	Artificially defined
Segmental parameter values	Non-existent	Estimated from geometric segment approximations
Environmental contact areas on terminal segments	Ill-defined shape-changing amorphic soft tissue contact patches	Artificially well-defined contact points
Joint kinematics	Non-stationary axes of rotation with changing orientation and position	Well-defined stationary axes of rotation assumed
Number of configurational degrees of freedom (coordinates)	$< 3 \times 10^7$	$>10^2$
Configurational coordinate histories	Inherently defined by motion of real biosystem	Experimentally observed by error-prone motion recording devices
First and second derivatives of coordinate histories	Defined a priori by dynamics of real biosystem	Computed by applying various filtering and derivative calculation techniques, results erroneous to varying degrees

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