# The effect of a multibody system model in the inverse dynamics problem in Biomechanics

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Abstract The inverse dynamics is a classic problem solved when human gait analysis is carried out. The solution is the vector of joint reactions and driving actions which is essential to perform a kinetic analysis of the human gait. Multibody system techniques are widely used to solve this problem. However, it is not clear in the literature if mathematical constrains of the joints should be fulfilled nor what is the effect of this constrains on the kinetic results. Moreover, it is necessary to have a procedure to evaluate the influence of the joint constrains on the kinetic results. Four different methods to solve the inverse kinematics and inverse kinetics problems were implemented in this work according to the fulfilment of the joint constrains, the procedure to fulfil them or the type of joint constrains imposed. Because of all the sources of errors present in a gait analysis measurement, the dynamic equations are not balanced. To balance them dynamic residuals are defined. These dynamic residuals were used in this work to evaluate the goodness of the procedures. Results showed that the imposition of kinematic constrains could lead to worse results in the kinetic results if the model is too simplistic. However, this kind of approach could be necessary if further studies were required as a force-shared problem, where the definition of reaction and driving actions should be made properly.

 $\mathbf{Keywords}$ Biomechanics  $\cdot$  Gait analysis  $\cdot$  Inverse dynamics problem  $\cdot$  Dynamic residuals

# **1** Introduction

Inverse dynamics is commonly used by the biomechanical community for analysis of human movement. Inverse dynamics implies measuring a certain movement and calculating the force and torque reactions at various body joints [38]. To perform

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the inverse dynamic analysis a model must be set. The musculo-skeletal system can be modeled as a multibody system which degrees of freedom depend on the number of segments considered as well as the kinematic constrains considered between them [34, 8]. Generally, at least three markers are located on each segment in order to measure the location and orientation of the segment, considered rigid, in space. Therefore, there is no need to consider kinematic constrains in the model as for each rigid body considered in the model six motion laws corresponding to three translations and three rotations are measured. These laws can be numerically derived twice to get the inertial forces. The approach, which does not consider kinematic constrains to model joints, allowing six degrees of freedom in each one, it's the most employed in the clinics field. This procedure is commonly used in commercial codes as Vicon [16] and by many other researchers [9, 5, 18]. As the motion of each segment is reconstructed separately, without modelling joint articulations with kinematical constraints, unrealistic motions such as important joint dislocations may occur. The use of kinematic constraints overcome this problem easily [35]. This approach, which reduces the number of degrees of freedom in the joints by adding kinematic constrains, is the preferred by the multibody community.

Despite widespread use, it is well recognized that inverse dynamics solutions are prone to errors. Errors can stem from a variety of sources including inaccuracies in body segmental parameters (BSP), inaccuracies in measurements, inaccuracies related to locating joint centers, etc. There are many studies in the literature that focus in one or several inaccuracies. Riemer et al. [32] present a comprehensive analysis of the uncertainties in joint torque estimates derived through inverse dynamics. Their analysis revealed that for the lower and upper extremity joints the main contributors to the total uncertainty were inaccuracies in segment angles. These inaccuracies are associated mainly with skin motion artifacts, what agrees with the findings of several authors [12] about the main source of error in the kinematic data obtained from marker-based motion capture system.

The skin motion articlate is also known as soft tissue articlate (STA). STA are interdependently caused by the inertial effects, the skin deformation and the deformations due to muscle contractions. Such perturbations typically contain frequencies similar to gait frequencies [13] and consequently cannot be removed by only filtering. Errors produced by STA have been characterized as task and subject dependent. Numerous studies have investigated thigh and shank STA for a variety of different motor tasks and the propagation of STA to the estimation of joint kinematics [14, 21, 7, 11, 3]. It has been shown that only motion about flexion axis of the hip, knees and ankles can be determined reliably. Motion about other axes at those articular joints should be regarded with much more caution as STA produces spurious effects with magnitudes comparable to the amount of motion actually occurring in those joints. Efforts have been made to improve measurement techniques to minimize STA [19] but they cannot be eliminated unless markers are applied to the bones directly or through bone-pins [25]. It is particularly important to develop and apply a corrective method that compensates for skin movement artifact. The motion of the skin makers can be minimized by least square methods [15,2] or redundancy as the cluster method or can be specifically modeled [10,35]. One of the methods belonging to the first category is called Local Optimization Method (LOM). This approach is based on a least squares pose estimator, separately for each body segment. The model-determined configuration of the markers is fitted to the measured configuration in a least squares sense. This method reconstructs the motion of each segment separately without kinematic constraints constraints. There are also methods belonging to the first category that impose kinematical constrains to avoid joints dislocations. In this case the optimization process is based on a minimization of the weighted sum of squared distances between experimental and model-determined marker positions, while ensuring kinematic consistency of the motion by applying kinematic constraints. This method is known as the Global Optimization Method (GOM). GOM is most used by the multibody community. It uses ideal joints to model biomechanical joints. A large number of models published in the specialized literature use simple joints as revolute, spherical or universal joints. Generally it is accepted that kinematic consistent data obtained with the model improve the kinematic reconstruction of the musculo-skeletal system. Reconstructed data does not present dislocated joints, but errors arising from an inadequate modelling of the joint articulation can strongly bias the estimated motion [26]. Using idealized knee joint constraints have the potential of limiting or eliminating actual bone motions [7, 20, 30]. As such, adding a spherical or revolute joint constraint becomes a potential source of error that is being introduced to minimize a second source of error (the STA)[4]. Adding joint constraints can improve the ability of skin markerbased kinematic data to represent the actual motion of the underlying bones only if the error introduced by the joint constraints is smaller than the STA error.

Data measure by the motion capture system can be processed in many different ways. Different choices should be made. For instance, whether kinematic constrains are implemented or whether methods to reduce STA errors are implemented. The selected procedure yields different inverse kinematics and consequently different inverse dynamics. It's difficult to know which procedure gives the better reconstructed data. A challenging problem in gait biomechanics is the experimental validation of the results[33]. Most methods for STA compensation have been tested using just numerical experiments [22,25]. GOM method has been theoretically validated by introducing an artificial noise to the marker trajectories obtained from a theoretical and kinematically consistent motion. By comparing the motion estimated with GOM with the original one, GOM showed to accurately reduce STA errors. However, this study did not consider modelling errors of the joint articulations. Few experimental validations have been conducted based on a comparison between the estimated motion and in vivo measured motion. Andersen et al.[4] used the data described by Benoit et al. [7], which includes simultaneously recorded skin and bone-mounted pin markers for the thigh and shank for six healthy male subjects measured during gait. Knee motion estimated with GOM using different kinematic models was compared to in vivo measurements concluding that the use of simple knee models produces errors in the analysis larger than those induced by the STA.

There are several published studies about the influence of different parameters in inverse dynamic solutions. These works use models without kinematic joints [32] or with them [29,6,28,31], but none of them analyze the influence of the use of simple kinematical joints. Six degree of freedom joints method presents measurement errors due principally to skin movement while including simple joints introduces errors associated to a predicted relative motion of the joints.



Fig. 1 MoPiG markers placement.

Dynamic residuals will be used as a measure of the goodness of the procedure. These residuals are defined to balance the Newton's equations which are not usually verified due to the errors introduced through the whole procedure.

## 2 Material and methods

## 2.1 Experimental setup

An experiment has been designed to obtain quantitative data of normal walking. Gait analysis was carried out on one adult male subject with no pathologies in gait using a modified Newington gait model (MoPiG) [26] as the Body Pose Reconstruction method 1. The marker trajectories were measured at 100 Hz using a Vicon six-camera motion capture system.

## 2.2 Kinematics

The position in the space of the musculo-skeletal system is described by means of the multibody system techniques. Thus, the position of the whole system is described by the position of each segment. A formulation based on dependent cartesian coordinates and Euler parameters is used[24] to define one segment and showed in equation 1.

$$\mathbf{q}_{\mathbf{i}} = \begin{bmatrix} x_i & y_i & z_i & e_{0_i} & e_{2_i} & e_{3_i} \end{bmatrix} = \begin{bmatrix} \mathbf{r}_{\mathbf{i}} & \mathbf{p}_{\mathbf{i}} \end{bmatrix}, \tag{1}$$



Fig. 2 Position and orientation of the segments obtained from the position of actual markers shown in blue (a), using UNO (b), KC (c) and GOM (d). In red, the model markers.

where  $\mathbf{q_i}$  is the vector which describes the position and orientation of the body i (Eq. 1) given by the coordinates of its center of mass and the Euler parameters, respectively.

The translational velocity of one segment can be obtained by the temporal derivative of the position coordinates of the segment,  $\mathbf{r_i}$ . The angular velocity vector  $\omega_i$  is defined by equation 2.

$$\tilde{\omega}_{\mathbf{i}} = \dot{\mathbf{A}}_{\mathbf{i}} \mathbf{A}_{\mathbf{i}}^{\mathrm{T}} \tag{2}$$

Where  $\mathbf{t}$  is the skew-sym operator of the vector  $\mathbf{t}$ ,  $\mathbf{A}_i$  is the rotation matrix of the segment *i* and  $\dot{\mathbf{A}}_i$  is the temporal derivative of the matrix rotation. The translational acceleration of one segment is obtained by the temporal derivative of the translational velocities,  $\mathbf{\dot{r}}_i$ , and angular accelerations are expressed by equations 3, taken from [24].

$$\dot{\omega_i} = 2\mathbf{G_i}\ddot{\mathbf{p}_i} \tag{3}$$

Where  $\ddot{\mathbf{p}}_i$  is the second temporal derivative of the Euler parameters and  $\mathbf{G}_i$  is a transformation matrix defined by means of the Euler parameters [24].

Motion equations defined this way are easy to implement. Modularity allows for joint constrains inter-changeability and the formulation is free from singularities. As an inconvenience, this formulation requires a higher computational effort because of the additional constrain equations introduced by the Euler parameters. In any case, the analysis developed in this work is independent of the formulation employed.

## 2.3 Body pose reconstruction methods

For different approaches have been implemented to reconstruct the position and orientation of the different segments of the human gait through the position of the markers attached to the skin. These methods can be classified in function of the inclusion of kinematic constrains or the reduction of the STA errors as is shown in figure 3.

	No kinematic constrains	Kinematic constrains
No STA reduction	UNO	КС
STA reduction	LOM	GOM

Fig. 3 Classification of the four methods implemented in this work.

UNO The method is based on the Newington-Helen Hayes gait model[16] and calculates biomechanical segment lengths (distance between the joint centres) from the static trial. Rigid segments are defined frame-by-frame. Each segment is defined by an origin (generally located at the proximal joint centre) along with three orthogonal axes which are defined at every frame from the external markers. This method yields dislocations and residuals, as the constant length segment does not coincide in every frame with the distance between the joints centres, nor coincides the local position of the markers obtained in the static trial, mainly due to STA. It is important to remark that the results obtained with UNO are completely independent of the way the joints are modelled.

KC The procedure proposed by Silva and Ambrosio[35] consists in assembling the model and using the independent coordinates obtained in the BPR as the parameters that locate and orient the model. In this procedure, independent coordinates are reconstructed as in the BPR used in UNO, while dependent coordinates are computed by imposing kinematic constraints. This method has been named KC, for kinematic constraint, in this work. It can be observed in figure 2 that the pelvis location and orientation are identical to those reconstructed with UNO, while in the femur, the orientation is the same, but the position is not. To eliminate the dislocation the femur is artificially moved, thus increasing its marker residuals. This method produces bigger residuals than the previous one but eliminates the dislocations, yielding kinematically consistent results.

LOM The goal of this procedure is to minimize the differences between the position of the markers experimentally obtained and the position of the markers obtained with a model where no kinematic constrains at the joints are defined. 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:

$$\mathbf{r}_i^m = \mathbf{r}_i + \mathbf{A}_i \mathbf{s'}_i^m \tag{4}$$

where  $\mathbf{A}_i$  is the rotation matrix of the body segment,  $\mathbf{r}_i$  is the position vector of the origin of the body segment, and  $\mathbf{s'}_i^m$  is the local position of the marker m in the body segment coordinate frame, obtained from a static trial to eliminate the effect of skin motion. A standing static trial is chosen to define subject specific functional parameters. As the segments are not perfectly rigid and the set of markers move relative to the segments due, mainly, to the STA, a marker residual vector  $\mathbf{res}_i^m$  is defined by subtracting the position of the marker obtained experimentally,  $\mathbf{r}_i^{m,exp}$  at time  $t_j$ , from the right hand side of equation (1), yielding:

$$\mathbf{res}_{i}^{m} = \mathbf{r}_{i} + \mathbf{A}_{i} \mathbf{s}_{i}^{\prime m} - \mathbf{r}_{i}^{m,exp} \tag{5}$$

The deviation of the current marker can be measured with the norm of the  $\mathbf{res}_{i}^{m}$  vector (equation 3).

$$\|\operatorname{\mathbf{res}}_{i}^{m}\| = \sqrt{\operatorname{\mathbf{res}}_{i}^{m^{T}}\operatorname{\mathbf{res}}_{i}^{m}} \tag{6}$$

The rotation matrix  $\mathbf{A}_i$  and the position vector  $\mathbf{r}_i$  of the body segment *i* at time  $t_j$  are searched to minimize the cost function, defined as the weighted sum of the squared residuals:

$$Min \quad \sum_{i=1}^{n_{bodies}} \mathbf{W}_{i} \frac{1}{n_{i}} \sum_{m=1}^{n_{i}} \| \mathbf{res}_{ij}^{m} \|^{2}$$
$$s.t. \quad \phi(q) = 0$$
(7)

where  $n_{bodies}$  is the number of bodies of the model and  $\phi(q) = 0$  are the set of constrains to normalize the sum of the squared Euler parameters for each segment.

GOM In GOM, optimization of the residuals is performed simultaneously in all segments. A set of parameters  $\mathbf{W}_i$  can be defined to weight the errors associated to the markers placed on the segment i [22]. For simplicity,  $\mathbf{W}_i$  are chosen to equally weight all the markers of a segment. However, a different weight is assigned to each segment, reflecting its average degree of STA. For this purpose, the segmental residuals using UNO are used as a guide, so that the segments with bigger residuals are assigned smaller weights, so not to affect much the global solution. For example, STA on the thigh are much bigger than on the pelvis and the shank [22]. Therefore, the weights assigned to the thigh are smaller than those assigned to the pelvis and the shank. So, the residual  $\mathbf{res}_{ij}^m$  for the marker m of the  $i^{th}$  body at time  $t_j$  is evaluated through equation (2) applied over the entire gait cycle to obtain its segmental averaged residual  $\mathbf{e}_i$  as:

$$\mathbf{e}_{i} = \frac{1}{n_{t}} \frac{1}{n_{i}} \sum_{j=1}^{n_{t}} \sum_{m=1}^{n_{i}} \| \mathbf{res}_{ij}^{m} \|$$
(8)

where  $n_t$  is the number of instants into which the gait cycle was divided and  $n_i$  the number of markers attached to the segment *i*. The segmental weight  $\mathbf{W}_i$  is then defined as:

$$\mathbf{W}_i = \frac{1}{e_i} \tag{9}$$

The rotation matrix  $\mathbf{A}_i$  and the position vector  $\mathbf{r}_i$  of the body segment *i* are searched to minimize the cost function, defined as the weighted sum of the squared residuals:

$$Min \quad \sum_{i=1}^{n_{bodies}} \mathbf{W}_{i} \frac{1}{n_{i}} \sum_{m=1}^{n_{i}} \| \mathbf{res}_{ij}^{m} \|^{2}$$
$$s.t. \quad \phi(q) = 0$$
(10)

where  $n_{bodies}$  is the number of bodies of the model and  $\phi(q) = 0$  are the set of kinematic constraints and the constraints to normalize the sum of the squared Euler parameters for each segment.

### 2.4 Velocities and accelerations problem

Once the position problem is solved, it is possible to obtain the velocities and accelerations by means of an inverse kinematics problem. In case of methods UNO and LOM, where no constrains are imposed (see figure 3), velocities and accelerations are obtained by temporal derivatives of the vector **q**. Angular velocities and accelerations result of the equations 2 and 3, respectively. These data yield a kinematic inconsistent problem in the three kinematic levels: position, velocity and acceleration.

In case of methods LOM and GOM, kinematic constrains are imposed (see figure 3). These kinematic constrains compose a non-linear system of equation,  $\phi_{\mathbf{k}}(\mathbf{q}) = 0$ . The additional equations required to determine the system are the driving equations associated with the degrees of freedom of the problem,  $\phi_{\mathbf{d}}(\mathbf{q}, t) = 0$ . The resultant system of equations is shown in equation 11.

$$\phi(\mathbf{q},t) = \begin{bmatrix} \phi_{\mathbf{k}}(\mathbf{q}) \\ \phi_{\mathbf{d}}(\mathbf{q},t) \end{bmatrix} = 0$$
(11)

It is clear that this methodology can be applied to the cases UNO and LOM considering that the system of equations would be composed only by driving equations  $(\phi(\mathbf{q},t) = \phi_{\mathbf{d}}(\mathbf{q},t) = 0)$ . To ensure kinematic consistency, the system  $\phi(\mathbf{q},t) = 0$  is imposed in velocity and accelerations levels by means of the jacobian matrix,  $\phi_{\mathbf{q}}$ , solving the systems shown in equation 12.

$$\mathbf{v} = \phi_{\mathbf{q}}^{-1} \boldsymbol{\nu}$$

$$\mathbf{a} = \phi_{\mathbf{q}}^{-1} \boldsymbol{\gamma}$$
(12)

Where **v** is the velocity vector defined by  $\dot{\mathbf{r}}$  and  $\omega$ , **a** is the acceleration vector defined by  $\ddot{\mathbf{r}}$  and  $\dot{\omega}$ , and  $\nu$  and  $\gamma$  are the independent terms.

## 2.5 Inverse kinetics

The motion of a multibody system is due to the forces and moments applied on it. This relation between the motion and the forces and moments can be described in several ways. The formulation employed in this work is presented in equation 13 and was taken from the work of Nikravesh[24].

$$\mathbf{M}\ddot{\mathbf{v}} = \mathbf{f}^{\mathbf{ext}} + \mathbf{h} + \mathbf{f}^{\mathbf{reac}} \tag{13}$$

where  $\mathbf{\ddot{y}}$  the acceleration vector of generalized coordinates. This vector of coordinates is defined in equation 14.

$$\ddot{\mathbf{y}} = \begin{bmatrix} \ddot{\mathbf{r}} \\ \dot{\omega}' \end{bmatrix} \tag{14}$$

Where  $\dot{\omega}'$  is the vector of angular accelerations defined in the local frame of each body. **M** is the mass matrix of the system. The adopted formulation defines the parts of the mass matrix associated to the moments as identities.  $\mathbf{f}^{\text{ext}}$  is the vector of external generalized forces containing the weights and the ground reaction forces. **h** is the vector of quadratic terms which appears due to the moments are defined in local coordinates.  $\mathbf{f}^{\text{reac}}$  the vector of generalized reactions. The reaction vector is related to kinematic constrains defined to model the links due to the joints. This reaction vector is defined by means of Lagrangian multipliers related to constrains equation. Thus, by replacing terms in equation 13 Lagrange's equations of the first kind are in the way expressed by equation 15.

$$\mathbf{M}\ddot{\mathbf{y}} - \mathbf{J}^{\mathbf{T}}\boldsymbol{\lambda} = \mathbf{f}^{\mathbf{ext}} + \mathbf{h} \tag{15}$$

which leads to the solution of the inverse dynamics problem.

Solving equations of motion for  $\lambda$  leads to a determined problem during the singlesupport phase because the motor torques can be derived by equating the corresponding generalized forces to those obtained with the external forces (the inertial forces, the weights and the ground reaction forces). However, during the doublesupport phase the problem results in an overdetermined system of equations because ground reaction forces are applied as input data instead of unknown external loads which originates the motion. The introduction of these extra measurements reduces the number of unknowns. The inverse dynamics problem for the case of measured ground reaction forces can be solved by introducing residuals forces and moments. These variables correspond to external forces and moments that would have to be applied to the model to make the input data and the model compatible. It is clear that these residuals would equal zero if the mechanical model reproduces perfectly the real system and if there were not errors in the input data. Since the models are far from perfect and the input data always contain some amount of error, the vector of residuals is always unequal zero. Therefore, the magnitude of the vector of residuals gives an idea of the relevancy of the simulation, including the kinematic data, the mechanical model and the ground reaction forces measurements.

Residuals forces appear to balance the inertial forces, the external forces and the ground reaction forces. Residual moments are introduced to balance the equilibrium of moments in a point of one solid, typically the pelvis. In the case of residual forces, these are equivalent to the driving forces in the pelvis obtained from the inverse problem. In the case of residual moments, these are calculated in one point of the pelvis: that one which separates the lower limbs from the upper limbs. In this model,

$$\mathbf{rd_{moment}} = \mathbf{M}_{\mathbf{driving}} + \sum_{i=1}^{N} \mathbf{M}_{\mathbf{joint}_{i}} + \mathbf{rx} \mathbf{F}_{\mathbf{driving}}$$
 (16)

# 2.6 Mechanical model

The mechanical model is composed of two feet, two shanks, two thighs, one pelvis, one trunk, one head, two upper-arms, two forearms and two hands. The masses, the centre of mass locations and the moment of inertia tensors were obtained from the literature [17] and scaled to the subject of this study using a linear method [36].

## 3 Results

Results section was divided in two subsections. First it was discussed whether the use of ideal kinematical constrains improves the kinematic and kinetic results. In the second subsection, a multibody model with imposed kinematic constrains was assumed. It was discussed the effect of considering kinematic consistent or inconsistent data.

## 3.1 On the use of kinematic constrains

A gait cycle has been analyzed (heel strike at 0 and 100% of the cycle) using four different approaches. The difference between these procedures may be the imposed kinematic constrains, or the method to reconstruct the kinematics or both. The first approach, used UNO (un-optimized), to reconstruct position. Velocity and acceleration vectors were got by double derivation of the position vector. No kinematic constrains were imposed. The model used in this work has 90 coordinates and 90 degrees of freedom. Therefore, all the coordinates were independent.

The second called used LOM, which did not impose the kinematic constrains neither, but it reconstructed the kinematics through a minimization of the markers residuals to minimize the STA as it was explained in section 2. Because kinematic constrains were not imposed, this approach also yielded joint dislocations, as it can be seen in figure 5. Logically, because of the optimization process applied, marker residuals were smaller than with the previous approach, as shown in figure 4.

The third procedure was the KC method. It imposed kinematic constrains but it did not use any additional method to reduce STA errors. Position, velocity and acceleration vectors were obtained from constrain equations, but independent coordinates were got directly from raw data, in the same way as UNO did. Therefore, the degree of freedom coordinates were contaminated by STA errors. In this work spheric joints had been selected for all joints, and therefore, the number of degrees of freedom reduced to 48. Marker residuals were shown in figure 4.

The fourth method, GOM, shared with KC that kinematic constrains were imposed. But, as LOM did, it reconstructed the kinematics minimizing the marker residuals to reduce STA errors. While LOM reconstructed each segment separately, GOM optimized all segments together as kinematic constrains should be satisfied. The method was implemented in two ways yielding the two last approaches. First, modelling all the joints as spheric joints. Second, modelling the knee joint as revolute joint. In this case the number of degrees of freedom reduced to 44.

Results shown were obtained for one subject and eight trials. Just one subject was analyzed because the main objective of the work was to show the influence on the



Fig. 4 Averaged values of marker residuals for the different approaches implemented in this work. Markers position shown in figure 1.



Fig. 5 Average values of dislocations at the lower limb joints (AJC: ankle. KJC: knee. HJC: hip) obtained with UNO and LOM.

kinematics and kinetics of different data manipulation using the same set of data. A statistical analysis would have partially hidden these differences. Only results for the lower limb were presented as they were the most relevant for gait analysis. In figure 6 joint angles calculated using the five procedures were compared. The implemented formulation yields the position and orientation of each segment. Once the position and orientation of each segment is calculated, joint angles are expressed as the rotation of one segment relative to other segment. These relative angles are expressed in the proximal body reference system (see equation 17.

$$\mathbf{A}(\mathbf{p_{rot}}) = \mathbf{A}(\mathbf{p_{parent}}) - \mathbf{A}(\mathbf{p_{child}})$$
(17)



Fig. 6 Temporal evolution of joint angles. In black and dotted lined, UNO. In green and dashed line, LOM. In blue and solid line, GOM with spheric joint. In red, and dot-dashed line, GOM with revolute joint.

Where  $\mathbf{A}(\mathbf{p_{rot}})$  is the matrix that defined the relative rotation between the parent and child segments as a function of the Euler parameters  $\mathbf{p_{rot}}$ .  $\mathbf{A}(\mathbf{p_{parent}})$  and  $\mathbf{A}(\mathbf{p_{child}})$  are the absolute rotations of the parent and child segments, respectively. It was observed that flexion angles were very similar while abduction-adduction and internal-external angles were much sensitive to the procedure implemented.

Inverse kinematics results using UNO and LOM were very similar in the ankle. The differences increased in knee and hip joints although time evolution was quite similar. The introduction of kinematic constrains using KC did not modify the independent coordinates evolution, as explained before. UNO and KC joints angles were identical. It did not occur the same with the dependent coordinates. Therefore, inertia forces using UNO and KC were very different, what it was crucial for kinetic results, as it will be seen later in this section. GOM changed kinematics out of sagittal plane significatively. To avoid dislocations, position and orientation should experiment significant changes.

It has been shown that imposition of kinematic constrains introduced great changes in kinematic variables. It did not happen the same with kinetic variables. The moments plotted in figure 7 were very similar no matter the procedure used, although there were slight differences. Moments in figure 7 had been calculated from the reaction actions expressed in the centre of masses of each segment.

Reaction forces would be those one which balance the external forces applied to the system, including the inertia forces, as stated in equation 15. In inverse kinetics, generalized reaction forces include generalized driving forces, as law motions for independent coordinates were introduced as kinematic constrains. Both the weights and the force plates reactions were independent of the procedure applied in the inverse kinematics. However, the joint angles changed as it was shown in figure 6, changing in consequence the accelerations and the inertial forces. It must be noticed that position, velocity and acceleration of independent coordinates vectors for KC were the same than the corresponding for the UNO formulation. However, although it had not been shown, the dependent coordinates for KC had different position, velocity and acceleration than the corresponding to UNO, as the calculation procedure was different. Also position changed from one procedure to the other, what affects to the moment equations 15. If the moments plotted in figure 7 were very similar no matter the procedure used though the differences in the positions and accelerations were substantial, specially in the abduction and internal rotation, it meant that these variables were not very significant in joint moment calculations .

The procedure used to carry out the dynamic analysis implemented the ground reaction forces as external forces. Because these forces were more important than inertial forces, the changes in these last ones had low influence in the global result, as it has been noticed in the literature[9]. It was important to consider that joint moments showed in figure 7 were driving moments in all cases with the exception of the case where the knee was modelled as a revolute joint. In this case the adduction and the internal rotation joint moment at the knee were reaction moments. This consideration is crucial in the estimation of muscles forces due to reaction moments are not included in the algorithm to estimate muscle forces but only the driving moment.

Analyzing figure 6 and 7, it was observed that standard kinetic results were achieved no matter the procedure used whereas kinematic results presented higher divergences. In other words, changes on kinematics (position, velocity and accel-



Fig. 7 Temporal evolution of joint moments. In black and dotted lined, UNO. In green and dashed line, LOM. In blue and solid line, GOM with spheric joint. In red, and dot-dashed line, GOM with revolute joint. In magenta and crosses, kc method.

eration) had a low effect on the kinetics. Moreover, the influence of the kinematic constrains was indirect since they affected to the kinematics. That is, kinetics results depend exclusively on the kinematic variables through the inertial forces and he moment arms. The vector of generalized reactions on the centres of masses is the same if the kinematics problem was solved. The definition of the ground reactions forces as external forces determines univocally the problem, no matter the kinematics constrains imposed.

Marker residuals were widely used in the literature [22, 1, 27] to quantify how well the model fit the experimental results. The total error measured by the marker residuals included not only the error due to the model but also the errors contained in the measurement process, being the STA the error with more importance in the gait analysis. The model was introduced, mainly, to reduce the STA. However, if the error due to the model was higher than the STA error, the results with UNO would be more accurate than results obtained with GOM. According to the figure 4, it seemed that LOM provided the lowest values of marker residuals, which could lead to conclude than LOM yielded the best kinematics. However, the estimation of marker residuals was not enough to evaluate the goodness of the procedure due to it was necessary to consider the value of the joint dislocations simultaneously [27]. Analyzing the figure 5 together with figure 4 UNO provided better results than LOM. Even, GOM appeared to be yield good results since this approach produced no dislocations. KC method provided the highest marker residuals because no optimization was carried out. Segments links were moved to prevent dislocations keeping their orientation.

The previous analysis was just a kinematic analysis. It was not discussed the validity of the approaches in a kinetic level. Therefore, the dynamic residuals were defined to carry out this analysis. The inertial forces, the weights and the ground reaction forces should be balanced. Because of the experimental and numerical errors in the procedure, three residual forces and three residual moments rose, which were represented in figure 8 in the five cases.

The obtained results showed that UNO was the procedure with lower values of dynamic residuals. These results were in agreements with experimental results using markers attached directly to the bones [4] and with data taken from the literature [37]. Andersen et al. [4] reported that spherical and revolute joint did not simulate properly the knee mobility.

Regarding the analysis carried out the evaluation of the different approaches should be made from three points of view: marker residuals, dislocations and dynamic residuals. UNO provided the best dynamic residuals although joint dislocations came up with this approach. LOM produced the lowest marker residuals but high joint dislocations were presented in this method. The approaches where kinematic constrains were imposed did not produced joint dislocations but they presented big marker residuals. Regarding kinetic results, these approaches, GOM and KC, also provided high dynamic residuals. However, no significant differences appeared if only the sagittal plane was considered. It could be observed, for instance, that the changes on the flexion angles were much smaller than the range of motion.



Fig. 8 Temporal evolution of dynamic residuals. In black and dotted lined, UNO. In green and dashed line, LOM. In blue and solid line, GOM with spheric joint. In red, and dot-dashed line, GOM with revolute joint. In magenta and crosses, kc method.

### 3.2 Kinematic consistency

The inclusion of kinematic constrains in the biomechanics model of the human locomotor system does not always lead to better results, as it was established in the previous section. However, it is a usual practice among the engineers that works on the motion analysis. It has been discussed in the literature that kinematic inconsistent data can produce fake moments to compensate joint dislocations. The objective of this section was to demonstrate that the employ of kinematic inconsistent data does not lead to unrealistic joint moments but the same moments than using an unconstrained formulation, that is, UNO method. Therefore, it does not have to produce worse results than kinematic consistent data.

Three approaches were analyzed in this section. First, a case with kinematic constrains imposed. It was the GOM approach in the previous section. The constrains were imposed in the three position, velocity and acceleration problems. Therefore, the data were kinematically consistent. Second, an approach where no kind of kinematic constrain was imposed. It was the UNO method defined previously. Finally, an approach where the position problem was obtained in the same manner than UNO did but the velocity and acceleration problems were solved imposing kinematic constrains corresponding to the spheric joints, as in GOM method. This method was called partially consistent method, PCM.

In figure and 9 were compared for a multibody model with only spherical joints. Results in green corresponded to kinematically inconsistent data, i.e., kinematics was identical to the one reconstructed by UNO. Consequently, kinetic results were also identical to the ones obtained by UNO, represented in figure 7. The discussion in the previous section showed that generalized reactions results only depend on the kinematics. Therefore, forces and moments were the same, keeping in mind that they could be reaction or driving actions. Results in blue were obtained with a fully kinematic data consistent with the model. Both kinematic and kinetic results



Fig. 9 Temporal evolution of joint moments. In blue and solid line, consistent kinematics, GOM. In red and dot-dashed line, inconsistent position and consistent velocities and accelerations, PCM. In green and dashed line, inconsistent kinematics, UNO.

were identical to the ones obtained with GOM, represented in figures 6 and 7. In red, partially consistent data were showed using PCM. Dynamic residuals were those represented in figure 10. For this simple model, model errors seemed to be greater than STA errors, and inconsistent data yielded better results.



Fig. 10 Temporal evolution of dynamic residuals. In blue and solid line, consistent kinematics, GOM. In red and dot-dashed line, inconsistent position and consistent velocities and accelerations, PCM. In green and dashed line, inconsistent kinematics, UNO.

## **4** Discussion

Inverse dynamic analysis implies measuring a certain movement and calculating forces that produce the measured movement. In biomechanics motor forces are exerted by muscles. As it is well known, the calculation of muscles yields the redundancy problem. So, usually the calculation is made in two steps. First, joint moments and forces are obtained from a traditional inverse dynamics problem. Then, using some kind of optimization process, muscles forces are estimated. The inclusion of kinematic constrains affects the muscle forces calculation in different ways. First of all, kinematics changes, as it has been shown in figure 6. Slight changes in position could yield large variations in muscles forces, as insertion points are very close to joints centers for some muscles. Secondly, joints moments also differ as shown in figure 7 and what it's more important, driving moment are determined by the joint model selected. For example, if knee joint is modeled by a spherical joint the three joint moments are used to calculate muscles forces, but if a revolute joint is used instead only flexion-extension moment is used, as the other two are reaction moments. When ideal joints are used, just kinematic equivalent mechanisms are been used, but not dynamic equivalent ones, so care must be taken about dynamic results obtained. The classical approaches only compute a whole joint reaction at the joint centre. This joint reaction, in the typical joint models (i.e., spherical, hinge, universal), represents both the joint contact and the ligament forces. The inclusion of "anatomically" consistent kinematic models [23] with joint contacts and ligaments allows a deeper understanding of the forces distribution through the different active and passive structures and a better view of the interactions acting into the musculo-skeletal system during gait.

## **5** Conclusions

The inverse dynamics problem had been solved in this work using four different approaches. It had been studied the influence of the multibody system model in the results and, in particular, the effect of the kinematic constrains and the kinematic consistency. It had been shown that no significance differences occur at the joint moments whereas remarkable variations had been observed in the kinematics.

If a multibody system composed by rigid bodies interconnected by kinematic joints is used to model the musculo-skeletal system, it is well known that the kinetic results do not depend only on the biomechanical model but also on the kinematic data provided as input. This three dimensional data can be obtained through the reconstruction of the measured human motion, as explained for UNO. This procedure alone does not ensure that the kinematic data is consistent with the biomechanical model adopted, because the underlying kinematic constraint equations are not necessarily satisfied. When using GOM or similar procedures, positions, velocities and accelerations are consistent with the multibody model.

In the published literature it can be found papers that hold that the consistency in the kinematic data led to results for the joints moments with better quality. It has been stated that the use of kinematically inconsistent data yields spurious joints reaction forces and net moments-of-force, associated to the constraint violations. Authors agree that consistent data should be used when a multibody model with joint constrains is used. However, the use of inconsistent data does not necessarily yield worse results. Computed joint moments depend on accelerations values and do not depend on the joint constrains between links. When floor-reaction forces are introduced as external forces, using Newton or Lagrange approaches, the reactions in the ankle, for example, if just a segment is used for the foot, are determined and depend only on the external forces and the inertia forces. The joint forces and moments values are the same if the ankle is modelled as a spherical, revolute or universal joint. So, joint moments obtained using a multibody model with constrains and UNO reconstructed kinematics are identical to joints moments using UNO over a model without constrains.

Dynamic residuals had been used as a tool to evaluate the goodness of each procedure. The use of kinematically consistent data with a multibody model with constrains will only yield better results that the same model with inconsistent data if the error introduced by the model is smaller than the error due to STA. However, definition of the kinematic constrains in a multibody model of the human locomotor system is absolutely necessary if a forward dynamics analysis is performed. If just an inverse dynamics analysis is desired, kinematic constrains are not essential but can have different functions. First, they can reduce the number of markers in the motion capture protocol. Most joints do not have 6 DOF so it is not necessary to use three markers in each segment. Although the number of markers can be drastically reduce, generally the markers set is designed to be redundant, so the kinematic analysis can still work even if a number of markers drop out. Secondly, kinematic constrains can also help to define the driving moments to be used in the muscular dynamics. If no constrains are defined it is not possible to distinguish between driving and reaction moments. Finally, kinematic constrains can be used to reduce STA errors.

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