Model-based approach for human kinematics reconstruction from markerless and marker-based motion analysis systems.

Sholukha, Victor; Bonnechère, Bruno Jean P; Salvia, Patrick; Moiseev, Fédor; Rooze, Marcel; Van Sint Jan, Sérgé

Published in:
Journal of Biomechanics

Publication date:
2013

Citation for published version (APA):
Model-based approach for human kinematics reconstruction from markerless and marker-based motion analysis systems

V. Sholukha\textsuperscript{a,b}, B. Bonnechere\textsuperscript{a}, P. Salvia\textsuperscript{a,c}, F. Moiseev\textsuperscript{a}, M. Rooze\textsuperscript{a}, S. Van Sint Jan\textsuperscript{a,c}

\textsuperscript{a} Laboratory of Anatomy, Biomechanics and Organogenesis (LABO), Faculty of Medicine Université Libre de Bruxelles (ULB), Belgium
\textsuperscript{b} Department of Applied Mathematics, Polytechnical University, Saint Petersburg, Russia
\textsuperscript{c} Center for Functional Evaluation, Faculty of Medicine, ULB, Belgium

\textbf{A R T I C L E   I N F O}

\textbf{Article history:}
Accepted 26 July 2013

\textbf{Keywords:}
Multibody system kinematics
Joint modeling
Constrained registration
Kinect\textsuperscript{™}
Computational modeling.

\textbf{A B S T R A C T}

Modeling tools related to the musculoskeletal system have been previously developed. However, the integration of the real underlying functional joint behavior is lacking and therefore available kinematic models do not reasonably replicate individual human motion. In order to improve our understanding of the relationships between muscle behavior, i.e. excursion and motion data, modeling tools must guarantee that the model of joint kinematics is correctly validated to ensure meaningful muscle behavior interpretation. This paper presents a model-based method that allows fusing accurate joint kinematic information with motion analysis data collected using either marker-based stereophotogrammetry (MBS) (i.e. bone displacement collected from reflective markers fixed on the subject’s skin) or markerless single-camera (MLS) hardware. This paper describes a model-based approach (MBA) for human motion data reconstruction by a scalable registration method for combining joint physiological kinematics with limb segment poses. The presented results and kinematics analysis show that model-based MBS and MLS methods lead to physiologically-acceptable human kinematics. The proposed method is therefore available for further exploitation of the underlying model that can then be used for further modeling, the quality of which will depend on the underlying kinematic model.

© 2013 Elsevier Ltd. All rights reserved.

1. Introduction

A number of neuromuscular pathologies lead to dysfunction of the locomotor system that can show a variety of disorders (i.e. spasticity, weakness, and lack of coordination). Among the clinically-relevant physiological signals to be analyzed are the joint and limb displacements using motion analysis methods associated or not with electromyography. One important challenge for clinicians is to understand the relationships between the observed motion patterns and muscle behavior (Dallmeijer et al., 2011). Unfortunately, no fully satisfactory data analysis tools are currently available to perform patient data interpretation (Van Sint Jan, 2011). Once a proper generic model (GM) is available, clinical individual input motion data must be fused accordingly. The obtained GM, once properly adjusted and validated, could then be used in further simulation to obtain clinically relevant muscle information (length, moment arms) that are difficult to estimate directly in clinical settings. Quality of the obtained muscle information strongly relies on the underlying bone and kinematic data used to create the joint models that will be crossed by the muscle spatial path.

By its nature, marker-based stereophotogrammetry (MBS) data might include important soft tissue artifact (STA) (Leardini et al., 2005). Therefore, using MBS data to estimate joint centers might lead to poor accuracy (Sholukha et al., 2011a). Several methods minimizing STA have been previously developed (Leardini et al., 2005). Some methods addressed each segment separately by computing the optimal bone pose from marker location (Soderkvist and Wedin, 1993; Challis, 1995). STA compensations can also be addressed by developing a mechanically-based model of the joints as further discussed in this paper. Several models of underlying functional joint behavior (Van Sint Jan, 2005). In order to improve our understanding about the relationships between muscle behavior (i.e. excursion) and motion data, modeling tools must guarantee that the joint kinematics in the model are correctly validated to ensure meaningful interpretation and avoid imprecise muscle estimation (Van Sint Jan, 2005). Once a proper generic model (GM) is available, clinical individual input motion data must be fused accordingly. The obtained GM, once properly adjusted and validated, could then be used in further simulation to obtain clinically relevant muscle information (length, moment arms) that are difficult to estimate directly in clinical settings. Quality of the obtained muscle information strongly relies on the underlying bone and kinematic data used to create the joint models that will be crossed by the muscle spatial path.

By its nature, marker-based stereophotogrammetry (MBS) data might include important soft tissue artifact (STA) (Leardini et al., 2005). Therefore, using MBS data to estimate joint centers might lead to poor accuracy (Sholukha et al., 2011a). Several methods minimizing STA have been previously developed (Leardini et al., 2005). Some methods addressed each segment separately by computing the optimal bone pose from marker location (Soderkvist and Wedin, 1993; Challis, 1995). STA compensations can also be addressed by developing a mechanically-based model of the joints as further discussed in this paper. Several models of...
the ankle and knee joints based on universal and hinge joints were previously proposed (Andersen et al., 2009, 2010; Reinbolt et al., 2005). Methods based on coupled degrees-of-freedom, or DoFs (Van Sint Jan et al., 2002), were also performed using spatial parallel mechanisms (Di Gregorio et al., 2007; Feikes et al., 2003) that take into account properties of anatomical structures (e.g., shape of articular surfaces or keeping ligament length constant). In order to be applicable in daily motion analysis, current models should integrate the above anatomical aspects using more advanced fusion methods.

Typically, a global optimization method based on mechanical modeling could be applied to adjust model parameters to specific motion. Different sets of joint constraints related to joint kinematics (e.g., joint surface geometry, ligament information and joint mechanism) were previously implemented in order to assess their influence on the lower limb kinematics during gait (Duprey et al., 2010). This approach requires implementation of collision detection and reaction mechanism procedures such as the ones available from commercial multibody dynamics software.

The method presented herein allows fusing validated joint kinematic information with relatively crude motion analysis (MA) data collected using either MBS or markerless single-camera (MLS) hardware. The obtained kinematical model can then be used for further modeling of muscle components (e.g. muscle moment arm or excursion by addition of relevant data).

This paper extends the model-based approach (MBA) (Fohanno et al., 2013; Marin et al., 2010; Nicolas et al., 2007; Poppe, 2007) for human motion data reconstruction using a novel scalable registration method that combines validated joint kinematics with limb segment poses. The new MBA proposed in this paper uses a scalable generic model with joint constraints to improve the realism of skeleton kinematics obtained from MBS or MLS systems. It has been applied for most large human joints (upper and lower limbs). This approach is an improvement of a previously published double-step registration method (Sholukha et al., 2006), developed for lower limbs MA.

2. Materials and methods

2.1. Morphology and joint kinematic data collection for model building

2.1.1. Human materials

Generic morphological bone models for the lower and upper limbs (LL and UpL, respectively) were collected during past European-funded projects (VAKHUM, see http://www.ulb.ac.be/project/vakhum/, LHDL, see http://www.livinghuman.org/ and DHERgo, see http://www.dhergo.org) from fresh-frozen cadaveric specimens obtained from the Université Libre de Bruxelles (ULB) Body Donation program using medical imaging (Van Sint Jan et al., 2002) (Fig. 1). Due to the complex methodology of the data collections, LL and UpL were obtained on different cadavers.

2.1.2. Lower limb data collection

Twelve of these specimens were used to collect in-vitro LL joint kinematics data for the hip, knee and ankle joints using 6 DoFs instrumented spatial linkage (Sholukha et al., 2004; Van Sint Jan et al., 2006). Hip kinematics data were obtained by manually mobilizing the thigh along each anatomical plane. Knee joint passive motion was collected from full flexion to full extension by pulling on the quadriceps muscle tendon against gravity. Ankle joint passive motion was obtained similarly from full dorsiflexion to full plantarflexion by pulling on the Achilles’ tendon. Results of polynomial fitting of the joint flexion/extension DoF versus five other DoFs for tibiofemoral motion were previously published (Sholukha et al., 2006). Patella-femoral joint six DoFs were fully guided by tibiofemoral joint flexion/extension DoF.

2.1.3. Shoulder complex data collection

Data related to the shoulder complex were not previously published and more details are given here. In-vitro joint kinematic data related to the shoulder complex were collected on 2 fresh-frozen specimens. Before data collection, technical frames (TFs) made of reflective markers were rigidly attached to the segments-of-interest. TF location relative to bone anatomical landmarks (ALs) were obtained from medical imaging by virtual palpation (Van Sint Jan, 2007). Similarly, in-vivo motion data related to the shoulder complex were obtained from 3 volunteers with TF clusters fixed on each segment-of-interest for which ALs were previously manually palpated (Salvia et al., 2009). Motion data were collected along each anatomical planes (passively and actively for the specimens and volunteers, respectively).

2.1.4. Other joints integrated in the model

The overall model also includes supplementary joint models next to the above-mentioned joint segments (see Table 1). These supplementary models are related to the spine, forearm, wrist and ankle joints. Comparison of MBS and MLS results is given in Annex B of the supplementary materials.

2.1.5. Joint center determination

For in-vivo data, all joint centers were obtained from medical imaging. Joint center determination was evaluated using previously-published work based on fitting by primitive geometrical objects (e.g., quadric surfaces for the femoral condyles, or spheres for the femoral head) (van der Helm and Pronk, 1995). The topology of the model is presented in Table 1.

from medical imaging by virtual palpation (Van Sint Jan, 2007). Similarly, in-vivo motion data related to the shoulder complex were obtained from 3 volunteers with TF clusters fixed on each segment-of-interest for which ALs were previously manually palpated (Salvia et al., 2009). Motion data were collected along each anatomical planes (passively and actively for the specimens and volunteers, respectively).

2.1.6. Joint kinematics representation

For the LL bones, anatomical frames (AFs) were built according to the recommendations of the ISB (Wu et al., 2005) to describe results according to clinical conventions. Distal segment (relative to thorax) and joint (relative to proximal link) motion data were derived using body pose representation by translation (origin to origin) and attitude vectors (helical rotation, Capuzzo et al., 1995; Woltring, 1994). For UpL bones, the projections of each DoF related to the clavicle, scapula and humerus pose vectors on the thorax anatomical frame were calculated and retained in an internal look-up table as part of the model. In total 144 (2 proximal bones, 2 linear and parabolic fitting, 6 DoF proximal and 6 DoFs humerus bones) plots were processed by linear and parabolic fittings. Then shoulder pose prediction was implemented as described in the next section.

2.1.7. Weighted multiple regression for the shoulder model

This approach allowed predicting the 6 DoFs-dependent motion of the clavicle and scapula from the combination of up to 6 DoFs humerus behavior relative to the thorax (Sholukha et al., 2011b). Let us define for the current frame of motion $Q_i = \{q_1, ..., q_6\}$, $i = 1, ..., 6$, where $c_i$ and $q_i$ are predefined binary (value 0 or 1) weight coefficients and the value of humerus ith DoF. Then, a set of normalized weight coefficients is defined as $w_i = \frac{q_i}{S}, i = 1, ..., 6$, where $S = \sum_{i=1}^{6} q_i$. These weight coefficients reflect the “weight” of particular humerus DoFs. Using these weights...
Table 1
Topology of the model presented in this paper: multibody system topology (columns 3,4) and segment local coordinate system (LCS, column 9) definitions. \(N_N, N_{ref}-current \) and parent (0 corresponds to GCS) segment numbers and number of joint DoFs respectively (see Fig. 1). Total model DoFs is 144. Column 1: segment index (used in Fig. 1); column 2: segment name. Columns 5–8 show the abbreviations of ALs (Van Sint Jan, 2007) used for segment local coordinate system. See text for further explanations.

<table>
<thead>
<tr>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
</tr>
</thead>
<tbody>
<tr>
<td>(N)</td>
<td>(N_N)</td>
<td>(N_{ref})</td>
<td>(G_1)</td>
<td>(G_2)</td>
<td>(G_3)</td>
<td>(G_4)</td>
<td>LCS</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Pelvis</td>
<td>0</td>
<td>6</td>
<td>(Pi) LIAS</td>
<td>LIPS</td>
<td>RIAS</td>
<td>RIPS</td>
<td>(G_C = (G_1 + G_3)/2; G_R = (G_2 + G_4)/2; v_1 = (G_1 - G_3); v_2 = (G_2 - G_4); Y = [v_0 \otimes v_0]; X = [v_0 \otimes v_1]; Z = [X \otimes Y])</td>
</tr>
<tr>
<td>Lower limbs [LL]</td>
<td>2</td>
<td>Right</td>
<td>1</td>
<td>3</td>
<td>(Th)</td>
<td>(Th)</td>
<td>(G_C = G_1; G_R = (G_1 + G_3)/2; v_1 = (G_1 - G_3); v_2 = (G_2 - G_4); Y = [v_0 \otimes v_1]; X = [v_0 \otimes Y]; Z = [X \otimes Y])</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>Thigh</td>
<td>2</td>
<td>6</td>
<td>RFLE</td>
<td>RFME</td>
<td>RFCH</td>
<td>(G_C = G_{12}; v_1 = (G_2 + G_3)/2; Y = [v_0 \otimes v_1]; Z = [v_0 \otimes Y]; X = [Y \otimes Z])</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>Left</td>
<td>3</td>
<td>6</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>Thigh</td>
<td>1</td>
<td>3</td>
<td>LFME</td>
<td>LFLE</td>
<td>LFCH</td>
<td>()</td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>()</td>
<td>8</td>
<td>6</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>()</td>
<td>9</td>
<td>6</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>Right shank</td>
<td>4</td>
<td>6</td>
<td>RTTC</td>
<td>RFAL</td>
<td>RFAX</td>
<td>RTAM</td>
</tr>
<tr>
<td></td>
<td>11</td>
<td>Left shank</td>
<td>10</td>
<td>6</td>
<td>LTTM</td>
<td>LTAM</td>
<td>LFA</td>
<td>LFL</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>Right foot</td>
<td>5</td>
<td>6</td>
<td>RFM5</td>
<td>RFM2</td>
<td>RFM1</td>
<td>RFCC</td>
</tr>
<tr>
<td></td>
<td>12</td>
<td>Left foot</td>
<td>11</td>
<td>6</td>
<td>LFMM</td>
<td>LFMM1</td>
<td>LFMM5</td>
<td>LFCC</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>Right patella</td>
<td>5</td>
<td>6</td>
<td>RPAX</td>
<td>RPLE</td>
<td>RPME</td>
<td>RPCE</td>
</tr>
<tr>
<td></td>
<td>13</td>
<td>Left patella</td>
<td>11</td>
<td>6</td>
<td>LPAX</td>
<td>LPLE</td>
<td>LPME</td>
<td>LPCE</td>
</tr>
<tr>
<td>Upper body [Upl]</td>
<td>2</td>
<td>Lumbar</td>
<td>1</td>
<td>6</td>
<td>MSJN</td>
<td>MSXS</td>
<td>MTV8</td>
<td>MTV2</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>Thorax</td>
<td>2</td>
<td>6</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>Cervical</td>
<td>3</td>
<td>6</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>Head</td>
<td>4</td>
<td>6</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>Right clavicle</td>
<td>3</td>
<td>3</td>
<td>(Cl)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>12</td>
<td>Left clavicle</td>
<td>3</td>
<td>3</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>Right scapula</td>
<td>6</td>
<td>3</td>
<td>RSRS</td>
<td>RSAA</td>
<td>RSA</td>
<td>RHCH</td>
</tr>
<tr>
<td></td>
<td>13</td>
<td>Left scapula</td>
<td>12</td>
<td>3</td>
<td>LSA</td>
<td>LSR</td>
<td>LSIA</td>
<td>LHCH</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>Right humerus</td>
<td>7</td>
<td>6</td>
<td>(Hu)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>14</td>
<td>Left humerus</td>
<td>13</td>
<td>6</td>
<td>RHLE</td>
<td>LHR</td>
<td>LHLE</td>
<td>LHCH</td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>Right ulna</td>
<td>8</td>
<td>3</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>15</td>
<td>Left ulna</td>
<td>14</td>
<td>3</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>Right radius</td>
<td>9</td>
<td>3</td>
<td>(Ro)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>16</td>
<td>Left radius</td>
<td>15</td>
<td>3</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>11</td>
<td>Right hand</td>
<td>10</td>
<td>3</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>17</td>
<td>Left hand</td>
<td>16</td>
<td>3</td>
<td>()</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

one can predict current values of dependent DoFs \(k = 1, 2\) (clavicle and scapula per three rotations and translations) as \(y^k = \sum_{i=1}^{3} w_i P^k_i(q_i), \quad i = 1, \ldots, 6\), where \(P^k_i(q_i)\) are polynomial regressions or fitting of the dependent DoFs versus humeral ones. In practice, we restricted these polynomials to parabolic representation and have selected only three humeral DoFs (two planar angular elevations, i.e. abduction and flexion, and humeral head vertical translation using \(c_3\)) by analyzing fitting residual values.

At this point, 3D joint models (including geometrical and kinematic data, and AL location) were available for further fusion with individual motion data collected during in-vivo activities using less complex procedures leading to less required anatomical data.

2.2. Individual in-vivo motion data

The method presented in this paper has been developed in order to be used with standard MBS systems (Vicon MX Titan) or single MLS camera (Microsoft Kinect™). Obviously, these two systems have different specifications and qualities. MBS systems have greater accuracy allowing complete 3D (6 DoF) analysis. However, they are relatively costly and time-consuming due to the manual placement of markers being analyzed. MLS on the other hand is less accurate, but is less expensive and allows faster data collection. Integrating both systems into one unique modeling pipeline would allow collecting data according to the user’s requirements and equipment.

Available data for data fusion from both systems are also different although they both allow anatomical landmark (AL) location. MBS systems collect AL data from reflective markers set directly on the subject skin or located through palpation (Van Sint Jan, 2005). The MBS marker model used in this paper was the so-called “Plug-in-gait” model (Vicon™) with supplementary markers on elbow, knee and ankle joints (Fig. 2). MLS ALs were determined from 3D mapping of the subject shape collected from the camera software, and provide estimation of the joint centers (Fig. 2) (Clark et al., 2012).

In-vivo MBS data were collected on 7 healthy adult volunteers. Subjects were asked to perform various movements (deep squatting and large free motion of the upper limbs). On two volunteers, MBS and MLS data were collected simultaneously.
Both MBS and MLS joint 3D pose data were processed frame by frame using a MBA method. The details of the developed multibody model used in this paper are described in Annex A (Supplementary materials). The MBA human skeleton (see Fig. 1) included two tree-structured parts (LL and Upl) both starting from the pelvis (segment 1 in Fig. 1). This allows organizing input data processing according to the available motion data: Upl motion only, LL motion only or simultaneous Upl and LL motions (i.e., during full body analysis).

For each model segment one local coordinate system (LCS) was built from the available ALs as following (see Table 1; columns 5–9). Let us assume \( G_i \), \( i = 7,7^a \) as vector columns \( G_i = (G_{ix}, G_{iy}, G_{iz})^T \) corresponding to the digitized segment AL locations defined in the global CS. The origin of each segment LCS was defined as \( G_i \). In Table 1 symbol \( \circ \) is defined as matrix cross product sign, \( |P| = P_+/P_- \) is norm of the vector column of point \( P \). In order to calculate the ALs in the LCS, let us define from column 9 a rotation matrix \( R = (X, Y, Z) \). In the upright pose left and right patella and shank had the same orientation. For the LL and Upl links (segments [3,4,9,10] and [3–5], respectively) the LCS origin was defined as the mean point of the most proximal surface relative to pelvis. Then, we obtained the vector columns \( I_r = R(G_i-G_r) \), \( r = 7,7^a \), where \( I_r \) are the ALs location in the LCS.

### 2.3. MBA model registration towards individual motion data

MBA registration to the captured motion data, either MBS or MLS, presented in Fig. 2, was based on an inverse kinematics (IK) approach. The purpose of the IK step is to find the set of generalized coordinates (joint angles and positions) for the model that best fits the motion data recorded for a particular subject. The IK process approaches each time step (i.e. motion frame) available from the motion dataset and computes generalized coordinate values which position the model in a pose that fits input AL coordinates for that particular time step. Mathematically, this AL fit was expressed as a weighted least squares problem with constraints, whose solution is aimed to minimize both AL and generalized coordinate errors. The weight coefficients must take into account the accuracy of the input ALs and generalized coordinates. This registration was achieved through the implementation of a multi-stage processing pipeline (Fig. 3). The entire motion reconstruction (IK & optimization) method has been implemented in MATLAB® using “Optimization Toolbox”.

The available subject’s MBS or MLS data are first analyzed to select the most appropriate generic model from the available above-described GM database. Then, the selected GM data are scaled to each subject’s data to create the final model including anatomically and physiologically acceptable joints and bones with relevant bony landmarks required for ALs processing. The next sections present the developed pipeline components.

#### 2.3.1. Input data and GM selection

The subject’s anthropometric data (Table 2) was used for generic model scale factors evaluation. Subject data related to segment kinematics were stored in global coordinate system (GCS). The dataset directly obtained from the MLS hardware (see Fig. 2) defined the spatial trajectories of the subject joints defined in the GCS. In order to get reliable data for GM selection and scaling a static upright pose of the volunteer must be captured. This pose also could be used to convert MLS data into MBS coordinate system for motion comparison (as illustrated in the video files available from the Supplementary material). The MBS data collection used in this paper protocol required 34 reflective markers (see Fig. 2). The amount of available DoFs was 144 (see Table 1), but depending on the task performed by the subject some DoFs kinematics could be constrained or frozen.

![Fig. 2](image.png)

**Fig. 2.** Data input required by the MBA model according to the available motion analysis systems. MBS dataset (small spheres in pictures) included 34 ALs corresponding to the Plug-in-Gait dataset with supplementary ALs located on the medial malleolus, medial femoral condyle, medial humeral condyle and humeral greater tuberosity. The 20 ALs available from the MLS dataset (large spheres) are directly obtained from the MLS hardware.

for results comparison. These particular motions were selected because of some constraints rising from the use of a single MLS camera. Indeed, a full gait is not possible with MLS, and a possibly useful alternative was found in squatting (performed mainly in the sagittal plane like walking). Upper limbs motions adopted in this study were based upon clinical tests such as the Mallet score (van der Sluijs et al., 2006).
surfaces of the ribs (see also supplementary movie (Ludewig et al., 2009, 2010; Lunden et al., 2010). The data has been palpation. A for a full description of the method algorithm).

Results

For the upper limb. Two of the main GM joint kinematic constraints were based on regression relationships between the estimated DoFs (e.g. joint flexion/extension or humerus relative to thoracic elevations) and the supplementary ones (e.g. clavicle and scapula poses). For the knee (including patello-femoral joint) and ankle joints a one-DoF mechanism was used (Sholukha et al., 2006). For the shoulder rhythm mechanism we used our own data (Sholukha et al., 2011b) compared with data available from the literature (Ludewig et al., 2009, 2010; Lunden et al., 2010). The data has been processed using the above-described shoulder rhythm algorithm. Similar to (Hill et al., 2008; van der Helm, 1994; Veeger and van der Helm, 2007) scapula motions were further constrained by ellipsoidal surfaces derived by fitting lateral exterior surfaces of the ribs (see also supplementary movie files).

Table 2

<table>
<thead>
<tr>
<th>N</th>
<th>Name</th>
<th>ALs</th>
<th>Distance (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Pelvis width</td>
<td>RIAS-LIAS</td>
<td>232</td>
</tr>
<tr>
<td>2</td>
<td>Trunk height</td>
<td>LS-C7</td>
<td>474</td>
</tr>
<tr>
<td>3</td>
<td>Trunk width</td>
<td>RCAJ-LCAJ</td>
<td>341</td>
</tr>
<tr>
<td>4</td>
<td>Right arm</td>
<td>RCAJ-RHLE</td>
<td>349</td>
</tr>
<tr>
<td>5</td>
<td>Right forearm</td>
<td>RHLE-RRSSP</td>
<td>270</td>
</tr>
<tr>
<td>6</td>
<td>Left arm</td>
<td>LCAJ-LHLE</td>
<td>346</td>
</tr>
<tr>
<td>7</td>
<td>Left forearm</td>
<td>LHLE-LRSSP</td>
<td>270</td>
</tr>
<tr>
<td>8</td>
<td>Right thigh</td>
<td>RFTC-RFLE</td>
<td>409</td>
</tr>
<tr>
<td>9</td>
<td>Right shank</td>
<td>RFAX-RFAL</td>
<td>379</td>
</tr>
<tr>
<td>10</td>
<td>Left thigh</td>
<td>LFTC-LFLE</td>
<td>404</td>
</tr>
<tr>
<td>11</td>
<td>Left shank</td>
<td>LFAX-LFAL</td>
<td>381</td>
</tr>
<tr>
<td>12</td>
<td>Right foot</td>
<td>RFCC-RFM2</td>
<td>186</td>
</tr>
<tr>
<td>13</td>
<td>Left foot</td>
<td>LFCC-LFM2</td>
<td>181</td>
</tr>
</tbody>
</table>

3. Results

Fig. 4 shows results of the GM-to-subject fusion using data obtained from a volunteer. LL GM contains (see Table 1) 13 links (each femoral bone was divided in three parts to allow neck and femoral condyle segments pose adaptation if individual subject specific data are available), 39 (13 × 3) heterogeneous scale factors and 72 (6+2 × 5 × 6 +2 × 3) DoFs. Joint ranges of motion were limited by box constrains with optional DoF freezing. Kinematic constraints for knee, patella and ankle joints were implemented following (Sholukha et al., 2006). The 3 parts of the femoral bones allowed adaptation of the femoral neck and condyles size according to the subject data.

Fig. 5 shows LL joint kinematics (i.e., angular velocity and accelerations) comparison (MBS versus MLS) for squat motion using (Grood and Suntay, 1983) convention versus joint flexion/extension motion. The MLS input data frequency was not constant and had to be reframed at equal frequency (25 frame/s), smoothed by cubic spline and synchronized with MBS data. The MBS input data was reframed accordingly to allow further comparison. The range and shape of the estimated accelerations plots are similar for both kinds of input data (e.g. [−200,200] deg/s²) for both knee flexion/extension (|0,120| deg). Both datasets show some hysteresis behavior of accelerations, which could be explained by a gravity factor or partly by soft tissue (reflective markers) motions. Comparable results are obtained for both MBS and MLS graphs (see also Tables 1 and 2 in the Annex B of the Supplementary materials). Mean differences varied from 1.2 to 11.9 for the lower limbs and from 1° to 14.8° for the upper limb. Note that larger discrepancies were expected for some DoFs (such as humerus internal/external rotation) due to the MLS hardware limits. For the hip joints, results are similar for joint amplitude until about 90°; for larger amplitude (>90°) discrepancies appear (up to 30°) because of the nature of the deep squatting movement, requiring a large hip and knee flexion, which led to a poor visibility of the hip area by the single camera MLS because the thigh is perpendicular to the camera.

Fig. 6 shows the results of the GM-to-subject fusion using data obtained from a volunteer. Upl. GM contains 17 links, 51 (17 × 3) scale factors, 72 (5 × 6+2 × 5 × 3 +2 × 6) DoFs. Joint range of motion was limited by box constrains with optional DoF freezing. Kinematic constraints for clavicle and scapula joints were implemented following the above-described shoulder rhythm and scapula-thoracic gliding constraints.

Fig. 7 shows the comparison between results obtained from MLS and MBS data for both humeral bones. Humeral elevations are angles in different planes due to natural motion of the humerus (see “Hand_Motion.mp4” in the Supplementary materials). The gleno-humeral joint center translations are given relative to the thorax LCS (see Table 1). Mean differences for the plots from Fig. 7 are presented in Table 3. The two last columns of the Table 3 report the maximal difference in the glenohumeral center position.

4. Discussion

The presented results and kinematics analysis show that MBS and MLS model-based reconstructions are comparable for the
shoulder, elbow, hip and knee joints (for more detailed results see Annex B). For MLS data, results for other joints (i.e., wrist, forearm, and ankle joint) are less accurate because of the intrinsic limitations of the MLS hardware that does not include enough raw information to represent the real joint behavior of the subject being analyzed. Spine behavior integrated in the model is entirely the results of optimization. The reconstructed shoulder rhythm agrees with the works of Ebaugh and Spinelli (2010) and San Juan and Karduna (2010). Also, knee motion, including patellar displacement in both models, agrees with the descriptions by Hinterwimmer, et al. (2004) and von Eisenhart-Rothe et al. (2004). Furthermore, for the joints for which MLS and MBS appear

Fig. 5. Kinematics comparison [(Grood and Suntay, 1983) convention] between MLS and MBS data for hip (A) and knee (B) joints. Flexion/extension angular velocity and acceleration versus joint flexion/extension are given for each side (right and left). Red and blue colors correspond to flexion and extension respectively. MLS results: small dots; MBS results: large dots. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Please cite this article as: Sholukha, V., et al., Model-based approach for human kinematics reconstruction from markerless and marker-based motion analysis systems. Journal of Biomechanics (2013), http://dx.doi.org/10.1016/j.jbiomech.2013.07.037
comparable, MLS data collection could then be an interesting alternative for collecting data in settings where a cumbersome MBS system is difficult to use (for example, at a patient’s home).

A model-based registration method allows fusion of motion analysis data with both 3D bone morphology, soft tissue information (e.g. muscle line-of-actions) and joint kinematics (Sholukha et al., 2011c). The major advantages of the new method compared to the previously-published method (Sholukha et al., 2006; Anguelov et al., 2005; Brubaker et al., 2010) is the fusion of an anatomically-detailed generic model (including bone models and joint kinematics model) with motion data obtained from specific subjects’ performing activities. The method presented in this paper has been implemented for motion data collected from conventional MBS systems and MLS cameras. The accurate underlying generic data and the presented method should allow further estimation of biomechanically-relevant information related to muscle behavior such as muscle excursion or moment arms.

Fusion results are, however, sensitive to the original accuracy of both morphological and kinematic data. Artifacts may arise due to the soft-tissue deformation during the data collection performed on the subject undergoing the clinical data collection. The iterative registration procedure described in this paper allows a relatively comfortable parameter adjustment in order to compensate for these artifacts. Validation and quality checking of the results was performed by analyzing the fusion residual error and by visualization of the final results (for example, a non-physiological joint

**Table 3**

<table>
<thead>
<tr>
<th></th>
<th>R_El (deg)</th>
<th>L_El (deg)</th>
<th>R_X (mm)</th>
<th>R_Y (mm)</th>
<th>L_X (mm)</th>
<th>L_Y (mm)</th>
<th>R_dist (mm)</th>
<th>L_dist (mm)</th>
<th>R_max (mm)</th>
<th>L_max (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>9.7</td>
<td>5.2</td>
<td>5.6</td>
<td>6.1</td>
<td>3.1</td>
<td>2.7</td>
<td>1.9</td>
<td>1.0</td>
<td>10.1</td>
<td>4.6</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Fig. 6.** Screen snapshots of simulation results from model-based GM registration to MLS data (large spheres). Both clavicle and scapula motion guided by humerus motion and gliding plane constraints (shoulder rhythm). See “Hand_Motion.mp4” file in the Supplementary materials.

**Fig. 7.** Humerus motion relative to thorax LCS. Top graphs: left humerus; bottom graphs: right humerus motions. Left graphs: humerus elevation. Right graphs: gleno-humeral joint center anterior (blue line) and superior (green line) translations. All data are given relative to time. MBS results—thick dashed lines; MLS results—thin lines. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)
behavior, such as joint segment penetration and dislocation, would indicate poor results).

Current drawbacks of the method include the need for large in-vitro range of motion matching the amplitude of the motion data collected from the analyzed subject; this can be a drawback when collecting in-vitro data required for GM building using elderly specimens with limited joint amplitude.

Results include data (6-DoFs joint kinematics, motion data and bone orientation with muscle attachment) of interest for fundamental and clinical analysis, and in medical education. Bone models are not directly obtained from the subject undergoing the motion analysis because it requires irradiation of the subject and time-consuming processing. Therefore, the morphology of the available generic bone models will not exactly reflect the specific subject’s morphology. Solutions to allow local bone deformations, e.g. both femoral bones, should help to solve this problem.

As the results indicated, some limited discrepancies appear between the MBS and MLS (e.g., for hip flexion higher to 90°). It means that MLS should not be used for analyzing such large hip motion amplitudes (note that in rehabilitation of severe joint disorders such amplitude is not required). Currently, we are developing an advanced post-processing algorithm based on the original 20 MLS points to obtain 34 points similar to the plug-in-gait model used by the MBS. This algorithm keeps the limb lengths constant (based on a reference upright static pose) taking into account external environment constraints (e.g. feet on the floor), and is based on joint physiological constraints (e.g. knee and elbow range of extension). This algorithm also includes point trajectories smoothing using smoothing parameters related to the nature of the motion being processed. These new developments will allow substantial improvements of the final results.

Further studies, using the presented methods, should improve the ability to interpret musculoskeletal mechanisms in biomechanical and clinical researches, for example by analyzing the muscle behavior (i.e., instantaneous muscle length and moment arms) in normal and pathological subjects (Sholukha et al., 2011c). Advanced computer graphics visualization and user interface allow animating fusion results (see supplementary movie) and measurement graphs simultaneously.

Conflict of interest

We also certify that there is no conflict of interest, and that this paper content has not been published or submitted elsewhere.

Acknowledgments

This work was funded by the European Commission through the VAKHUM (IST-1999-10954), LHDIL (IST-2004-026932) and DHCP (SCP-7a-2008-218525) projects, and by the Brussels Government through the ICT4Rehab project (2010/PFS-ICT03). Special thanks to Mr. H. Bajou and J.-L. Sterckx for their technical assistance.

Appendix A. Supplementary materials

Supplementary material associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.jbiomech.2013.07.037.

References


