HBM2 - Reference Manual

HBM-Gait

SW011-7001-1.0

Preface

Motek provides innovative products for rehabilitation, orthopedics, neurology, performance enhancements and research. Motion platforms, instrumented treadmills, motion-capture systems and surround sound are combined with integrated Virtual Reality (VR) environments to train movement functions and improve (dynamic) stability.

We hope you will enjoy using the HBM and that it helps you to improve clinical care.

Regards,
Motek

Contents

1. Introduction

This document describes the Human Body Model for clinical gait analysis (HBM-Gait) developed by Motek, which is a partial model of the HBM as described by van den Bogert et al. (2013). The model is specifically designed for real-time biomechanical analysis of joint kinematics and kinetics, as well as estimation and visualization of muscle function during gait. HBM was updated in 2017 to meet the current state of the art in the field of gait analysis and biomechanical research. This version of the model was adapted to meet the gait conventions used in clinical practice.

Marker movement and (ground) reaction forces are measured and provided as input in a biomechanical model to calculate joint angles and joint torques produced by the skeletal muscles. The HBM model takes it one step further by using an optimized muscle model to calculate muscle forces. These real-time calculated muscle parameters and motion variables can be used to provide immediate feedback to both operator and subject. The HBM model can also be applied off-line using the Gait Offline Analysis Tool.

Kinematic analysis is done using a global optimization method. This makes the model less sensitive to marker drop-outs and skin artifacts, which are inevitable in motion capture.

The muscle model used in HBM contains information on muscle locations and parameters which is not subject specific, but based on data of healthy adults. This needs to be taken into consideration when using the muscle outputs of the model in subjects in which the control of muscles or the parameters of the muscle have changed.

Changes in the 2017 update

Originally, HBM was initialized by recording an initialization pose in which subjects had to stand straight and symmetrically, with feet pointing forward. However, not all subjects are able to assume this pose due to for example spasms or bone deformities. This might lead to incorrect locations of the knee and ankle joint axis and therefore incorrect data. The updated HBM uses medial markers on the knee and ankle to make the model initialization less pose dependent. Furthermore, joint centers of the knees and hips can now also be estimated using functional calibration methods. All changes incorporated in the updated model are listed below:

- The model is now available with or without a trunk segment.
- The predictive method used in hip joint estimation is changed from the method proposed by Bell et al. (1989) to linear regression equations proposed by Harrington et al. (2007).
- The proximal trunk joint has been relocated to the T10/T11 joint based on data from Bruno et al. (2015).
- Medial epicondyle and medial malleolus markers (LMEK, RMEK, LMM and RMM) are added. These markers are only used during calibration and can be removed during the walking trial.
- Segment definitions have been changed to match ISB recommendations (Wu et al. 2005) and clinical gait analysis practice more closely (see Section 4).
- Functional hip and knee calibration procedures, using separate range of motion trials, to determine hip and knee joint center and knee joint axis are available.

- Muscle volume weighting is now applied in muscle solver.
- Internal muscle model updated to gait2392 model (Delp et al. 2007).

Changes in marker set

- The C7 marker is added to the trunk segment to improve accuracy of trunk movement analysis.
- LGTRO and RGTRO (greater trochanter) markers are removed to avoid soft tissue artifacts associated with this marker.
- SACR (sacrum) and NAVE (navel) markers are removed as they are no longer necessary for visualization, and to avoid soft tissue artifacts associated with these markers.
- The TOE marker is moved from the tip of the big toe to the caput of the 2nd metatarsal bone, and is now called MT2.
- Several marker names are changed. STRN marker is now called JN (jugular notch), XYPH changed to XIPH, FLTHI/FRTHI changed to LLTHI/RLTHI, and LATI/RATI are now called LLSHA/RLSHA.
- The placement of the thigh and shank markers has changed.

2. Marker set

HBM-Gait uses a marker set containing 26 markers (Figure 1, Table 1) to create a skeleton model and to solve skeleton motion. This includes four trunk markers which can optionally be placed depending on the kinematic parameters of interest. Each marker is assigned to a certain body segment and has its own weighting for the appropriate segment.

The bold markers in Table 1 and green markers in Figure 1 are anatomical markers needed to define the joint centers and segments of the model during initialization. These markers need to be placed accurately in order to get reliable results. The other markers are technical markers providing redundancy and robustness for the model. Therefore, placement of these markers is less critical. They are also used for the functional calibration of the knee and hip.

Note that the medial markers on the knee and ankle (LMEK, LMM, RMEK, and RMM) can be removed after model initialization since these are only used during initialization to determine joint centers and segment reference frames. This feature was added because these markers often tend to detach during gait.

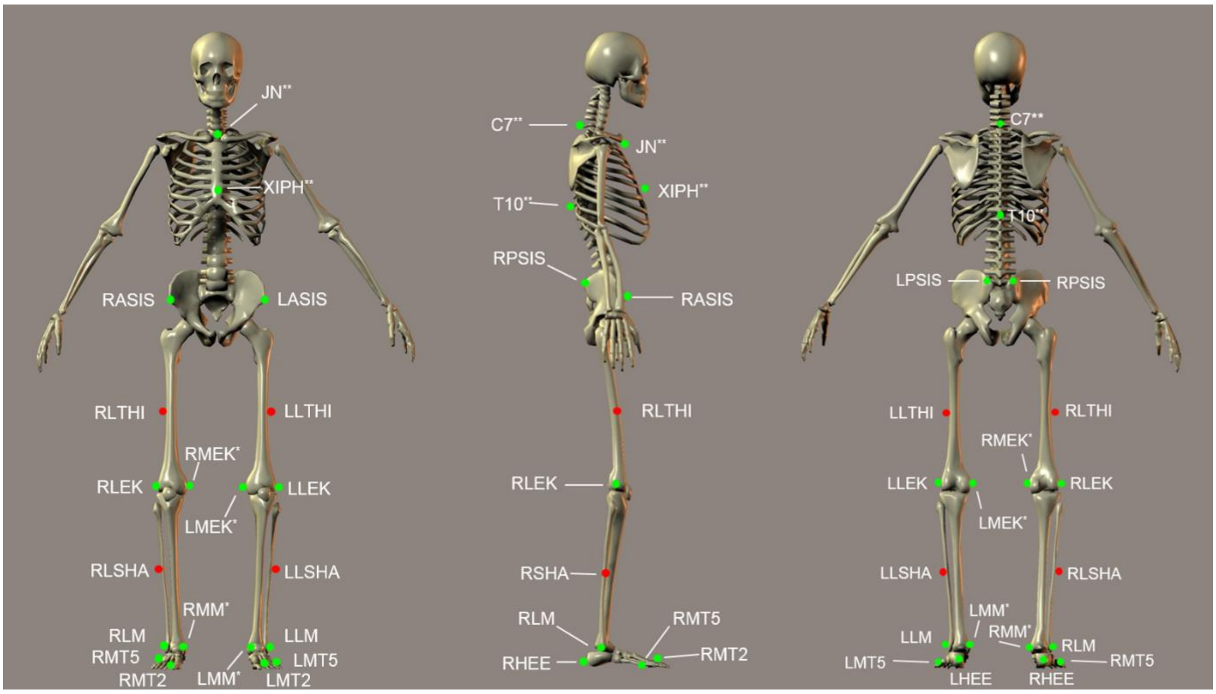

Figure 1. Front, side, and rear view of the marker set used in HBM-Gait. Green markers are anatomical markers used to define the skeleton during initialization.
*These markers are optional. If used, they may be removed after model initialization.
** These markers are optional and only need to be used if trunk kinematics are desired.

Table 1. Marker placement of the marker setup used in HBM-Gait. Bold markers are anatomical markers used to define the skeleton during initialization.

No.	**Marker**	**Position**	**Placement remarks**
1	**C7****	**C7**	**On the 7th cervical vertebra**
2	**T10****	**T10**	**On the 10th thoracic vertebra**
3	**XIPH****	**Xiphoid process**	**Xiphoid process of the sternum**
4	**JN****	**Jugular notch**	**On the jugular notch of the sternum**

5	**LASIS**	**Pelvic bone left front**	**Left anterior superior iliac spine**
6	**RASIS**	**Pelvic bone right front**	**Right anterior superior iliac spine**
7	**LPSIS**	**Pelvic bone left back**	**Right posterior superior iliac spine**
8	**RPSIS**	**Pelvic bone right back**	**Right posterior superior iliac spine**
9	LLTHI	Left thigh, lateral	1/2 on the line between the left greater trochanter and LLEK
10	**LLEK**	**Left lateral epicondyle of the knee**	**On the lateral side of the joint axis**
11	**LMEK***	**Left medial epicondyle of the knee**	**On the medial side of the joint axis. Check by holding both points and bending the knee; markers should not/hardly move.**
12	LLSHA	Left shank, lateral	1/2 on the line between LLEK and LLM
13	**LLM**	**Left lateral malleolus of the ankle**	**The center of the left lateral malleolus**
14	**LMM***	**Left medial malleolus of the ankle**	**Most pronounced part of the left medial malleolus**
15	**LHEE**	**Left heel**	**Center of the heel at the same height as LMT2**
16	**LMT2**	**Left 2nd meta tarsal**	**Caput of the 2nd meta tarsal bone, on joint line midfoot/toes**
17	**LMT5**	**Left 5th meta tarsal**	**Caput of the 5th meta tarsal bone, on joint line midfoot/toes**
18	RLTHI	Right thigh, lateral	1/2 on the line between the right greater trochanter and RLEK
19	**RLEK**	**Right lateral epicondyle of the knee**	**On the lateral side of the joint axis**
20	**RMEK***	**Right medial epicondyle of the knee**	**On the medial side of the joint axis. Check by holding both points and bending the knee; markers should not/hardly move.**
21	RLSHA	Right shank, lateral	1/2 on the line between RLEK and RLM
22	**RLM**	**Right lateral malleolus of the ankle**	**The center of the right lateral malleolus**
23	**RMM***	**Right medial malleolus of the ankle**	**Most pronounced part of the right medial malleolus**
24	**RHEE**	**Right heel**	**Center of the heel at the same height as RMT2**
25	**RMT2**	**Right 2nd meta tarsal**	**Caput of the 2nd meta tarsal bone, on joint line midfoot/toes**
26	**RMT5**	**Right 5th meta tarsal**	**Caput of the 5th meta tarsal bone, on joint line midfoot/toes**

*These markers are optional. If used, they may be removed after model initialization.

** These markers are optional and only need to be used if trunk kinematics are desired.

3.Model Initialization

Static initialization of the model is done by recording an initialization pose. Optionally, functional hip and knee joint calibrations can be performed. The functional calibrations have to be performed before the static calibration, to be incorporated in the model. When the static calibration is done prior to the functional calibration, the functional calibration will remain unused until a new static calibration is performed.

For most patients, static model calibration is preferred as functional joint calibration requires the subject to perform complex calibration motions with extensive ranges of motion in both the hip as well as the knee. Recent research also suggests that locating the hip joint center using the Harrington equations generally works as well as, or better than, functional calibration (Peters et al. 2012; Sangeux et al. 2011; Sangeux et al. 2014).

3.1 Static Initialization

The static calibration can be done with or without the use of medial knee and ankle markers. In earlier versions of HBM, these medial markers were not included in the marker set. Using the medial markers makes the initialization less pose dependent, which will especially be helpful with subjects who are not able to assume the initialization pose. The calibration without medial markers is still available.

During initialization the position of joint centers, bone lengths, and joint axes are estimated based on:

- Marker coordinates during initialization pose
- Marker diameter [m]
- Knee width [m] (when no medial markers are used)
- Ankle width [m] (when no medial markers are used)

To estimate mass properties of the body segments, the following additional information is needed:

- Subject weight [kg]
- Subject gender

To perform the static initialization, the subject is placed in an initialization pose. The exact execution of the pose is essential when no medial markers are used, since the calibration will be pose dependent in that case. However, even when medial markers are used try to meet the following guidelines as well as possible:

- The subject should stand upright, looking forward. The direction the subjects is facing is not important, since the software automatically compensates for this direction.
- Feet should be pointing forward, approximately at hip width. This can be confirmed by doing knee bends in which the distance between the knees should remain constant.

3.2 Functional hip joint calibration

A functional hip joint calibration can be performed to determine the joint center of the hip. Subjects should start by standing upright, thereafter; the subject has to perform a star arc movement, which was found to be the movement which leads to the most accurate results according to Camomilla et al. (2006). The star arc movement described in Camomilla et al. (2006) is slightly adapted since excessive hip extension causes significant skin movement artifacts. The adapted star arc consists of five different movements as described below (Figure 2):

1. Hip flexion, then back to neutral.
2. Combination of hip flexion and abduction, then back to neutral.
3. Hip abduction, then back to neutral.
4. Combination of hip extension and abduction, then back to neutral.
5. A full circumduction movement is made with the hip.

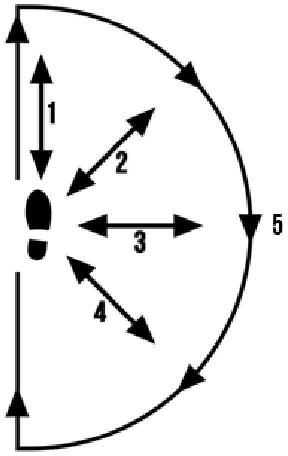

Figure 2. Transverse view of the five movements of the star arc for the calibration of the right hip.

To create as little as possible soft tissue movement in the thigh, subjects should be asked to avoid internal and external rotation of the hip and to minimize frontal rotation of the pelvis (Leardini et al. 1999). Please note that the star motion has to be performed for each leg individually. To use the functional hip calibration, HBM requires a minimal range of motion of 60 degrees of flexion/extension and 30 degrees of abduction (Kainz et al. 2015).

3.3 Functional knee joint calibration

Similar to the functional hip joint calibration, subjects should start by standing upright. Subjects should flex and extend the knee about five times through a range of approximately 0 to 90° of flexion. This calibration also needs to be done for each leg individually.

4. Skeleton Model

The skeleton model is designed for real-time biomechanical analysis of the lower body (especially gait analysis), and involves all kinematic degrees of freedom (DOF) in the lower limbs which are controlled by muscles. The optional trunk is modeled as two segments which are coupled to give three degrees of freedom. Figure 3 shows the 9-segment skeleton model, which has a total of 21 DOF.

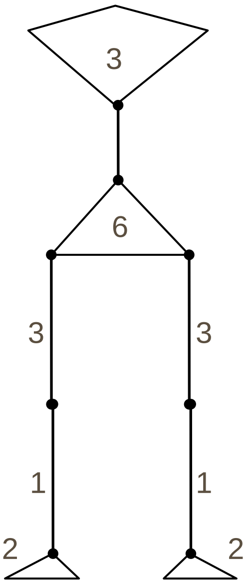

Figure 3. Hierarchy of the skeleton model: The pelvis is the root segment, which has six degrees of freedom (DOF) relative to the world. Numbers besides the segments represent the DOF added by that segment. The two DOFs of ankle and subtalar joint are combined in this diagram. The total number of DOF of the skeleton model is 21.

HBM generates the following list of body segment names:

- Pelvis
- Abdomen
- Thorax
- RFemur
- LFemur
- RShank
- LShank
- RFoot
- LFoot

For each segment a reference frame is needed to define the equations of motion (Figure 4). These segment reference frames are defined only once during model initialization. Thereafter, the segments' marker coordinates and joint centers are expressed as constants relative to these reference frames. During motion, the markers and joints define skeleton motion via the inverse kinematics as described in Section 5.1.

As a general principle, the origin of each segment is placed in the proximal joint (i.e. the connection onto the parent bone), except for pelvis, which is the root of the hierarchy. As a general rule, the segment Z-axis is defined to go through its distal joint (when available). This is also consistent with de Leva (1996), so that the local X- and Y-coordinates of the center of mass, for all segments, are zero. The segment Z-axis will generally point up when standing upright. This means the centers of mass in the leg segments have negative Z-coordinates. The advantage of defining the Z-axis this way is that the model stands perfectly straight when all rotations are zero (except in the ankles). Rotations are then easier to interpret.

Joint axes are defined so that kinematic data are compatible with standards used in clinical gait analysis. These are based on the ISB standards (Wu et al. 1995, 2002, 2005), unless when these are not practical for clinical use.

Joint axes are also needed to constrain the motion of the model, so that the model represents muscle function, and not the small motions (e.g. knee abduction and rotation, joint translations) that are not controlled by muscles. Compared to the full body model, the positive angles reported in HBM-Gait are adapted to meet standards used in clinical gait analysis. These angles will be found in the .mox files recorded with D-Flow as well as in the gait reports of the Gait Off-line Analysis Tool. They will deviate from angles in the .txt file recorded by D-Flow, since this file contains the angles from the original full body HBM. The following adaptations are applied to the angles:

Joint kinematics

- Pelvic flexion: Inverted
- Pelvic rotation: 180 (or -180) degrees offset to get the pelvic rotation near zero during a neutral pose
- Left hip abduction: Inverted
- Right hip abduction: Inverted
- Left ankle flexion: inverted and a 90 degrees offset to get the ankle flexion near zero during a neutral pose
- Right ankle flexion: inverted and a 90 degrees offset to get the ankle flexion near zero during a neutral pose

The remainder of this section describes the definitions of the segments and how these are constructed during the model initialization. As the origin of each segment is placed in the proximal joint, the segments are described bottom up starting with most distal joint (the foot) working back up towards the parent segment and end with the trunk. For each segment the construction of the proximal joint center is described first, as this will be the origin for the segment reference frame (which is described second). Finally the joint axes and joint angles are described.

4.1 Foot

Joint centers

Ankle joint

The ankle joint center is assumed to be the midpoint between the lateral and medial malleolus. If both lateral and medial ankle markers are available, the ankle joint center is defined as midpoint between these two markers. When no medial malleolus marker is used, the ankle joint center will be defined as ‘half of ankle width + marker radius’ medial to the lateral marker. Medial direction in this case is a horizontal projection of the vector from RASIS to LASIS.

Subtalar joint

According to van den Bogert et al. (1994) the subtalar joint center is defined 12mm below the ankle joint center. In HBM, this is implemented as a displacement along the X-axis of the foot. This proposed 12mm was scaled by tibia length as follows:

$$\text{Tibia length}/0.375 * 12$$

in which tibia length is the distance between lateral knee and ankle markers.

Reference frame

The origin of the foot is located in the subtalar joint center. The Z-axis is parallel to the vector from MT2 to HEE markers (which should be horizontally when the foot is flat on the ground) and points posteriorly. In this way HBM will report a 90° flexion angle when standing in neutral pose. The X-axis is based on the Z-axis and a temporal Y-axis, for which two possibilities exist, depending on the presence of the medial ankle marker. When a medial marker is present, a temporal Y-axis between the lateral and medial malleolus pointing to the left is defined. In case the medial marker is not present, the temporal Y-axis is parallel to the vector between the two ASIS markers and pointing to the left. The X-axis is the cross product of the temporal Y-axis and the Z-axis, and will point dorsally. The Y-axis is the cross product of the Z- and X-axis.

Note that in the HBM-Gait the 90° flexion angle is reported as 0° to suit with clinical standards. Since the flexion angle is inverted, a positive angle means dorsal flexion and a negative angle means plantar flexion relative to the neutral position.

Joint axes and joint angles (degrees of freedom)

The ankle is modeled as two hinges, based on Isman's normative data (van den Bogert, et al. 1994; Isman and Inman 1969). Using three hinges would lead to overestimation of muscle forces as in Burdett (1982), a problem nicely described by Glitsch and Baumann (1997). Between the two joint axes a distance of 12 mm is assumed according to van den Bogert et al. (1994) which is scaled in HBM by tibia length as mentioned above. A talus segment is not explicitly defined, since its mass can be ignored and only has a kinematic role. The ankle thus has two degrees of freedom, which are plantar flexion (rotation about the Y-axis of the shank reference frame; dorsal flexion is positive) and pronation/supination (rotation about the pronation/supination axis; pronation is positive). The pronation/supination axis is not aligned with the foot coordinate axes, but is defined in the foot reference frame using the average subtalar joint (STJ) in Isman and Inman (1969) and points forward. According to Isman and Inman, the STJ is inclined 42 degrees from the horizontal plane, and deviates 23 degrees medially from the sagittal plane. Therefore, our STJ axis is for the right foot:

$$STJ = \begin{bmatrix} \cos(42°)\cos(23°) \\ \cos(42°)\sin(23°) \\ \sin(42°) \end{bmatrix}$$

4.2 Shank

Knee joint center

Three different methods can be used to determine the knee joint center. Two different methods for static initialization are available, and one method is available for functional knee calibration. The knee joint center is assumed to be the midpoint between the lateral and medial epicondyle. If both lateral and medial knee markers are available during static initialization, the knee joint center is defined as midpoint between these two markers. When no medial knee marker is used, the knee joint center will be defined as 'half of knee width + marker radius' medial to the lateral marker. Medial direction in this case is a horizontal projection of the vector from RASIS to LASIS.

In case of functional knee calibration, knee axes are estimated using the axis of rotation estimation method by Gamage and Lasenby (2002), as was recommended by Van Campen et al. (2011) and MacWilliams (2008). This method assumes that the markers on the shank (LM, MM, and LSHA) rotate about a fixed axis of rotation relatively to the thigh. A least squares cost function is used to find the best fitting axis. The knee joint center is defined as the projection of the midpoint between the medial and lateral epicondyle onto this axis.

Reference frame

The origin of the shank is located in the knee joint center. The negative Z-axis points towards the ankle joint center. A temporal Y-axis is constructed along the ankle axis and points to the left (see section 4.1). The X-axis is the cross product of the Z-axis and the temporal Y-axis. The Y-axis is the cross product of the Z- and X-axis to ensure orthonormality.

Joint axes and joint angles (degrees of freedom)

The knee is modeled as one hinge, since Glitsch and Baumann (1997) have shown that this is best for the analysis of muscle function and estimation of muscle forces. Also, the abduction/adduction range of motion is very small. As to internal/external rotation, the knee does have a 45 degrees range of motion when flexed 90 degrees. During gait however, the knee is extended so there will be little internal/external rotation. Therefore, modeling these movements would most likely reflect inherent crosstalk errors in the 3D kinematic calculations, rather than a true anatomical movement (Ramakrishnan & Kadaba 1991). Thus, the knee has one degree of freedom, which is flexion/extension (rotation around the Y-axis; flexion is positive). Ab/adduction and internal/external rotation angles are constant, set during initialization.

4.3 Thigh

Hip joint center

A predictive method has to be used to determine the hip joint center (HJC) in case of the static model initialization, while a functional approach is used in case of functional hip calibration. Several studies comparing different methods of HJC estimation (Assi et al. 2016; Kainz et al. 2016; Peters et al. 2012; Sangeux et al. 2011; Sangeux et al. 2014) showed that the method of Harrington et al. (2007) is the most accurate predictive method.

The most accurate functional approach was found to be the geometric sphere fit method by Gamage and Lasenby (2002) (Kainz et al. 2015; MacWilliams 2008; Sangeux et al. 2011; Sangeux et al. 2014). Hence, these two methods are implemented in the HBM.

Harrington equations

The Harrington equations (Harrington et al. 2007) are linear regression equations to predict the location of the HJC based on pelvic width and pelvic depth. Pelvic width is defined as the distance between the two ASIS markers, while pelvic depth is defined as the distance between the midpoints of the line segments connecting the two ASIS and the two PSIS.

Geometric sphere fit

The “bias compensated least squares method” by Halvorsen (2003), based on the geometric sphere fit method by Gamage and Lasenby (2002) is used to estimate the HJC. This method assumes that each marker on the thigh (LTHI, LEK, and MEK) is moving along a trajectory on the surface of a sphere with the center at the HJC. The location of the HJC is estimated based on these markers during an iterative algorithm, in which a correction for the bias due to measurement noise is performed every iteration until convergence is reached.

Reference frame

The origin of the thigh is located at the hip joint center. The negative Z-axis points towards the knee joint center. A temporal Y-axis is constructed along the knee axis and points to the left. When only static model initialization is used, this is a vector through the lateral epicondyle and the knee joint center. Note that when medial markers are used to determine the knee joint center, a misplacement of these markers will result in a rotated thigh reference frame. This in turn will result in an offset in the internal or external hip rotation. In case of the functional knee calibration, the temporal Y-axis is along the functional axis of rotation. The X-axis is the cross product of the Z-axis and the temporal Y-axis. The Y-axis is the cross product of the Z- and X-axis.

Joint axes and joint angles (degrees of freedom)

The hip has three degrees of freedom, which are rotations around the Y-axis (hip flexion; flexion is positive), X-axis (hip ab/adduction; adduction is positive), and Z-axis (hip rotation; internal rotation is positive).

4.4 Pelvis

Reference frame

The origin of the pelvis is defined as the midpoint between the two ASIS markers. The Y-axis is defined as the vector from RASIS to LASIS. The Z-axis is the cross product of the Y-axis and a temporal X-axis, which is a vector from the midpoint between the two PSIS markers to the midpoint between the two ASIS markers. Subsequently, the X-axis is the cross product of Y and Z.

Joint axes and joint angles (degrees of freedom)

The pelvis has six degrees of freedom relative to the lab origin, which are implemented as three global translations (X, Y, and Z) of the pelvis origin, and rotations about the Y-axis (pelvic tilt; forward tilt is positive), X-axis (pelvic obliquity; Left drop/right lift is positive), and Z-axis (pelvic rotation; left twist is positive).

4.5 Trunk

The trunk is modeled as two rigid segments for which statistical models were used that predict mass properties (de Leva 1996). These segments are coupled so that there are only three degrees of freedom. This allows the trunk to flex, bend, and twist realistically without having to solve extra degrees of freedom which would be noisy and sensitive to marker wobble due to soft tissue artifacts.

Joint centers

S1/L5 joint

The joint center of the S1/L5 joint (joint between pelvis and trunk) is defined based on the data from Reynolds et al. (1982) and as described by the algorithm below. The algorithm calculates the joint center based on pelvic width and pelvic depth, which are calculated from the pelvic markers. Due to the anatomical differences between the male and female pelvis, the algorithm provides different calculations according to gender. Note that the algorithm below is expressed in a reference frame in which X is anterior, Y is to the left, and Z is up are assumed.

$Y_{S1L5} = 0$

For male subjects:
$X_{S1L5} = X_{midASIS} - 0.498888 * pelvic\_depth$
$Z_{S1L5} = Z_{midASIS} + 0.111790 * pelvic\_width$

For female subjects:
$X_{S1L5} = X_{midASIS} - 0.543004 * pelvic\_depth$
$Z_{S1L5} = Z_{midASIS} + 0.102756 * pelvic\_width$

Superior trunk joint

The joint center of the proximal trunk joint (joint between abdomen and thorax segments) is located at the T10-T11 joint. The location of the T10-T11 joint is defined at 26% along the line from T10 to XIPH as derived from an OpenSim model of the full thoracolumbar spine and ribcage (Bruno et al. 2015).

Segment reference frames

Abdomen

The origin of the abdomen is located in the S1/L5 joint center. The Z-axis points to the superior trunk joint. The X-axis is the cross product of the Z-axis and the pelvic Y-axis. The Y-axis is the cross product of the Z- axis and X-axis.

Thorax

The origin of the thorax is located in the superior trunk joint center. The Z-axis is a vector connecting the midpoint between XIPH and T10 and the midpoint between JN and C7. The Y-axis is a vector perpendicular to the plane formed by JN, C7, and the midpoint between XIPH and T10, pointing to the left. The X-axis is the cross product of the Y and Z-axis, pointing anteriorly.

Joint axes and joint angles (degrees of freedom)

The trunk has three degrees of freedom, which are rotations about the Y-axis (trunk tilt; forward lean is positive), X-axis (trunk lateroflexion; right lean is positive), and Z-axis (trunk rotation; left twist is positive).

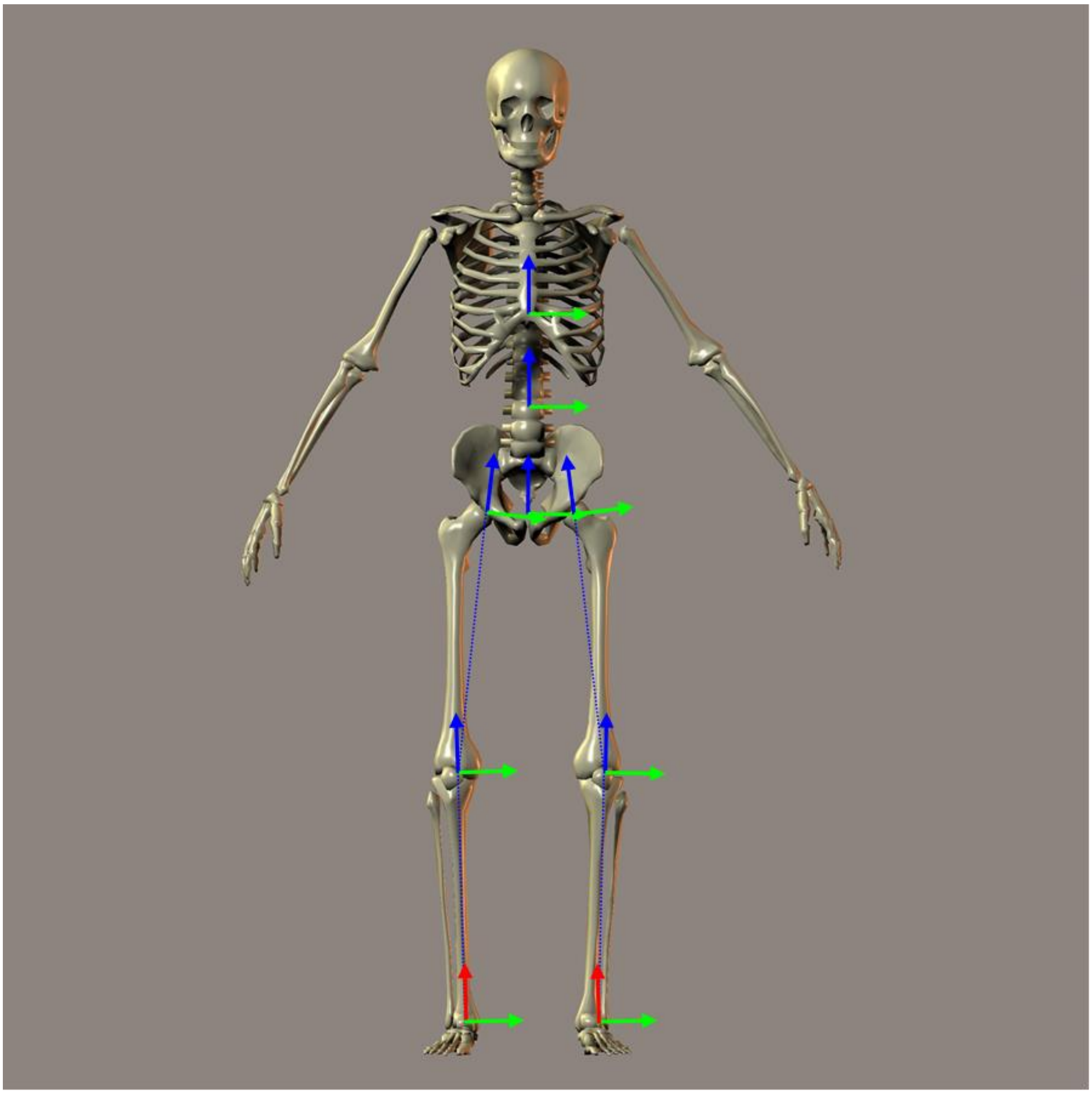

Figure 4. Front view of segment reference frames used in the HBM-Gait. X-, Y-, and Z-axes are indicated by red, green, and blue arrows, respectively. Segment origins generally are located at the proximal joint center, and negative Z-axes go through the distal joint center when available (except for the pelvis). The Z-axes of the feet point posteriorly.

4.6 Mass properties

During subject initialization, mass properties of each body segment are estimated based on segment lengths (distance between joint centers), gender, and total body mass. Segment mass, location of the center of mass, and the inertia tensor of each segment are estimated using parameters from Table 4 from de Leva (1996) which provides the following information:

- Segment mass as a percentage of total body mass: mperc
- Segment center of mass location as a percentage of segment length: cmperc

- Radii of gyration for the sagittal, frontal and transversal plane, expressed as a percentage of segment length: rsag, rfro, rtra.

Segment mass ($m_{segment}$) is calculated from $mperc$ and the total body mass (m_{total}):

$$m_{segment} = \frac{mperc}{100} * m_{total} \tag{1}$$

The center of mass of a given segment ($\vec{r}_{CM}$) is expressed in the segment's reference frame and is located on the longitudinal axis:

$$\vec{r}_{CM} = \frac{cmperc}{100}\begin{bmatrix}0\\0\\1\end{bmatrix} \tag{2}$$

Inertia tensors for each segment are also expressed in the segment's reference frame:

$$\mathbf{I} = m_{segment}\left(\frac{L_{segment}}{100}\right)^2 \begin{bmatrix} rsag^2 & 0 & 0 \\ 0 & rfro^2 & 0 \\ 0 & 0 & rtra^2 \end{bmatrix} \tag{3}$$

In which $L_{segment}$ is the length of the segment.

5. Biomechanical Analysis

Biomechanical analysis in HBM is done in five steps. First, inverse kinematics is used to describe skeletal motion. Second, the data is low pass filtered which is needed to calculate the first and second derivative (velocity and acceleration) without too much noise. Third, an inverse dynamics analysis is performed to calculate the generalized forces (forces and moments actuating the degrees of freedom). In the two final steps muscles moment arms and muscle forces are estimated.

5.1 Kinematics

Kinematic degrees of freedom

Based on the segment description in section 4, there are 21 kinematic degrees of freedom, and they have been given the following names. Each degree of freedom has a kinematic variable associated with it. These are also known as "generalized coordinates".

- PelvisX (not present in mox output)
- PelvisY (not present in mox output)
- PelvisZ (not present in mox output)
- PelvicTil
- PelvicObl
- PelvicRot
- TrunkTilt
- TrunkFlex
- TrunkRot
- RHipFlex
- LHipFlex
- RHipAbAd
- LHipAbAd
- RHipRot
- LHipRot
- RKneeFlex
- LKneeFlex
- RAnkleFlex
- LAnkleFlex
- RAnklePron
- LAnklePron

Inverse kinematics

In contrast to conventional six degrees of freedom models that calculate each segment orientation independently using at least three markers per segment, the joint angles in HBM are calculated all at once. During calibration HBM determines the segment reference frames based on the marker positions. For each frame these segments are fitted onto the marker data by minimizing the error between the measured marker data and the predicted marker data. Because all available markers are used in this optimization, fewer markers are required per segment than in the conventional models. Technically, HBM would only require the anatomical markers (bold in Table 1) to solve kinematics. However, additional technical markers are added to HBM (Table 1) to provide redundancy and robustness for the model in case of marker drop outs.

The inverse kinematics method used in HBM is based on van den Bogert and Su (2008). The skeleton model is defined with 21 DOF, represented by the generalized coordinates $\boldsymbol{q} = [\boldsymbol{q}_1 \dots \boldsymbol{q}_{21}]^T$, in which for example q_1 is PelvisX, q_2 is PelvisY, etcetera (see above). Since all segment reference frames are known from the marker data, the position vector $\boldsymbol{r} = [x, y, z]^T$ and orientation matrix $\boldsymbol{R}$ of each segment expressed in the global reference frame can be computed as a function of $\boldsymbol{q}$. Furthermore, the position of each marker in the segment reference frame ($\boldsymbol{p}$) is known. Therefore, the coordinates of each marker in the global reference frame can be expressed as a function of $\boldsymbol{q}$, by adding $\boldsymbol{R}(\boldsymbol{q}) \cdot \boldsymbol{p}$ (i.e. the position of a marker in the segment reference frame, rotated to the global reference frame) to the position vector of the segment origin in the global reference frame ($\boldsymbol{r}(\boldsymbol{q})$). Thus, the position of a certain marker i in the global reference frame is

$$\boldsymbol{r}_i = \boldsymbol{r}(\boldsymbol{q}) + \boldsymbol{R}(\boldsymbol{q}) \cdot \boldsymbol{p}_i \equiv \boldsymbol{f}_i(\boldsymbol{q}) \qquad (5)$$

The optimal estimate for the skeleton pose $\boldsymbol{q}$ can then be obtained by minimizing the squared difference between the measured coordinates of the markers in the global reference frame and their position expressed as a function of $\boldsymbol{q}$. If M markers are placed, the optimization is

$$\boldsymbol{F}(\boldsymbol{q}) = \sum_{i=1}^{M} \|\boldsymbol{r}_i - \boldsymbol{f}_i(\boldsymbol{q})\|^2 \qquad (6)$$

Note that in three dimensions, the right hand side is a sum of $3M$ squares, since the squares of x, y, and z distances are added. This optimization method is known as global optimization (Lu & O'Connor 1999), in which global refers to the fact that the entire skeleton is modeled at once, instead of modeling each segment individually. This makes the model less sensitive to marker drop-outs and skin artifacts. In HBM, equation 6 is minimized using the Levenberg-Marquardt algorithm, adapted from Numerical Recipes (Press et al. 1992). In this way, the generalized coordinates ($\boldsymbol{q}$) for each frame are calculated within 1ms of computation time.

Filtering and differentiation

The calculation of joint moments and muscle forces depends on the acceleration and velocity of the skeleton, which are the first and second derivative of skeleton movement ($\boldsymbol{q}$). To prevent these derivatives from being too noisy, $\boldsymbol{q}$ has to be smoothed using a filter.

The HBM software has a built-in real-time 2nd order low pass Butterworth filter. Higher order filters may reject noise better, but will also increase the time delay. Therefore, the used filter is considered to be a good compromise to be used in HBM. The state variable technique is used instead of the more common recursive digital filter, which allows processing data with varying sample rates (which occurs if the motion capture system drops a frame). Furthermore, this technique automatically generates first and second derivatives.

The cutoff frequency of the filter can be adjusted by the user to a maximum of 20 Hz. Higher frequencies are not allowed because these are unnecessary for human movement and would increase computation time. The default cutoff frequency is set to 6Hz, since this was found to be the highest frequency in kinematics related to gait (Winter et al. 1974). To prevent artifacts in joint movements, force plate data are processed with the same low pass filter as the kinematics (Bisseling and Hof 2006; van den Bogert and De Koning 1996).

5.2 Kinetics

Generalized forces

Each DOF is actuated with a force (for translational DOFs) or moment (for rotational DOFs). These forces and moments are also known as “generalized forces”. The signs of these are defined such that a positive force or moment would generate a movement in which the corresponding generalized coordinate is increasing. These (internal) moments and forces are solved using inverse dynamics. Furthermore, mechanical work can be computed as the product of the amount of change in the generalized coordinate and the amount of generalized force. The powers are presented per joint axis as most of the literature that reports on joint power presents a 2D sagittal plane analysis. When comparing HBM results with those results, only the flexion-extension power should be used. If preferred, the individual powers per joint can easily be summed to calculate the total joint power since they are scalars.

There are a few exceptions to the correspondence between generalized coordinates and generalized forces. Similarly as in the joint kinematics, some kinetic parameters are adapted to meet standards used in clinical gait analysis. The following adaptations are applied to the joint moments:

- Left hip flexion moment: Inverted
- Right hip flexion moment: Inverted
- Right hip Abduction moment: Inverted
- Left knee flexion moment: Inverted
- Right knee flexion moment: Inverted

There is one more exception, which are the pelvis moments that have been defined as Cartesian XYZ components in the world reference frame, rather than as moments on the yaw, pitch, and roll axes. Thus, the first six generalized forces are residual loads exerted by the outside world on the pelvis. When all external forces are measured and accounted for in the inverse dynamics, these loads should be zero.

An overview of all joint moments outputted by HBM is listed below:

- HipFlex: Extension is positive
- HipAbAd: Abduction is positive
- HipRot: External rotation is positive
- KneeFlex: Extension is positive
- KneeAbAd: Abduction is positive (constraint moment)
- KneeRot: External rotation is positive (constraint moment)
- AnkleFlex: Extension is positive (plantar flexion)
- AnklePron: Pronation is positive
- AnkleAbAd: constant value (zero)
- AnkleRot: constant value (zero)

Inverse dynamics

The generalized forces are calculated in an inverse dynamic analysis, which has the low pass filtered kinematics and the ground reaction forces as input. Like the inverse kinematic solution does for the generalized coordinates, the inverse dynamic analysis calculates all generalized forces ($\boldsymbol{\tau}$) at once using the following equation from van den Bogert et al. (2013):

$$\boldsymbol{\tau} = \boldsymbol{M}(\boldsymbol{q})\ddot{\boldsymbol{q}} + \boldsymbol{c}(\boldsymbol{q},\dot{\boldsymbol{q}}) + \boldsymbol{B}(\boldsymbol{q})\boldsymbol{\tau}_{\boldsymbol{ext}} \qquad (7)$$

In this equation $\boldsymbol{M}$ is a square matrix containing mass properties of the segments, $\boldsymbol{c}$ are terms related to Coriolis and centrifugal effects and gravity, and $\boldsymbol{B}(\boldsymbol{q})\boldsymbol{\tau}_{\boldsymbol{ext}}$ are the measured external forces (force plate data).

It is assumed that full ground reaction force data is available. When two force plates are used and each plate registers 3D forces and 3D moments, $\boldsymbol{\tau}_{\boldsymbol{ext}}$ contains 12 variables. Furthermore it is assumed that all DOFs of the model are actuated, which implies that $\boldsymbol{\tau}$ contains one variable for each DOF of the model. Thus, the solution also includes 3D force and moment acting on the root segment (pelvis). These values will be non-zero, even though it is known these values are exactly zero. Allowing this error has the advantage that there is an exact solution for $\boldsymbol{\tau}$. Also, joint moments are only influenced by inertial effects distal to the joint.

5.3 Muscle properties

HBM includes 43 lower limb muscles (for each limb, Table 2) which are modeled according the Gait2392 model (Delp et al. 2007). For each muscle maximal isometric force (F_{max}), and polynomial equations for muscle length as a function of joint angles are available. HBM is able to estimate muscle force (F) and activation level (F/F_{max}) using these parameters and skeletal pose. A list of all muscles included in HBM is shown in Table 2.

Table 2. Muscles included in the HBM-Gait.

Muscles in HBM-Gait	
Gluteus Medius 1	Psoas
Gluteus Medius 2	Quadratis Femoris
Gluteus Medius 3	Gemelli
Gluteus Minimus 1	Piriformis
Gluteus Minimus 2	Rectus Femoris
Gluteus Minimus 3	Biceps Femoris SH
Semimembranosus	Vastus Medialis
Semitendinosus	Vastus Intermedius
Biceps Femoris LH	Vastus Lateralis
Sartorius	Medial Gastrocnemius
Adductor Longus	Lateral Gastrocnemius
Adductor Brevis	Soleus

Adductor Magnus 1	Tibialis Posterior
Adductor Magnus 2	Flexor Digitorum Longus
Adductor Magnus 3	Flexor Hallicus Longus
Tensor Fascia Lata	Tibialis Anterior
Pectineus	Peroneus Brevis
Gracilis	Peroneus Longus
Gluteus Maximus 1	Peroneus Tertius
Gluteus Maximus 2	Extensor Digitorum Longus
Gluteus Maximus 3	Extensor Hallicus Longus
Iliacus	

Muscle moment arms

Muscle moment arms were estimated using the method of van den Bogert et al. (2013). In this method the coupling between muscles and skeleton is represented by a polynomial function which describes muscle length as a function of skeleton pose.

$$L(\boldsymbol{q}) = \sum_{i=1}^{N_{terms}} c_i \prod_{j=1}^{N_{DOF}} q_j^{e_{ij}} \tag{8}$$

In this equation, N_{terms} is the number of polynomial terms, $q_1 \dots q_{N_{DOF}}$ are values of the joint angles between origin and insertion of the muscle. The coefficients c_i, and the exponents e_{ij} are the model parameters.

The moment arm d_k can be obtained by partial differentiation with respect to the k^{th} joint angle as was described by An et al. (1984).

$$d_k(\boldsymbol{q}) = \frac{\partial L}{\partial q_k} = \sum_{i=1}^{N_{terms}} c_i \, e_{ik} \prod_{j=1}^{N_{DOF}} q_j^{e_{ij}-\delta_{jk}} \tag{9}$$

The model was loaded into OpenSim (Delp et al. 2007), in which the skeleton was systematically moved through many combinations of joint angles. For each skeleton pose, moment arms of all muscles and the corresponding joint angles were exported to a database. A stepwise regression was then used to fit the model to these data, in order to obtain values of the model parameters c_i and e_{ij}.

Muscle force estimation

A matrix $\boldsymbol{D}(\boldsymbol{q})$ is constructed which contains muscle moment arms of all muscles with respect to all generalized coordinates. Since all moment arms (d_k) and all joint moments ($\boldsymbol{\tau}$) are known, muscle forces ($\boldsymbol{F}$) can be estimated. This is done for all muscles at once using a static optimization which minimizes the squared activation levels (equation 10) (van der Helm 1994), while satisfying the known joint moments $\boldsymbol{\tau}$. The optimization is weighted by muscle volume (V_i) to make the solutions independent of the level of discretization of the muscular anatomy (van den Bogert et al. 2013; Holmberg and Klarbring 2012). Muscle volumes were assumed to be proportional to the product of maximal force and fiber length. These muscle properties were taken from the original models (Chadwick et al. 2009; Delp et al. 1990; Lambrecht et al. 2009).

$$\boldsymbol{F} = \sum_{i=1}^{n} V_i \left(\frac{F_i}{F_{max}}\right)^2 \qquad (10)$$

Subject to linear equality constraints

$\boldsymbol{D}(\boldsymbol{q})\boldsymbol{F} = \boldsymbol{\tau}$

And bound constraints

$F_i \geq 0$

This is a quadratic programming problem, which is solved in HBM in real time using a recurrent neural network as described by Xia and Feng (2005).

Activation levels are guaranteed to be positive, but are not guaranteed to be less than 1. The F_{max} values used in the optimization are derived from cadaveric data (Delp et al. 1990). These values are meant to be interpreted as relative muscle strengths, so activation levels may be higher than 1 when capturing above average strong subjects.

6. Gait Analysis

As HBM-Gait is specifically adapted to clinical gait analysis, the model reports spatial and temporal gait parameters often used to assess gait.

Walking speed

The walking speed is calculated based on the average horizontal displacement of the pelvis markers. When walking on a treadmill, the treadmill speed is added to this calculated speed.

Step time/stride time

Step time is the time span between two consecutive contralateral heel strikes. Stride time is the time span between two consecutive ipsilateral heel strikes.

Step length/stride length

Step length is the difference in anterior/posterior position in the global reference frame of the HEE markers during subsequent heel strikes plus the traversed distance of the treadmill between the heel strikes. The traversed distance is calculated by taking the integral of belt speed over time. Stride length is the sum of two consecutive contralateral step lengths.

Step width

Step width is the difference in medio-lateral position in the global reference frame of the HEE markers during subsequent contralateral heel strikes.

Stance time/swing time

Stance time is the time between heel strike and toe off. Swing time is the time between toe off and heel strike. Both stance time and swing will also be reported as percentage of the gait cycle.

Foot progression angle

Foot progression is the angle of the foot in the horizontal plane relative to the direction of walking. A foot pointing medially is defined as a positive angle.

7. References

An, K.N. et al., 1984. Determination of muscle orientations and moment arms. *Journal of biomechanical engineering*, 106(3), pp.280–2.

Assi, A. et al., 2016. Validation of hip joint center localization methods during gait analysis using 3D EOS imaging in typically developing and cerebral palsy children. *Gait and Posture*, 48, pp.30–35.

Bell, A.L., Brand, R.A. & Pedersen, D.R., 1989. Prediction of hip joint centre location from external landmarks. *Human Movement Science*, 8(1), pp.3–16.

Bisseling, R.W. & Hof, A.L., 2006. Handling of impact forces in inverse dynamics. *Journal of Biomechanics*, 39(13), pp.2438–2444.

van den Bogert, A.J. et al., 2013. A real-time system for biomechanical analysis of human movement and muscle function. *Medical & Biological Engineering & Computing*, 51(10), pp.1069–1077.

van den Bogert, A.J. & De Koning, J.J., 1996. On optimal filtering for inverse dynamics analysis. In *Proceedings of the IXth biennial conference of the Canadian society for biomechanics*. pp. 214–215.

van den Bogert, A.J., Smith, G.D. & Nigg, B.M., 1994. In vivo determination of the anatomical axes of the ankle joint complex: An optimization approach. *Journal of Biomechanics*, 27(12), pp.1477–1488.

van den Bogert, A.J. & Su, A., 2008. A weighted least squares method for inverse dynamic analysis. *Computer methods in biomechanics and biomedical engineering*, 11(1), pp.3–9.

Bruno, A.G., Bouxsein, M.L. & Anderson, D.E., 2015. Development and Validation of a Musculoskeletal Model of the Fully Articulated Thoracolumbar Spine and Rib Cage. *Journal of biomechanical engineering*, 137(8), p.81003.

Burdett, R.G., 1982. Forces predicted at the ankle during running. *Medicine and science in sports and exercise*, 14(4), pp.308–316.

Camomilla, V. et al., 2006. An optimized protocol for hip joint centre determination using the functional method. *Journal of Biomechanics*, 39(6), pp.1096–1106.

van Campen, A. et al., 2011. Functional knee axis based on isokinetic dynamometry data: Comparison of two methods, MRI validation, and effect on knee joint kinematics. *Journal of Biomechanics*, 44(15), pp.2595–2600.

Chadwick, E.K. et al., 2009. A Real-Time, 3-D Musculoskeletal Model for Dynamic Simulation of Arm Movements. *Biomedical Engineering, IEEE Transactions on*, 56(4), pp.941–948.

Delp, S.L. et al., 1990. An Interactive Graphics-Based Model of the Lower Extremity to Study Orthopaedic Surgical Procedures. *IEEE Transactions on Biomedical Engineering*, 37(8), pp.757–767.

Delp, S.L. et al., 2007. OpenSim: Open source to create and analyze dynamic simulations of movement. *IEEE transactions on bio-medical engineering*, 54(11), pp.1940–1950.

Gamage, S.S.H.U. & Lasenby, J., 2002. New least squares solutions for estimating the average centre of rotation and the axis of rotation. *Journal of Biomechanics*, 35(1), pp.87–93.

Glitsch, U. & Baumann, W., 1997. The three-dimensional determination of internal loads in the lower extremity. *Journal of Biomechanics*, 30(11–12), pp.1123–1131.

Halvorsen, K., 2003. Bias compensated least squares estimate of the center of rotation. *Journal of Biomechanics*, 36(7), pp.999–1008.

Harrington, M.E. et al., 2007. Prediction of the hip joint centre in adults, children, and patients with cerebral palsy based on magnetic resonance imaging. *Journal of Biomechanics*, 40, pp.595–602.

van der Helm, F.C.T., 1994. A finite element musculoskeletal model of the shoulder mechanism. *Journal of Biomechanics*, 27(5), pp.551–569.

Holmberg, L.J. & Klarbring, A., 2012. Muscle decomposition and recruitment criteria influence muscle force estimates. *Multibody System Dynamics*, 28(3), pp.283–289.

Isman, R. & Inman, V., 1969. Anthropometric Studies of the Human Foot and Ankle. *Foot And Ankle*, 11, pp.97–129.

Kainz, H. et al., 2015. Estimation of the hip joint centre in human motion analysis: A systematic review. *Clinical Biomechanics*, 30(4), pp.319–329.

Kainz, H. et al., 2016. Joint kinematic calculation based on clinical direct kinematic versus inverse kinematic gait models. *Journal of Biomechanics*, 49(9), pp.1658–1669.

Lambrecht, J.M. et al., 2009. Musculoskeletal model of trunk and hips for development of seated-posture-control neuroprosthesis. *Journal of rehabilitation research and development*, 46(4), pp.515–28.

Leardini, A. et al., 1999. Validation of a functional method for the estimation of hip joint centre location. *Journal of Biomechanics*, 32(1), pp.99–103.

de Leva, P., 1996. Adjustments to Zatsiorsky-Seluyanov's segment inertia parameters. *Journal of biomechanics*, 29(9), pp.1223–1230.

Lu, T.W. & O'Connor, J.J., 1999. Bone position estimation from skin marker co-ordinates using global optimisation with joint constraints. *Journal of Biomechanics*, 32(2), pp.129–134.

MacWilliams, B. a., 2008. A comparison of four functional methods to determine centers and axes of rotations. *Gait and Posture*, 28(4), pp.673–679.

Peters, A. et al., 2012. A comparison of hip joint centre localisation techniques with 3-DUS for clinical gait analysis in children with cerebral palsy. *Gait and Posture*, 36(2), pp.282–286.

Press, W.H. et al., 1992. *Numerical recipes in C (2nd ed.): the art of scientific computing*,

Ramakrishnan, H.K. & Kadaba, M.P., 1991. On the estimation of joint kinematics during gait. *Journal of biomechanics*, 24(10), pp.969–977.

Reynolds, H.M., Snow, C.C. & Young, J.W., 1982. *Spatial geometry of the human pelvis*, Oklahoma City: DTIC Document.

Sangeux, M., Peters, A. & Baker, R., 2011. Hip joint centre localization: Evaluation on normal subjects in the context of gait analysis. *Gait and Posture*, 34(3), pp.324–328.

Sangeux, M., Pillet, H. & Skalli, W., 2014. Which method of hip joint centre localisation should be used in gait analysis? *Gait and Posture*, 40, pp.20–25.

Winter, D.A., Sidwall, H.G. & Hobson, D.A., 1974. Measurement and reduction of noise in kinematics of locomotion. *Journal of Biomechanics*, 7(2), pp.157–159.

Wu, G. et al., 2002. ISB recommendation on definitions of joint coordinate system of various joints for the reporting of human joint motion--part I: ankle, hip, and spine. International Society of Biomechanics. *Journal of biomechanics*, 35, pp.543–548.

Wu, G. et al., 2005. ISB recommendation on definitions of joint coordinate systems of various joints for the reporting of human joint motion -- Part II: Shoulder, elbow, wrist and hand. *Journal of Biomechanics*, 38(5), pp.981–992.

Wu, G. & Cavanagh, P.R., 1995. ISB Recommendations in the Reporting for Standardization of Kinematic Data. *J Biomechanics*, 28(10), pp.1257–1261.

Xia, Y. & Feng, G., 2005. An improved neural network for convex quadratic optimization with application to real-time beamforming. *Neurocomputing*, 64(1–4 SPEC. ISS.), pp.359–374.

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