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The conventional gait model, an open-source implementation that reproduces the past but prepares for the future

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ABSTRACT

Background: The Conventional Gait Model (CGM), known by a variety of different names, is widely used in clinical gait analysis. We present pyCGM2, an open-source implementation of the CGM with two versions. The first, CGM1.0, is a clone of Vicon Plug In Gait (PiG) with all its variants. CGM1.0 provides a platform to test the effect of modifications to the CGM on data collected and processed retrospectively or to provide backward compatibility.

The second version, CGM1.1, offers some practical modifications and includes three well documented improvements.

Research question: How do improvements of the conventional gait model affect joint kinematics and kinetics?

Method: The practical modifications include the possibility to use a medial knee epicondyle marker, during static calibration only, to define the medio-lateral axis of the femur in place of the knee alignment device. The three improvements correspond to the change of pelvis angle decomposition sequence, the adoption of a single tibia coordinate system, and the default decomposition of the joint moments in the joint coordinate system. We validated the outputs of version CGM1.0 against Vicon-PiG, and estimated the effect of the modifications included in version CGM1.1 using gait data collected in 16 healthy participants.

Results: Kinematics and kinetics of CGM1.0 were superimposed with that of Vicon-PiG, with root mean square differences less than 0.04° for kinematics and less than 0.05 N.m.kg-1 for kinetics.

Significance: The differences between the CGM1.1 and CGM1.0 were minimal in the healthy participant cohort but we discussed the expected difference in participants with different gait pathologies.

We hope that the pyCGM2 will facilitate the systematic testing and the use of improved processing methods for the conventional gait model.

1. Introduction

The Conventional Gait Model (CGM) is the predominant biomechanical model used in clinical gait analysis [1]. Originating in the 1970's and developed by various individuals [1,2], the strengths associated with the CGM include being understandable by a large community, even non-experts in Biomechanics [1]. The CGM became popular because it was distributed as a package (first Vicon Clinical Manager, then Plug in Gait) within the Vicon (Oxford Metrics, UK) clinical motion capture software.

Extensive application of the CGM in clinics and medical research [2,3] have exposed the model to criticism. For example, the lack of accuracy in positioning the thigh and shank segment wand-mounted markers has been responsible for large errors in the definition of the coronal planes for these segments [4,5]. The Knee Alignment Device (KAD) [6] was introduced to reduce these errors, by improving the location of the Knee Joint Centre (KJC) and the alignment of the medio-lateral axis of the femur with the trans-epicondylar axis. However, use of the KAD may be outdated now that most clinical gait analysis systems have resolutions sufficient to capture a small (i.e. < 9 mm in diameter) additional reflective marker on the medial femoral epicondyle.

Similarly, the clinical relevance of CGM outputs may benefit from research that has been published since its inception but have not been implemented yet. For example, Baker et al. [7] demonstrated that the CGM's angular decomposition does not correspond to the clinical

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definition of the terms for the pelvis. Pelvis tilt is defined clinically as the rotation of the pelvis around its medio-lateral axis, but it is calculated by the CGM as the rotation around the medio-lateral axis of the laboratory's coordinate system.

Schache et al. [8] showed that the decomposition of joint moments in different coordinate systems leads to different outputs. In a further study [9], they suggested the Joint Coordinate System (JCS) was more indicative of clinical understanding and may be preferred for the reporting of joint moments. However, the current implementation of the CGM does not allow to decompose in the JCS, it only allows to decompose the joint moments in the proximal or the distal segment's coordinate system. In addition, decomposition in the distal segment is the default option but Passmore and Sangeux [10] have shown that decomposition in the distal segment is problematic for the hip joint when the subject presents with torsional deformities in the lower limb, which is a common clinical problem.

Various projects have attempted to replicate the CGM. The *Advanced Gait Work Flow*, distributed by Vicon and written in Matlab (The Mathworks Inc., Natick, USA) has been proposed but is not validated against the CGM. Open-source versions, including pyCGM [11] in python, the Biomechanical Toolkit project in C + + [12] and BiomechZoo in Matlab [13], have also been proposed. However, these implementations have only tackled the basic CGM options, they did not include improvement of the static calibration with the KAD, precluding utility to many users.

The commercial software Visual 3D (C-Motion, Inc., Germantown, USA) has implemented all CGM variants, but has not replicated Vicon-PiG outputs exactly [14]. In Visual 3D, the segment pose is estimated through least-square segment fitting, which is different from CGM's direct kinematics [1].

This paper aims to present an open-source implementation of the CGM, pyCGM2 [15]. The pyCGM2 package proposes two versions: the CGM1.0 which replicates outputs of the Vicon-PiG implementation, and the CGM1.1 which addresses the shortcomings of the Vicon-PiG implementation without modifying the core of the model.

We present a comprehensive overview of the current Vicon-PiG variants and the improvements we implemented in the pyCGM2 version CGM1.1. We validated the implementation of the CGM1.0 against the Vicon-PiG outputs, and determined the differences between the CGM1.0 and CGM1.1 versions in a healthy population.

2. Method

2.1. Variants of the CGM

The original version of the CGM as implemented in Vicon-PiG is well described (Fig. 1a) [16]. An improved variant, using the knee alignment device (KAD), was introduced but was not clearly referenced in the literature [6]. The KAD is clamped to the medial and lateral epicondyles of the knee and defines the coronal plane of the femur (Fig. 1b, the KAD variant). Rotational offsets between the KAD and the thigh and shank wand markers are stored in the parameter file during static calibration and applied during the processing of dynamic trials.

A second variant (Fig. 1c, the KAD-med variant) added the use of a calibration marker on the ankle medial malleolus to define the trans-malleolar axis and the coronal plane of the tibia. Tibial torsion can then be calculated during static calibration (and output as knee rotation kinematics in the static trial) and the tibia is modelled as two segments: one, proximal aligned with the femur, and one, distal aligned with the trans-malleolar axis. During dynamic processing, the proximal tibia section is used to calculate knee kinematics, whereas the distal tibia section is used to calculate ankle kinematics. This explains why Vicon-PiG knee rotation kinematics has a mean value over the gait cycle that is approximately zero, since the medio-lateral axes of the femur and proximal tibia coordinate systems were aligned during static calibration. Without the use of a proximal tibia coordinate system to calculate knee kinematics, knee rotation kinematics would oscillate around the value of tibial torsion. The average knee rotation kinematics over the gait cycle would therefore be non-zero since tibial torsion is non-zero in normal subjects, because the ankle transmalleolar axis is known to be externally rotated with respect to the femoral epicondyles. Our experience indicates that most gait analysts are not aware of this subtlety in Vicon-PiG.

We also identified a processing error due to the complexity of dealing with two tibia coordinate systems. During static calibration the heel marker (HEE) may be used to determine the alignment of the longitudinal axis of the foot (defined as the vector from HEE to the forefoot marker, TOE) with respect to the vector from the ankle joint centre (AJC) to the TOE marker. This process allows to remove the HEE marker during dynamic trial and may be used to adjust for sole height differences [17,18]. The alignment of the longitudinal axis of the foot is stored as two parameters: the static plantarflexion and rotation offsets obtained through decomposing the orientation of the HEE-TOE axis compared to the AJC-TOE axis with respect to the medio-lateral and longitudinal axes of the static distal tibia coordinate system, respectively. However, these parameters are applied to the proximal tibia coordinate system during dynamic processing which introduces a small error in the ankle inversion/eversion kinematics.

2.2. pyCGM2 implementation

The pyCGM2 package has been developed as an open-source platform to replicate the CGM, to allow users to explore the code, and to provide a common platform to integrate improved processing methods. The pyCGM2 is written in python and employs standard python packages for numerical computation. The pyCGM2 is supplemented with the Biomechanical ToolKit (BTK) [12] and its evolution Open Movement Analysis (OpenMA) [19]. Both offer convenient methods for handling c3d files.

A pyCGM2 program is composed of a series of blocks or filters, each performing a specific operation, like computation of kinematics or kinetics. The pyCGM2 can be used to replicate the processing and outputs of the Vicon-PiG operations exactly. Therefore, the operations called *PiG static* and *Pig Dynamic* within Vicon Nexus have been implemented and named *pyCGM2 Calibration* and *pyCGM2 Fitting* respectively. The *Calibration* operation constructs a geometric multi-segment model by locating joint centres and computing segment offsets, and outputs static joint angles. The *Fitting* operation fits the calibrated model to the marker data and performs the kinematics and kinetics analyses.

In its CGM1.0 version, the pyCGM2 was designed to replicate Vicon-PiG outputs exactly. The kinematics are obtained using the same Cardan angle decomposition sequences and adopt the same sign conventions. The KAD-med variant includes two tibia coordinate systems and we reproduced the processing error pertaining to the offset parameters that describe the alignment of the longitudinal axis of the foot.

The kinetics are computed from inverse dynamics using anthropometric segment measurements according to Dempster [20]. Inverse dynamic calculations follow the iterative Newton-Euler equations described in Dumas et al. [21], where linear velocities and accelerations are computed with quintic-spline fitting derivation (function : splev of the Numpy package [22]) and 2nd order numerical differentiation of the rotation matrix for angular quantities.

2.3. CGM1.1: a CGM as it should work

2.3.1. Practical improvement

Most current gait analysis services are equipped with motion capture systems able to collect the position of medial knee markers. The CGM1.1 allows the option of using medial epicondyle knee markers instead of a KAD while maintaining the same logic as the KAD or KAD-med variants. The medial epicondyle knee markers can be removed after static calibration to avoid subject discomfort during dynamic

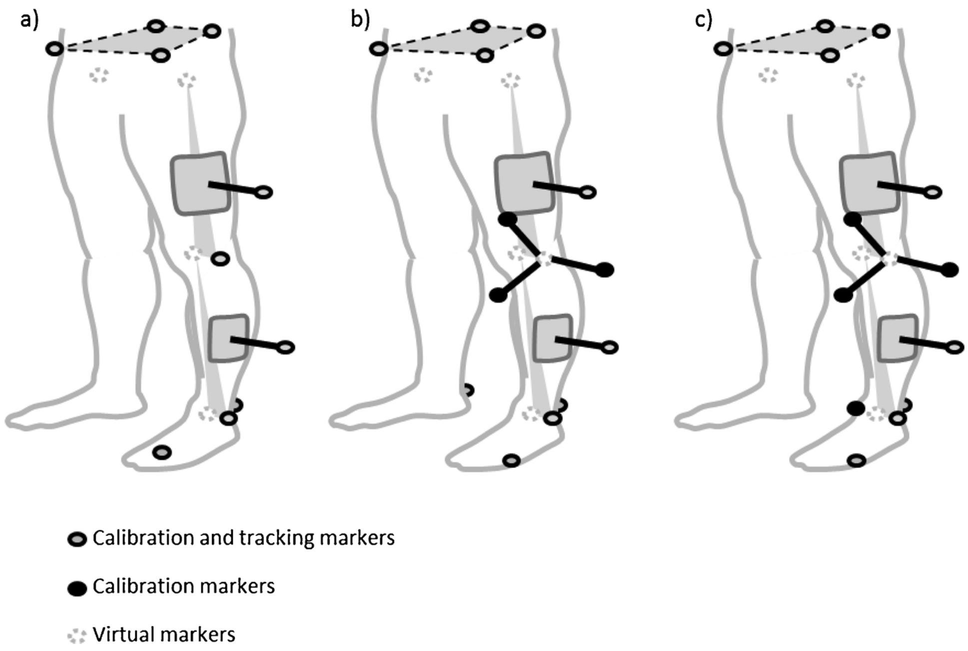

Fig. 1. The three calibration variants of the CGM as implemented in Vicon-PiG. Initial variant (a) defines coronal plane of the femur using the wand-mounted markers. The KAD variant (b) clamped the Knee Alignment Device to the knee condyles to define the coronal plane of the femur. The KAD-MED variant (b) places a marker on the medial malleolus in addition to the KAD. Tibial torsion is calculated and the tibia is modelled as two segments. During static calibration, the medio-lateral axis of the proximal tibia segment is defined from that of the femur (using the KAD), and the medio-lateral axis of the distal tibia is defined from the trans-malleolar axis.

trials. This is already the case for the medial malleolus ankle markers. We also corrected the processing error pertaining to the offset parameters that describe the alignment of the longitudinal axis of the foot.

2.3.2. Clinically relevant methods

After almost three decades of extensive use and testing in the clinical setting, we believe there are three modifications to the CGM that are required immediately. It is important to note that these modifications do not alter the core characteristics of the CGM as a model but aim to clarify the clinical interpretation of the kinematic or kinetic outputs.

Firstly, the Cardan sequence for the pelvis kinematics is modified to a Rotation-Obliquity-Tilt mobile axes sequence. This choice ensures that pelvis rotation reflects the rotation of the pelvis with respect to the vertical axis of the laboratory, and that pelvis tilt is the rotation of the pelvis around its medio-lateral axis, and not around the medio-lateral axis of the laboratory [7]. Secondly, the CGM1.1 implements a single tibia coordinate system using the transmalleolar axis to avoid the confusion between Vicon-PiG static (which uses the torsioned tibia) and dynamic (which uses the untorsioned tibia) knee rotation outputs. Thirdly, the default projection of the joint moments is in the JCS rather than in the distal segment coordinate system to improve clinical interpretation of kinetic graphs [9,10,23].

2.4. Validation

A dataset comprised of 3D gait data of 16 healthy adult participants (8 males and 8 females, with a mean age of 33 ± 17 years, height of 1.68 ± 0.10 m, mass of 64 ± 15 kg and Body Mass Index (BMI) of 23.0 ± 3.6 kg/m^2) was used to validate the replication of Vicon-PiG (CGM1.0) and to estimate the differences induced by the modifications implemented in the CGM1.1. Static calibration was carried out with the KAD-Med variant. Joint moments were decomposed into the distal segment for both Vicon-PiG-KAD-Med and its clone (CGM1.0-KAD-Med). Quantification of differences were calculated using the Root Mean Square Difference (RMSD):

$$RMSD = \left(\frac{1}{n} \sum_{i=1}^{n} (q^{CGM}(i) - q^{PiG}(i))^2 \right)$$

where q represents either kinematic of kinetic outputs, and n is the number of frame (i.e. 101).

Although ankle inversion/eversion is calculated by the conventional gait model, the default markerset used for the foot segment does not allow an accurate measurement for this parameter. We included ankle inversion/eversion in our comparison only to provide a comprehensive comparison.

Table 1
Root mean square difference between Vicon-PiG (KAD-MED Variant) and both pyCGM2 versions: CGM1.0 (the PiG clone) and CGM1.1 (the PiG as it should (have) work(ed)). Zero indicates a value inferior to 0.01.

	Version	Angles (°) Mean(sd)			Moment (Nm. kg^{-1}) Mean(sd)			Power (W. kg^{-1}) Mean(sd)
		Sagittal	Coronal	Transversal	sagittal	coronal	transversal	
Pelvis	CGM1.0	0	0	0	–	–	–	–
	CGM1.1	0.21(0.13)	0.76(0.42)	0.42(0.24)	–	–	–	–
Hip	CGM1.0	0	0.01(0.05)	0.03(0.14)	0.04(0.02)	0.02(0.01)	0	0
	CGM1.1	0	0.01(0.05)	0.03(0.14)	0.07(0.02)	0.06(0.04)	0	0.06(0.04)
Knee	CGM1.0	0.01(0.05)	0.01(0.05)	0.03(0.14)	0.02(0)	0	0	0
	CGM1.1	0.01(0.05)	0.02(0.11)	17.3(7.4)	0.03(0.01)	0.04(0.02)	0	0.08(0.03)
Ankle	CGM1.0	0.04(0.26)	0.02(0.11)	0.02(0.11)	0.01(0)	0	0	0
	CGM1.1	0.16(0.27)	3.21(1.72)	0.48(0.37)	0.01(0)	0	0.02(0.01)	0.06(0.03)
Foot	CGM1.0	–	–	0.02(0.11)	–	–	–	–
	CGM1.1	–	–	0.48(0.37)	–	–	–	–

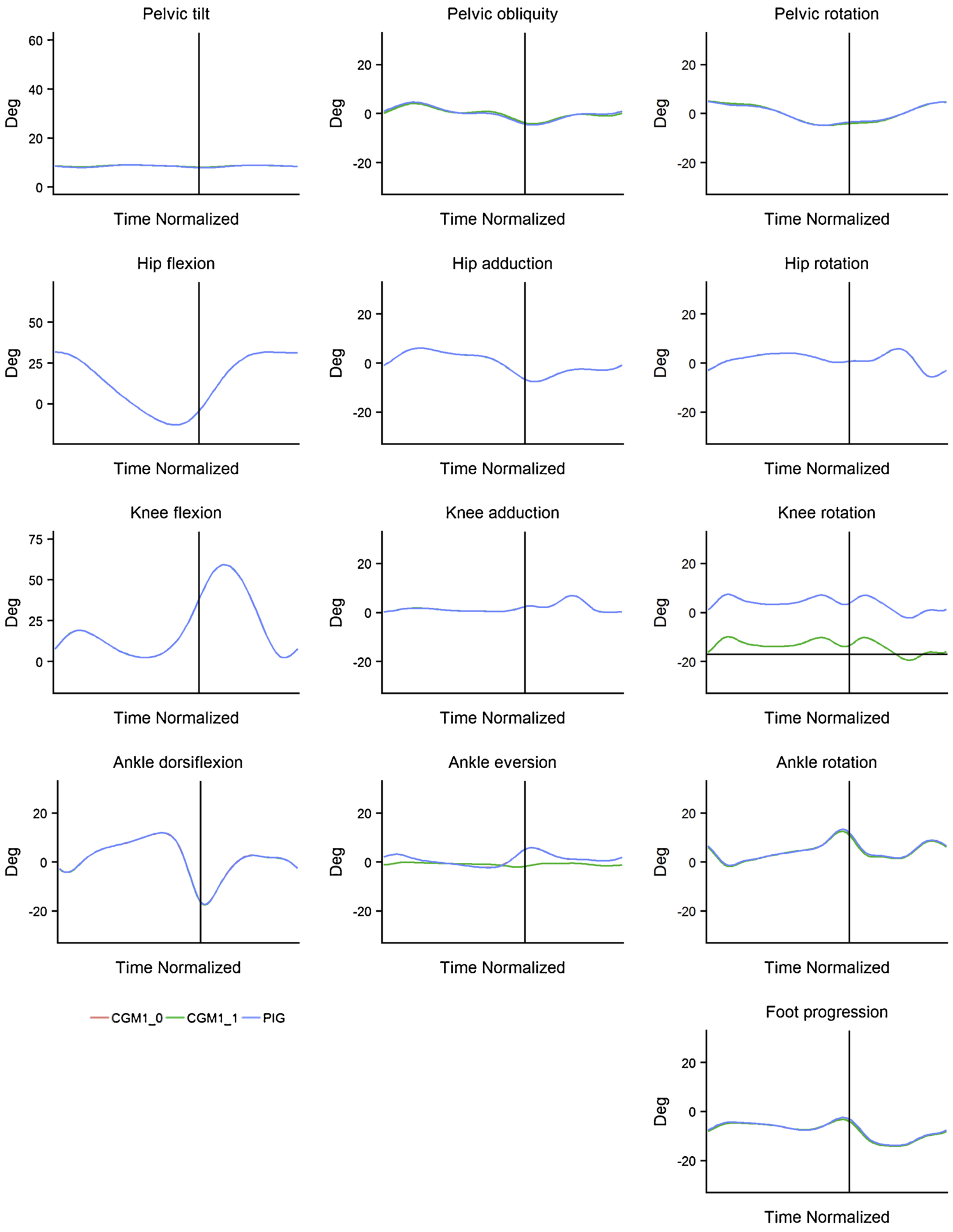

Fig. 2. Kinematic gait panel provided using Vicon PiG (KAD-med variant), the CGM1.0 and CGM1.1 versions. The data plotted is the mean curves for the entire cohort of healthy participants. The red curves (CGM1.0) are mostly not visible because it is almost exactly superimposed by Vicon-PiG curves in blue. The horizontal line in the knee rotation graph displays the value of tibial torsion calculated by Vicon PiG (or the CGM1.0 clone) using the additional medial ankle marker during static calibration. The vertical line represents the average toe-off instant.

2.5. Results

Table 1 presents the difference between Vicon-PiG-KAD-Med, pyCGM2 clone (CGM1.0-KAD-Med) and the new version (CGM1.1-KAD-Med). The CGM1.0 kinematic outputs were almost identical to Vicon-PiG. Maximal RMSD was 0.04° for ankle dorsi/plantar-flexion. Maximum RMSD was 0.05 N.m.kg-1 for the hip flexion/extension moment (Fig. 2).

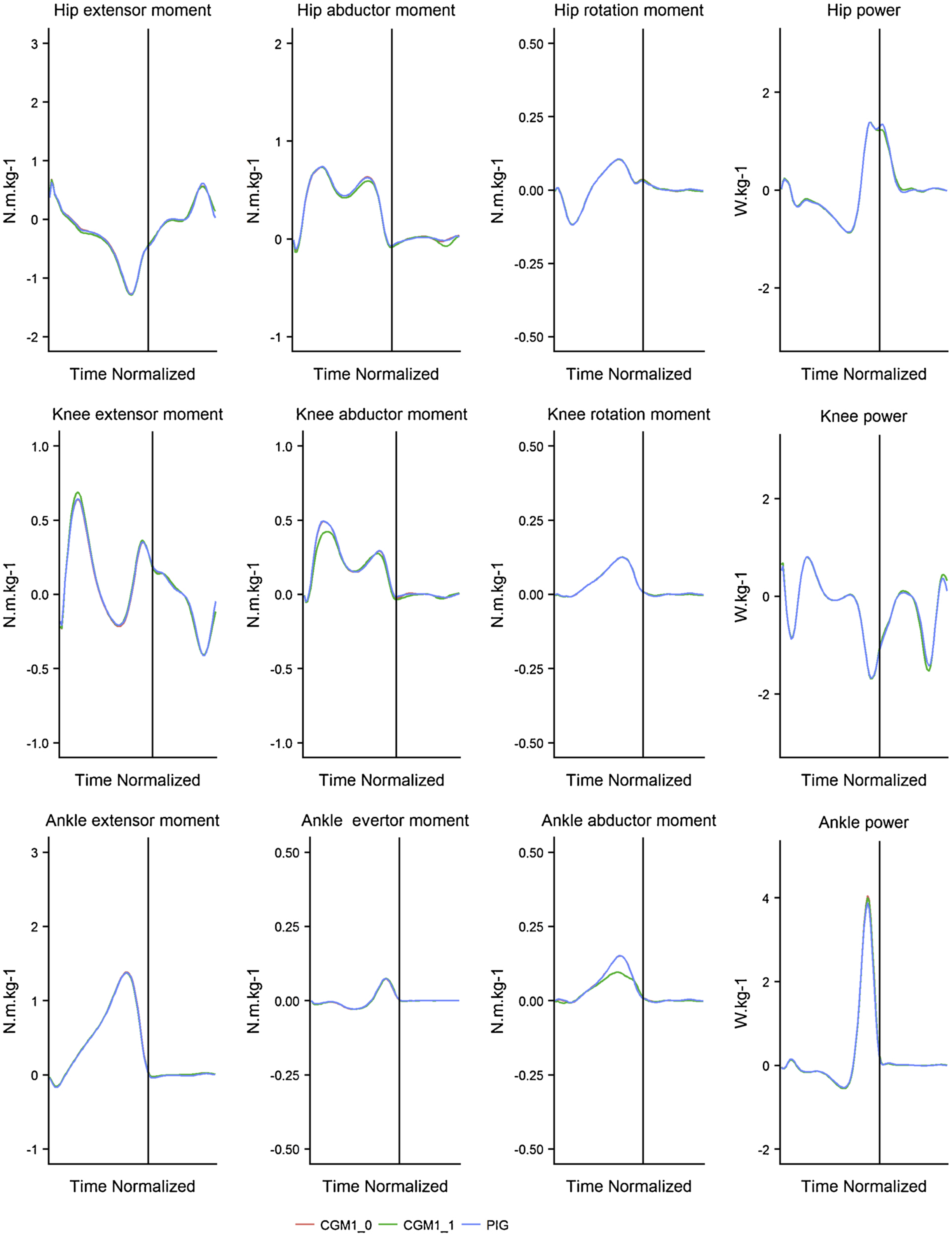

Fig. 3. Kinetic gait panel provided from Vicon PiG (KAD-med variant), the CGM1.0 and CGM1.1. The data plotted is the mean curves for the entire cohort of healthy participants. The red curves (CGM1.0) are mostly not visible because it is almost exactly superimposed by Vicon-PiG curves in blue. For Vicon-PiG and CGM1.0, the joint moments were decomposed into the distal segment coordinate system, whereas CGM1.1 projected them into the JCS. The vertical line represents the average toe-off instant.

Regarding the comparison between CGM1.0 and CGM1.1, the change in Cardan angle decomposition sequence at the pelvis had minimal effect. RMSD in the three planes were less than 0.8°. As expected, the knee rotation trace (Fig. 1) exhibited a large RMSD (17.2°) which matched average tibial torsion (17°). The Vicon-PiG exhibited a marked ankle eversion in swing phase, whereas ankle eversion was neutral with CGM1.1. Finally, the projection of moments into the JCS instead of the distal segment did not result in marked differences in our healthy cohort (Fig. 3).

3. Discussion

We have proposed pyCGM2, an open-source platform to replicate the CGM as implemented in Vicon-PiG in its version CGM1.0, and to implement three clinically relevant improvements in its version CGM1.1. The three improvements were: (i) change of angle decomposition sequence for the pelvis, (ii) adoption of a single segment definition for the tibia, and (iii) default decomposition of the moments in the JCS coordinate system. Vicon-PiG was compared to CGM1.0 in a cohort of 16 healthy participants to validate our implementation and was compared to CGM1.1 to estimate the differences induced by the improvements in normative reference datasets.

We showed that pyCGM2 version CGM1.0 produces almost identical outputs compared to Vicon-PiG's implementation of the CGM. Therefore, gait analysts may use one or the other interchangeably. The improved version, CGM1.1, produced similar outputs in a healthy cohort, with the exception of knee rotation kinematics which oscillates around the value calculated for tibial torsion during static calibration for CGM 1.1, rather than zero with CGM 1.0.

Similar outputs for CGM 1.0 and 1.1 in a healthy cohort are desirable for practical reasons since it indicates that the effect of these CGM versions will be minimal on published, or laboratory-based, normative datasets. It is important to note however that data collected by the different clinical gait centres for their normative datasets may be readily reprocessed using CGM1.1.

The absence of major differences in this study's healthy cohort does not imply there would be no differences in individuals with gait pathologies, depending on their pathology. The differences to expect between CGM1.0 and CGM1.1 in individuals with gait pathologies are well documented for each of the three modifications we included in CGM1.1.

Baker et al. showed that the change of the pelvis angular decomposition sequence primarily affects subjects walking with large pelvis rotation or large pelvic obliquity, which are two common clinical presentations [7].

The adoption of a unique segment definition for the tibia clarifies the interpretation of knee rotation kinematics as composed of tibial torsion plus the knee dynamic rotation. Many individuals with pathology undergoing clinical gait analysis present with large tibial torsion. With Vicon-PiG, or CGM1.0, the value of tibial torsion is hidden in the parameter file and does not appear in the knee rotation kinematics. This sometimes leads to inefficient reasoning, whereby clinicians need to add multiple transverse plane kinematics (pelvis, hip, knee, ankle and foot progression) to estimate a static parameter, tibial torsion, that is readily available in the parameter file but not apparent in the kinematics graph. With the CGM1.1 version, tibial torsion appears in the knee rotation kinematics graph directly. We believe this may not only clarify, but probably even fast-track clinical interpretation. Furthermore, it is likely to facilitate comparison with alternative models that also use a single definition for the tibia [9,10].

The use of the joint coordinate system as the default option to project the 3D vector of the net joint moment leads to major differences whenever transverse plane joint rotations are large, for example in subjects with large internal/external hip rotation or large internal/external knee rotation [10]. The default setting in Vicon-PiG is to decompose the moment in the distal segment coordinate system. As a result, the component of the net joint moment vector lying in the sagittal plane of the femur, rather than that of the pelvis, is currently called hip extensor/flexor moment. Similarly, when using a single tibia coordinate system, the component of the knee moment vector projected in the sagittal plane of the tibia (determined using the ankle transmalleolar axis) is labelled knee flexor/extensor moment.

On the contrary, the default choice of the joint coordinate system aligns well with the interpretation of muscle groups acting as motor torques, although the limitations of such interpretation need to be considered carefully [23].

In conclusion, this study has produced an open-source package, pyCGM2, that delivers both a clone to Vicon-PiG and an updated version of the CGM, CGM 1.1, that addresses what we believe are the most pressing improvements to the CGM. The open-source package intends to serve as a platform to test new methods, to evaluate the changes induced by the new methods systematically, and to support multicentric studies.

Conflict of interest

We confirm that the manuscript has been read and approved by all named authors and that there are no other persons who satisfied the criteria for authorship but are not listed. We further confirm that the order of authors listed in the manuscript has been approved by all of us.

We further confirm that any aspect of the work covered in this manuscript that has involved humans has been conducted with the ethical approval of all relevant bodies and that such approvals are acknowledged within the manuscript.

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