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In vivo Ankle Joint Kinematics from Dynamic Magnetic Resonance Imaging using a Registration-based Framework

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Abstract

In this paper, we propose a method for non-invasively measuring three-dimensional *in vivo* kinematics of the ankle joint from a dynamic MRI acquisition of a single range-of-motion cycle. The proposed approach relies on an intensity-based registration method to estimate motion from multi-plane dynamic MRI data. Our approach recovers not only the movement of the skeleton, but also the possibly non-rigid temporal deformation of the joint. First, the rigid motion of each ankle bone is estimated. Second, a four-dimensional (3D+time) high-resolution dynamic MRI sequence is estimated through the use of the log-euclidean framework for the computation of temporal dense deformation fields. This approach has been then applied and evaluated on *in vivo* dynamic MRI data acquired for a pilot study on six healthy pediatric cohort in order to establish *in vivo* normative joint biomechanics. Results demonstrate the robustness of the proposed pipeline and very promising high resolution visualization of the ankle joint.

Keywords : dynamic MRI, ankle, motion estimation, high-resolution reconstruction, intensity-based registration, locally rigid transformation

1. Introduction

To better understand the biomechanics of the pediatric ankle joint, it is crucial to establish *in vivo* normative joint biomechanics [7] before focusing on pathomechanics studies. This approach would likely contribute to a better long-term follow-up for childhood disabilities such as cerebral palsy.

Conventional MRI techniques have been used for accurate diagnosis of the ankle and foot disorders given the complexity of their anatomy [5]. Dynamic MRI was originally developed to study cardiovascular functions towards the end of the 1980s [18]. Since then, MRI acquisition and reconstruction techniques have improved by leaps and bounds with current sequences such as Fast-PC MRI, ultrafast MRI, and Fast Field Echo FFE. These techniques have been successfully employed to quantify the knee joint kinematics [22, 8], and to analyze *in vivo* 3D

12 musculoskeletal dynamics [6, 25], non-invasively. Sequences such as cine-PC MRI [17, 26] or
13 fast-PC MRI [23, 19] can provide *in vivo* joint velocity field measurements. However, these
14 data require long acquisition times with a high number of repeated cycles. Sequences such
15 as ultrafast MRI [9] allow faster scan speed by exploiting spatio-temporal redundancy and
16 can acquire images during a single cycle. However, they require slow motion of the joint
17 making the movement quasi-static. Thus, both these types of sequences are not appropriate
18 to acquire dynamic *in vivo* data for children especially with musculoskeletal disorders. In
19 this work, we use real-time FFE sequences [20] which are less sensitive to motion artifacts
20 and which reduce the scanning time to 18 seconds to acquire the dorsi-plantarflexion cycle.

21 Furthermore, post-processing of acquired dynamic images remains a challenging task due
22 to low resolution and motion artifacts. In [22], the displacement of specific points on each bone
23 were quantified by integrating the velocity data using a three-dimensional Fourier tracking
24 method [29]. Clarke *et al.* [9] determined *in vivo* muscle moment arms during ankle movement
25 using a 3D mesh-based registration method. They estimated bone motions by registering
26 the high-resolution joint geometry from MRI scans of the stationary joint to low-resolution
27 geometries from ultrafast MRI scans of the slowly moving joint. However, in addition to
28 the segmentation of the high-resolution static scan, it was needed to manually segment each
29 low-resolution time-frame which was time-consuming and prone to segmentation bias.

30 In this study, the spatial information of the high-resolution static MRI data and the temporal
31 information of the dynamic data were combined using a log-euclidean polyrigid framework
32 (*LEPF*). The purpose of this study was twofold : 1) to estimate bone motion, allowing to
33 derive the 3D kinematics of the joint, 2) to compute temporal dense deformation fields of the
34 joint, allowing to reconstruct a high-resolution dynamic MRI sequence from a low-resolution
35 dynamic MRI sequence and one high-resolution MR image.

36 The use of the *LEPF* proposed by Arsigny *et al.* [4, 3, 2] has been investigated for registration
37 of structures such as the hip and knee joint in mouse CT images [16], human hands from 2D
38 hand radiographs [14], bones in lower-abdomen area [11], and also intra-subject mandible
39 3D datasets [21].

40 In this work, we adapted this framework to deal with 4-dimensional MRI data by pro-
41 posing a fast and accurate algorithm to compute the dense deformation fields in regular
42 grids. In fact, we propose to compute the exponential mapping of the *LEPF* using matrix
43 eigendecomposition instead of the scaling and squaring method used in the literature [2, 11].

44 2. Materials and methods

45 2.1. Subject recruitment

46 Six typically developing children with a mean age of 12 years and with a mean weight
47 of 35.8 kg participated in this study which was approved by the regional ethics committee.
48 Children were selected with no contraindications to MRI and with no history of lower limb
49 musculo-skeletal injury or surgery in the past six months. MRI data were acquired in a single
50 visit after parents signed informed consent forms.

51 *2.2. Data Acquisition*

52 MRI data have been acquired using a 3T MR scanner (Achieva dStream, Philips Medical
53 Systems, Best, Netherlands). An MRI-compatible orthotic fixture was used to perform dy-
54 namic movements inside the scanner(Figure 1). Individual range-of-motion was checked by
55 the cilnician outside the MRI scanner and stops were placed on wire guides for controlling
56 the range-of-motion inside the scanner. Each dynamic scan lasted for 18 seconds and ankle
57 joint was moved (actively or passively) through the range-of-motion for each subject within
58 18 seconds with a rotation speed of $4^\circ/s$ to $5^\circ/s$ (depending on the range). Both passive
59 and active acquisitions were standardized for all subjects as detailed in [Annexe A](#). Dynamic
60 images were acquired in the oblique axis of the ankle motion. This was done by acquiring
61 axial dynamic scans first and then obliquely orienting the scanning plane for images to be
62 acquired in sagittal plane.

63 The scanning protocol included one high-resolution static 3D scan of the ankle joint
64 with a resolution of $0.26 \times 0.26 \times 0.8mm$ (T1-weighted gradient-echo, flip angle 10° , matrix
65 576×576 , FOV $150mm \times 150mm$, TR/TE 7.81/2.75 ms, mean acquisition duration : 424.32
66 s), and three low-resolution dynamic sequences per child : two passive sequences for repeata-
67 bility measures and one active sequence, all acquired with knee angle kept at full extension
68 (approximately between 0° to 10°). Each sequence is composed of 15 time frames with a
69 voxel size of $0.57 \times 0.57 \times 8mm$ (flip angle 15° , matrix 352×352 , FOV $200mm \times 200mm$,
70 TR/TE 20.61/1.8 ms, acquisition duration : 18.98 s).

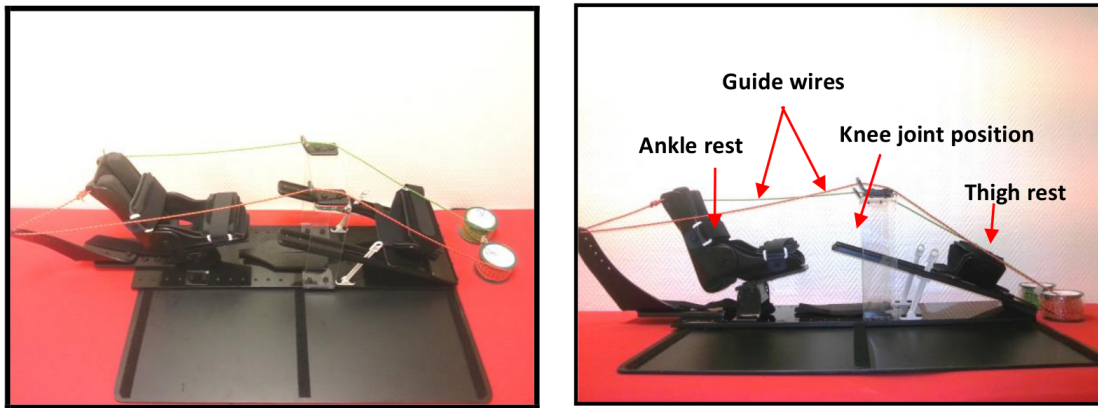


FIGURE 1 : Orthotic fixture specially designed to acquire MRI data on pediatric ankle joint. The entire fixture is made out of MRI-compatible material. Guide wires helped the technician to control and operate the passive plantar-dorsi flexion movements of the ankle joint while rest of the limb is fixed using straps at foot, tibia and mid thigh locations. Position of the ankle rest can be adjusted based on the limb length. Knee angle can be adjusted from full extension to 45° flexion. Cushioned ankle rest supports the foot to be imaged.

71 *2.3. Data post-processing*

72 Temporal tracking of the ankle bones is a challenging task because of nonlinearly articu-
73 lated joint motion. Image registration is an *iterative* process maximizing a similarity measure

74 between two images (source and target) in order to find the optimal geometric transforma-
 75 tion that best align them. In this work, we used a locally-linear intensity-based registration
 76 method to estimate bone motion, and then we fused these local transformations to compute
 77 temporal dense deformation fields.

78 2.3.1. Motion estimation

79 The bones of interest were manually segmented in the high-resolution static image (Fi-
 80 gure 2) and then automatically propagated throughout the dynamic low-resolution sequence
 81 using intensity-based registration.

82 The proposed approach for motion estimation consisted in two steps : 1) estimating a map-
 83 ping for each bone between static MRI data and dynamic sequences, 2) estimating the
 84 relative bone motions using the dynamic sequence.

85 **step1** : The first step was to compute the transformations from the static image to the
 86 dynamic images. In order to make this step robust, the multi-resolution registration was
 87 carried out in two steps : *First*, the static image was globally (and rigidly) registered to each
 88 low-resolution time frame $\{D_k\}_{k \in 1 \dots K}$. This provided a set of rigid transforms $\{T_{S \rightarrow D_k}\}_{k \in 1 \dots K}$.
 89 *Second*, initialized with the set of global rigid transforms $\{T_{S \rightarrow D_k}\}_{k \in 1 \dots K}$, the temporal posi-
 90 tion of each bone was refined thanks to a local rigid registration using bone masks. In this
 91 step, the static image is registered to each dynamic image $\{D_k\}_{k \in 1 \dots K}$ using input weights on
 92 each of the bones separately. This provided another set of rigid transforms $\{T_{S \rightarrow D_k}^i\}_{k=1, \dots, K}^{i=1, \dots, 3}$.
 93 To maximize the robustness of the algorithm, an image D_{k^*} from the dynamic sequence whose
 94 the content is the closest to the static image, was automatically detected. The underlying
 95 assumption is that the registration process is much simpler to converge for transformations
 96 close to the identity. To this end, the image of the sequence for which the overlap between
 97 regions of interest before and after bone-dependent registration was maximum, was selected
 98 as the reference image which served as a starting point for the motion estimation within the
 99 dynamic sequence.

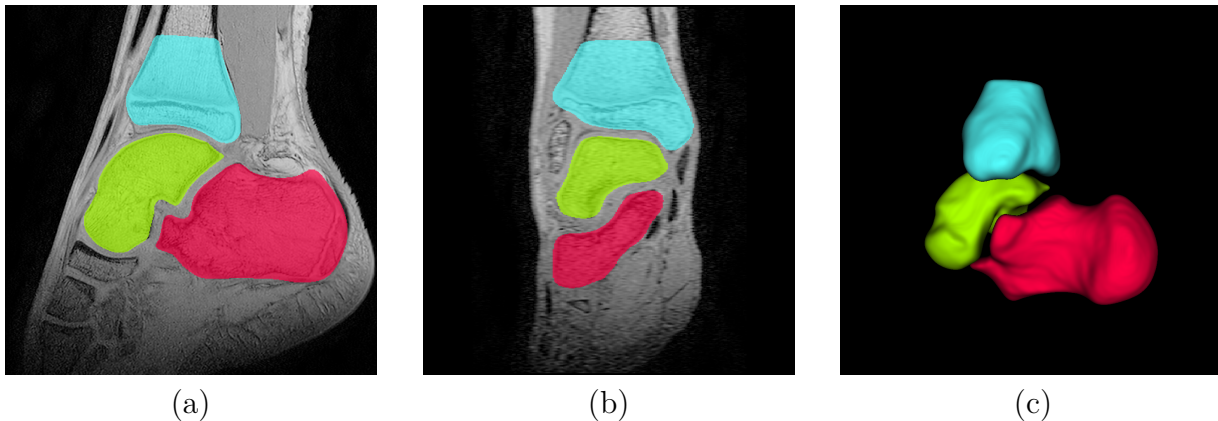


FIGURE 2 : Bones of interest : calcaneus (red), talus (green) and tibia (cyan). (a) : Mid-sagittal image from the high-resolution static scan ; (b) : Mid-coronal image from the high-resolution static scan ; (c) : Three dimensional rendering of segmented bones.

100 **step2** : The second step focused on the estimation of bone motion during the dynamic
 101 sequence. To do this, we proposed to take advantage of the temporal regularity of the data
 102 by propagating the bone masks in the dynamic sequence. For each bone, a rigid transform
 103 was estimated between successive images. *i.e.* local and rigid registrations were conducted
 104 from the reference image D_{k^*} towards first and last images of the sequence. To go forward
 105 and backward in time, only one interpolation was needed to propagate segmentation from
 106 D_{k^*} to each time frame D_k by composing a set of successive rigid transforms in order to
 107 avoid the propagation of interpolation errors as much as possible. Temporal bone rotations
 108 were optimized based on their quaternion representations [15], making the segmentation
 109 propagation more robust.
 110 The overall algorithm for bone motion estimation is described in [Annexe B](#).

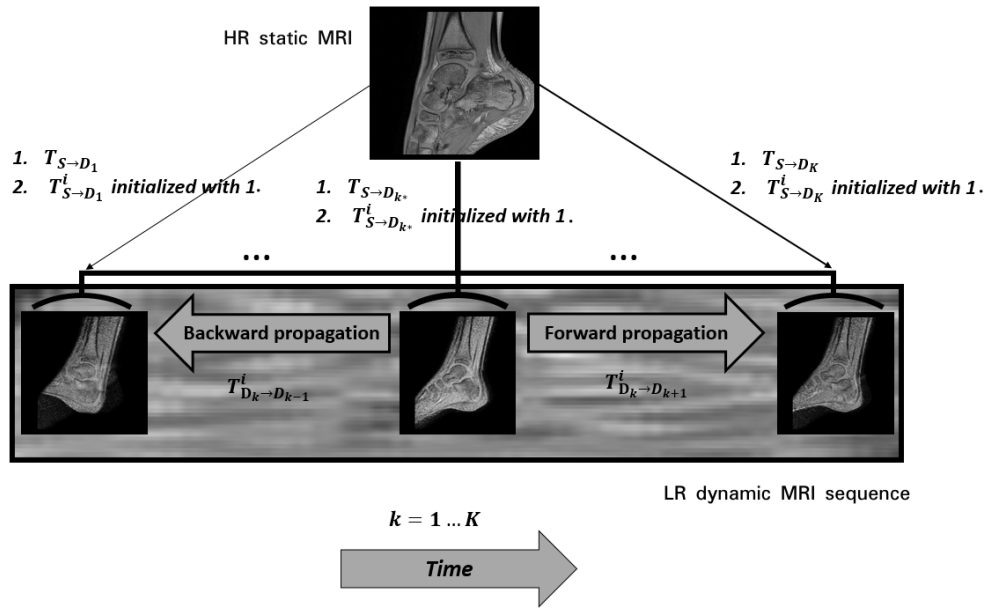


FIGURE 3 : Proposed pipeline for ankle motion estimation : Bones of interest are segmented in the high-resolution static image. This high-resolution MR image is globally (and rigidly) registered to each MR image of the dynamic sequence (1.), and the position of each bone is refined thanks to a local rigid registration using bone segmentations (2.). This allows to identify the dynamic MR image which is closest to the high resolution image and which will serve as a starting point for the motion estimation within the dynamic sequence. Last, local and rigid registrations are conducted from the reference towards the sequence first and last images.

111 2.3.2. Computation of temporal dense deformation fields

112 A dense deformation map of the joint from the static to each time frame was obtained by
 113 fusing rigid transforms corresponding to the bones of interest. For each bone, a non-negative
 114 weighting function was computed based on a distance to the mask [10]. Each weighting
 115 function reflects the local influence of the rigid transform of each bone. For each voxel x , the

116 weighting functions were computed as follows :

$$117 \quad w_{D_k}^i(x) = \frac{1}{1 + dist^2(x, M_{D_k}^i)} \quad (1)$$

118 where : $dist(x, M_{D_k}^i)$ is the Euclidean distance between the point x and the mask of the bone
119 i propagated onto the dynamic image D_k .

120 Given a point x in the high-resolution static image, the target location of this point in
121 the dynamic image D_k can be computed with the following equation [4] :

$$122 \quad \mathcal{T}_{S \rightarrow D_k}(x) = \exp \left(\sum_{i=1}^N \tilde{w}_{D_k}^i(x) \log(T_{S \rightarrow D_k}^i) \right) .x \quad (2)$$

123 where $\mathcal{T}_{S \rightarrow D_k}$ is the dense *invertible* deformation field from the static image S to the dynamic
124 image D_k , $\tilde{w}_{D_k}^i$ is a normalized weighting function (*i.e.* $\sum_{i=1}^N \tilde{w}_{D_k}^i(x) = 1, \forall x \in D_k$).

125 2.3.3. Fast computation of dense deformation fields

126 In this section, we describe an efficient algorithm to compute deformation fields in dense
127 regular grid based on the algebraic properties of the Log-Euclidean polyrigid framework.
128 In [3, 2], the matrix exponential was recursively *approximated* with a certain level of accuracy
129 using the *scaling and squaring* method by taking into account that the matrix exponential is
130 much simpler to compute for matrices close to zero via the Padé approximant. In this work,
131 we computed the exponential mapping of equation 2 *exactly* using eigen decomposition. As-
132 suming the log-euclidean mean of linear transformations $L(x) = \sum_{i=1}^N \tilde{w}_{D_k}^i(x) \log(T_{S \rightarrow D_k}^i)$
133 to be *diagonalizable* (*i.e.* $L(x)$ can be expressed in homogenous coordinates as : $L(x) =$
134 $P.D.P^{-1}(x)$, where the columns of P contains the eigenvectors $\{v_k(x)\}_{k \in \{0 \dots 4\}}$ corresponding
135 to the complex eigenvalues of $L(x)$, $\{\lambda_1(x), \lambda_2(x), \lambda_3(x), 1\}$), we broadcasted the exponen-
136 tiation of transformation eigenvalues over all grid points using the following Equation :

$$137 \quad e^{L(x)} = P e^D P^{-1}(x) = P \begin{pmatrix} e^{\lambda_1} & 0 & 0 & 0 \\ 0 & e^{\lambda_2} & 0 & 0 \\ 0 & 0 & e^{\lambda_3} & 0 \\ 0 & 0 & 0 & e \end{pmatrix} P^{-1}(x) \quad (3)$$

138 2.4. Determination of ankle joint biomechanics

139 2.4.1. Definition of anatomically based coordinate systems

140 Anatomical coordinate systems $\{R_i\}_{i=1, \dots, N}$ were defined on each bone in the high-
141 resolution image S following the same protocols used in [24] as illustrated in Figure 4,

142 and then mapped into the neutral position D_n using the estimated local-rigid transforms
 143 $\{T_{S \rightarrow D_n}^i\}_{i=1, \dots, N}$. The neutral dorsi-plantarflexion position was defined at an ankle angle of
 144 90° as recommended by the ISB standards committee [28]. However, the above defined neu-
 145 tral position cannot be always achieved during dynamic scanning. Therefore, the image in
 146 which the foot position was closest to a dorsi-plantarflexion position of zero degrees was
 147 selected as the neutral position.

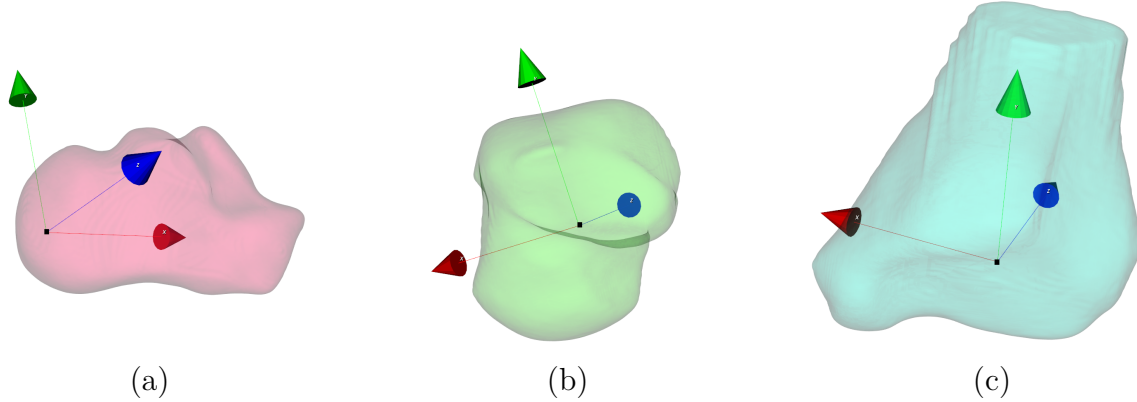


FIGURE 4 : Anatomical coordinate systems for one subject's calcaneus (a), talus (b), and tibia(c) as per ISB.

148 2.4.2. Quantification of ankle joint kinematics

149 In this study, the kinematics were defined through the 3D registration of the entire
 150 bone volume. More precisely, rotations and translations of each bone i were determined
 151 from estimated rigid transforms $\{T_{D_k \rightarrow D_{k+1}}^i\}_{i=1, \dots, N}$. Ranges of motion were estimated using
 152 low-resolution image data on multiple dynamic images (15 ankle positions). Kinematics
 153 of talocrural joint, subtalar joint, and calcaneal-tibial complex were then derived from
 154 $\{T_{D_k \rightarrow D_{k+1}}^i\}_{i=1, \dots, N}$.

155 Given the image coordinate system $R_I = (O, \vec{x}, \vec{y}, \vec{z})$, we defined the transformation, $M_{R_I \rightarrow R_j}$,
 156 that mapped R_I to an anatomical bone-based coordinate system $R_j = (O^j, \vec{x}^j, \vec{y}^j, \vec{z}^j)$. This
 157 transformation changed a representation from the R_j system to the R_I system.

158 Individual bone transformation matrices expressed in R_I were then converted into the trans-
 159 formation matrices expressed in the new anatomical coordinate systems R_j as follows :

$$160 T_j^i(k) = (M_{R_I \rightarrow R_j} \times T_{D_k \rightarrow D_{k+1}}^i \times M_{R_I \rightarrow R_j}^{-1})_{k=1, \dots, K-1; i=1, \dots, N; j=1, \dots, N} \text{ where :}$$

- 161 — $T_j^i(k)$: 4×4 rigid transformation matrix of the i^{th} bone relative to the j^{th} local bone
 162 coordinate system at time k .
- 163 — $M_{R_I \rightarrow R_j}$: the change of basis matrix.

164 2.5. Method evaluation

165 To evaluate the proposed registration approach for bone motion estimation, the propa-
 166 gated mask of each bone through the dynamic sequence was compared with a manually
 167 delineated bone on each time frame. The accuracy of the estimations of the successive rigid

168 transforms was assessed by computing the DICE coefficient $Dice(B_k^i, B_{m_k}^i)$ and the RMS
 169 error $RMSE(B_k^i, B_{m_k}^i)$ where B_k^i was the propagated mask of the bone i on dynamic image
 170 D_k and $B_{m_k}^i$ was a manually delineated mask of the same bone on the dynamic image D_k . A
 171 DICE value close to one indicates that the bone masks have been well propagated through
 172 the entire dynamic sequence.

173 The RMS error was computed as follows :

174 $RMSE(B_k^i, B_{m_k}^i) = \sqrt{1/n_c \cdot \sum_{x_c=1}^{n_c} dist^2(x_c, \zeta_{B_k^i})}$ where n_c is the total number of voxels of
 175 ground-truth contours (i.e. contours of $B_{m_k}^i$) and $dist(x_c, \zeta_{B_k^i})$ is the Euclidean distance
 176 between x_c and the contour of B_k^i .

177 3. Results

178 Results on bone motion estimation were reported in Figures 8-9 for the six subjects of the
 179 pilot study. In most of the cases, the DICE coefficient was greater than 0.8 and the RMSE was
 180 smaller than 0.6 indicating accurate propagations of bone masks over the dynamic sequence,
 181 for both passive and active motions. From the set of rigid transforms of each bone over the
 182 dynamic sequence, it was then possible to compute temporal dense deformation fields to
 183 synthesize a high-resolution dynamic MRI sequence. Using the fast computation technique
 184 described in Section 2.3.3, a dense deformation field was computed in $3min$ on an Intel[®]
 185 Xeon[®] Processor E3-1271 v3 3.60 GHz on a $576 \times 576 \times 90$ regular grid and in $15min$ on
 186 a very high dimensional space ($576 \times 576 \times 202 \simeq 67$ million deformation vectors) which
 187 required a high capacity RAM because computations were performed in the complex domain
 188 for the purpose of enhancing the accuracy. Figure 10 illustrates, for one subject (A6), such
 189 high-resolution reconstructed data.

190 Three-dimensional kinematics of the joint under both active and passive ankle dorsi-
 191 plantarflexion movement using the current 3D dynamic MRI method were presented in
 192 Figures 5 to 7. Kinematics of all ankles (except A5) were derived from the estimated tem-
 193 poral rigid transforms of each bone of interest, converted into the matrices of the calcaneus
 194 relative to the tibia, the talus relative to the tibia, and the calcaneus relative to the talus.
 195 The talus mistracking for the ankle A5 was caused by the considerable missing portion from
 196 the bone in intermediate time frames due to the inappropriate initial placement of the flex
 197 coils.

198 The mean rotation about the Inferior-Superior and about the Posterior-Anterior axes (ave-
 199 raged across time for all subjects) was close to 0 degrees for both active and passive motion.
 200 The mean range of passive rotation about the Medial- Lateral axis for talocrural and calcaneal-
 201 tibial joints was between -11 degrees of maximal dorsiflexion and $+32$ degrees of maximum
 202 plantarflexion with full extended knee. This demonstrates excellent correspondance with the
 203 mean range of passive rotation reported in [1] and validated for 245 healthy children between
 204 7 and 14 years old.

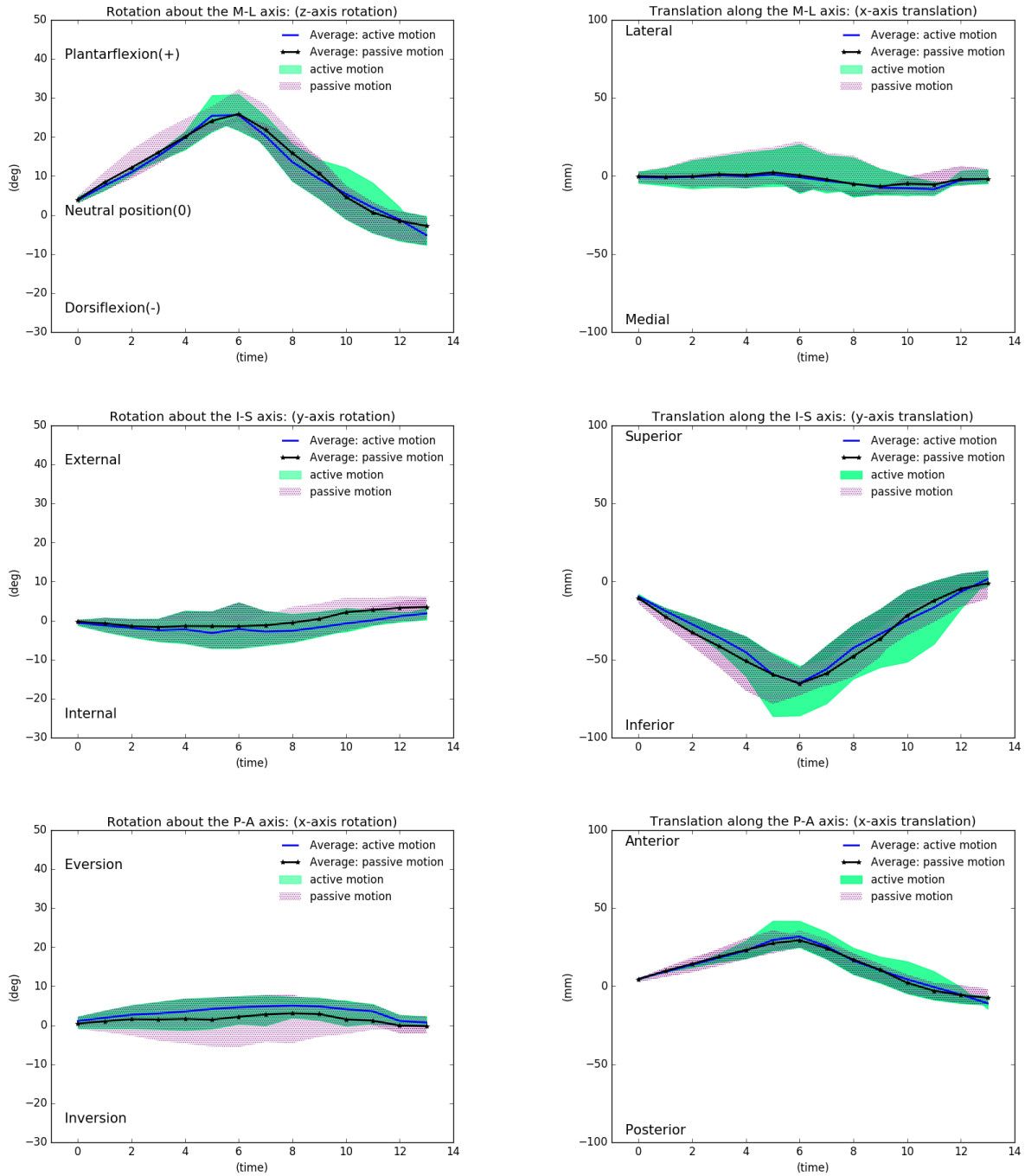


FIGURE 5 : 3D normative kinematics of the calcaneal-tibial complex using the proposed image processing method. The kinematics of the calcaneus are represented relative to the tibial coordinate system defined in neutral position. Average rotation and translation were computed for both passive and active motion for the studied ankles. Standard deviation above and below the average line are shown (hatched shaded area for passive motion and green shaded area for active motion).

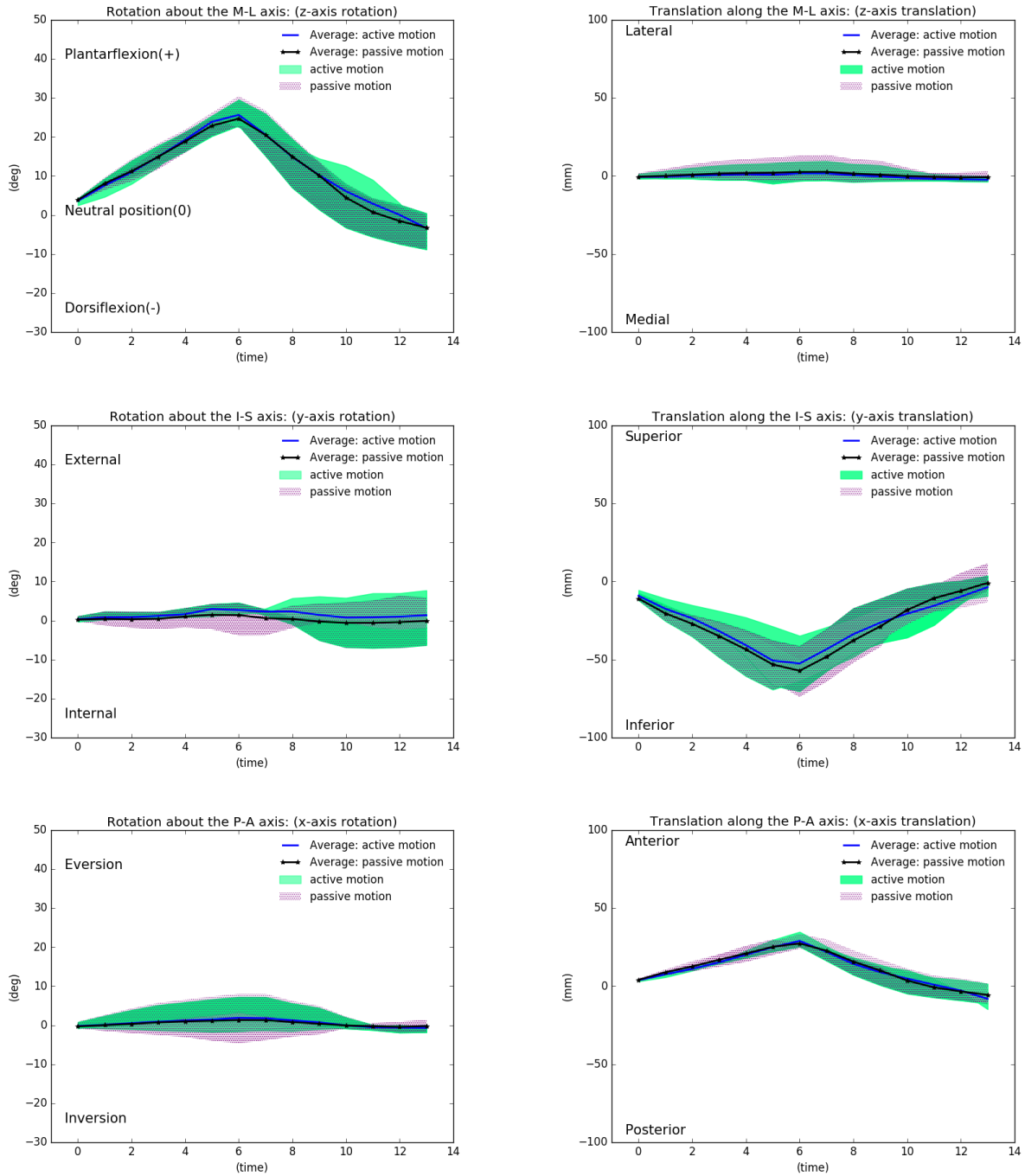


FIGURE 6 : 3D normative kinematics of the talocrural (talar-tibial) joint using the proposed image processing method. The kinematics of the talus are represented relative to the tibial coordinate system in neutral position. Average rotation and translation were computed for both passive and active motion for the studied ankles. Standard deviation above and below the average line are shown (hatched shaded area for passive motion and green shaded area for active motion).

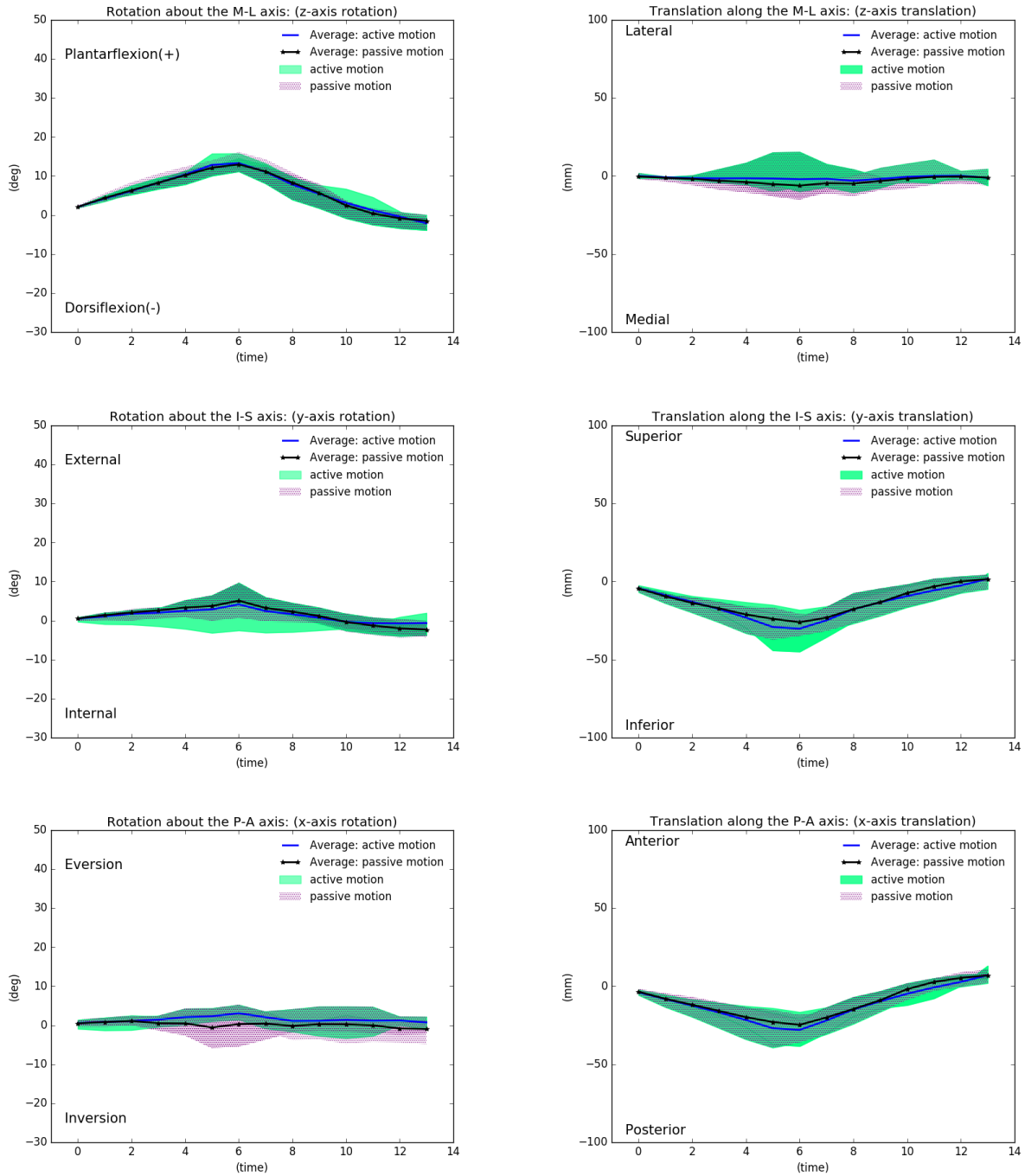


FIGURE 7 : 3D normative kinematics of the subtalar joint using the proposed image processing method. The kinematics of the calcaneus are represented relative to the talar coordinate system in neutral position. Average rotation and translation were computed for both passive and active motion for the studied ankles. Standard deviation above and below the average line are shown (hatched shaded area for passive motion and green shaded area for active motion).

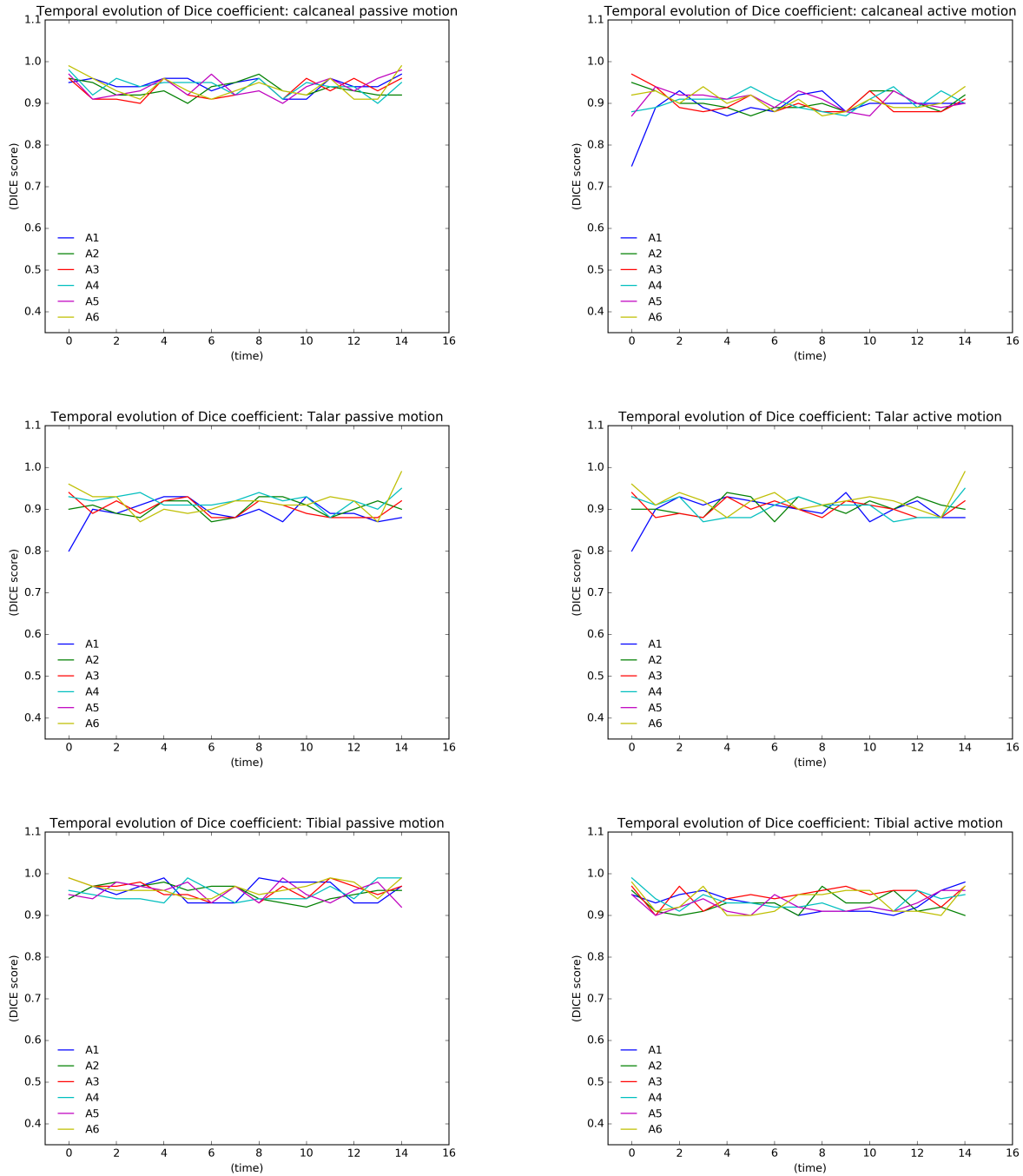


FIGURE 8 : 3D DICE coefficients between manual and automatic bone segmentation maps for the six subjects of the pilot study taking account of the whole set of bone trajectories. Results for passive (left column) and active motion (right column) are separated. A dice value of 1 indicates perfect geometric alignment between automatic and ground truth segmentations.

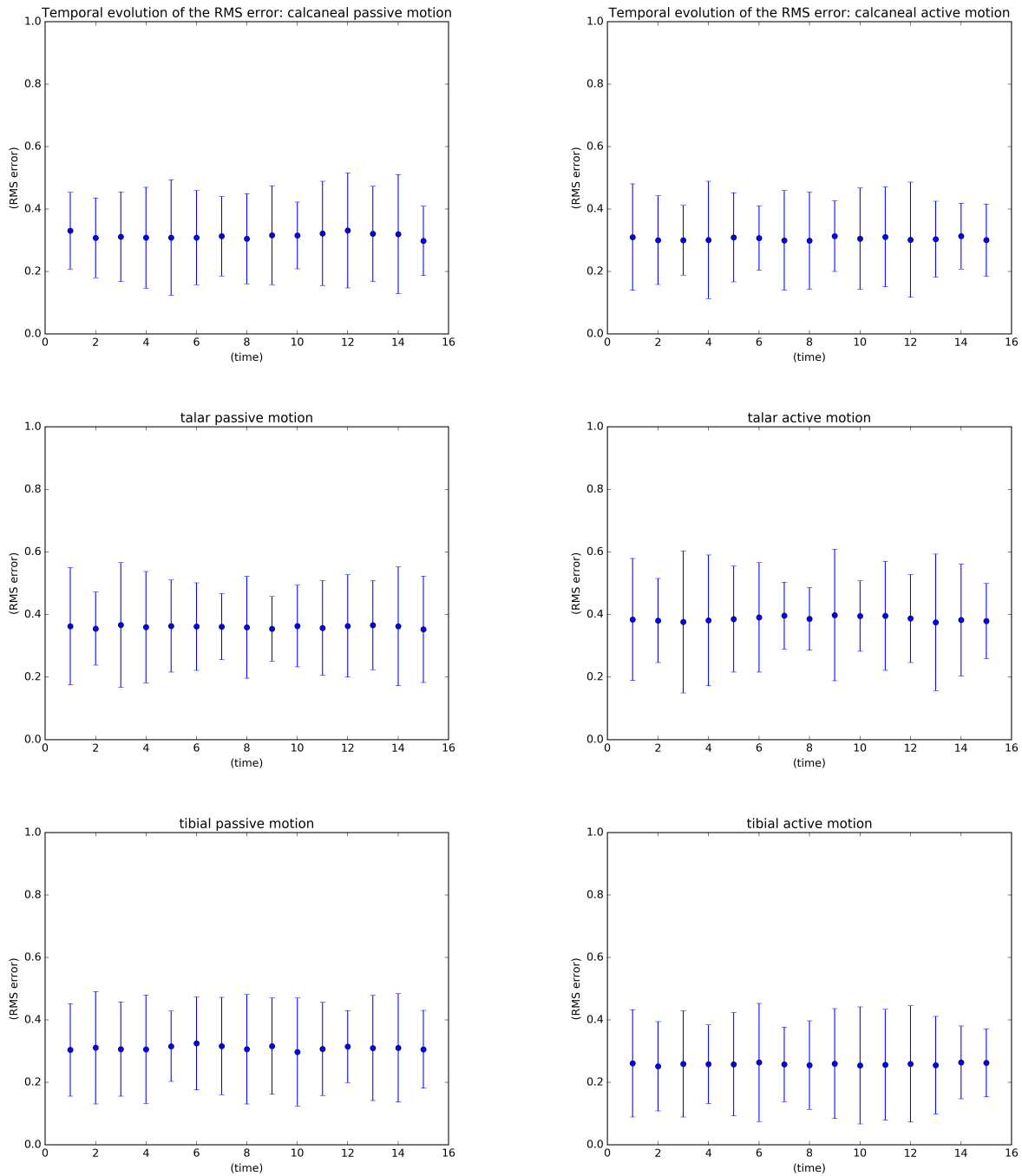


FIGURE 9 : Temporal evolution of the root-mean-square error (RMSE in voxels) between manual and automatic bone segmentations for subjects of the pilot study. Errors are represented using error bars. The average is shown with a dotted line with one standard deviation above and below this line. Results for passive (left column) and active motion (right column) are separated.

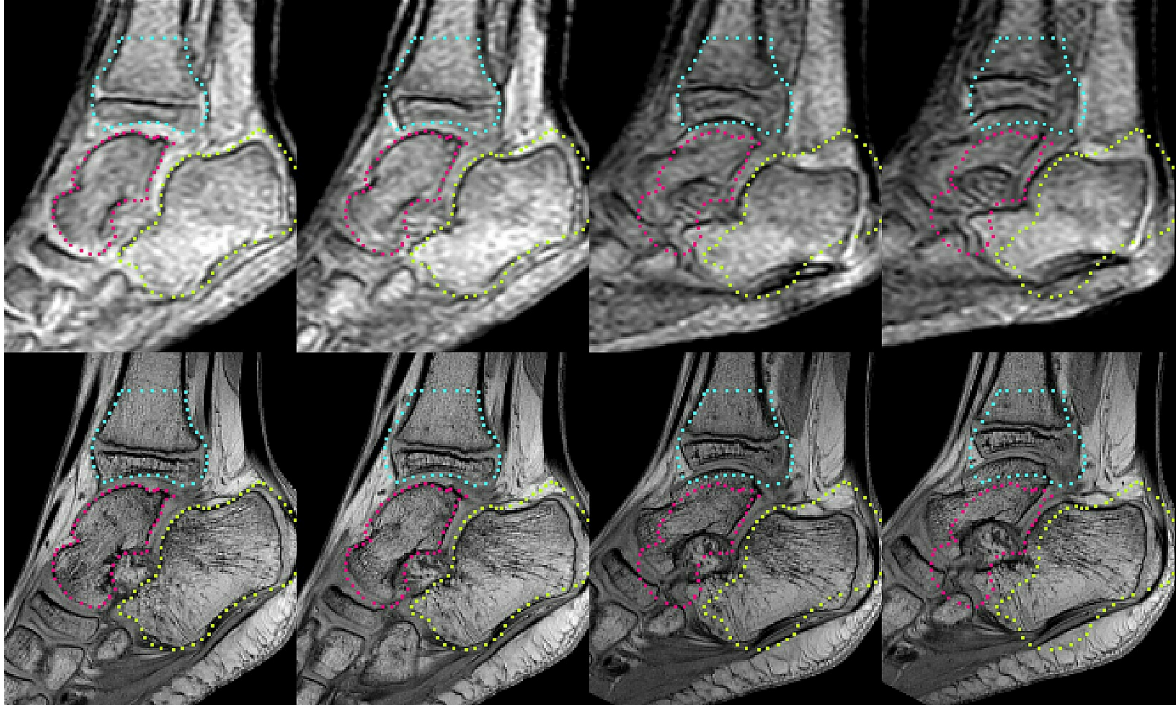


FIGURE 10 : High resolution temporal reconstruction for one subject (subject 6 : passive motion). First row : original dynamic images, second row : corresponding high-resolution reconstructed images, downsampled to resemble to the original low-resolution images in order to validate the reconstruction accuracy. Each column corresponds to one time frame. Contours of the first time frame show the reconstruction accuracy (column 1) and the joint motion (columns 2 to 4).

205 4. Discussion

206 In this study, we have presented a method to determine full 3D-kinematics of the ankle
 207 joint from dynamic anatomical MRI data. An intensity-based registration pipeline has been
 208 proposed to estimate bone motion through the dynamic sequence. The robustness of this
 209 approach for both passive and active motion has been evaluated on *in vivo* data acquired for
 210 a pilot control cohort study. Although based on a successive estimation of transformations,
 211 the proposed approach demonstrates advantages in efficiency, reliability and robustness for
 212 all subjects.

213 The proposed algorithm is robust enough to image quality as well as motion artefacts in a
 214 way that it can determine kinematics even for unconstrained motion. This was evaluated
 215 by changing the delta-time Δk separating each couple of source/target images during the
 216 successive rigid registrations and the algorithm is still robust even for $\Delta k = 5$.

217
 218 Normative passive kinematics show that the subjects maintained a consistent movement
 219 trajectory. Three-dimensional kinematics of the joint under passive ankle movement using
 220 the proposed method (Figures 5 to 7) were similar to ankle joint kinematics reported in
 221 other studies using velocity data [24]. Normative active kinematics show that the subjects

222 were able to perform voluntary plantar-dorsiflexion between the extreme positions with the
223 same temporal regularity as for passive motion. The comparison between passive and active
224 kinematics shows closest temporal averages despite some temporal fluctuation of the stan-
225 dard deviation across subjects.

226

227 Although the fact that both our method and other motion methods tend toward the same
228 goal which is bone motion tracking, there are some technical differences making it difficult
229 to perform an objective comparison based on a common error parameter.

230 In [9], the authors were more interested in the Achilles tendon moment arms and the accu-
231 racy and precision of bone motion tracking were not reported. Clarke et al. [9] have discussed
232 some limitations in their methods which can be particularly useful in adults. They have ex-
233 plicitly mentioned that their protocols require some modifications to be useful in the smaller
234 joints of children. To satisfy the mesh density requirements for using the ICP algorithm,
235 they have recommended the reduction of the slice gap for the dynamic scanning protocol
236 while increasing the number of slices per time frame so that the slices span the joint width.
237 However, assuming that they have used ultrafast MRI sequences (with 8 sagittal slices/time
238 frame compared to 6 slices in our work, and taking around 2 min to acquire 10 to 20 time
239 frames compared to only 18 sec to acquire 15 time frames in our work), increasing the num-
240 ber of slices will increase the scanning time of dynamic data to more than 2 min which will
241 be uncomfortable especially for the pathological subjects. The authors have also notified
242 that the rotation speed for their study was slow (mean $1^\circ/\text{s}$ compared to $4.2^\circ/\text{s}$ in our work)
243 in order to reduce the effects of motion artifacts, so the motion itself is reduced to almost
244 static or quasi-static nature where no real functionality can be assessed. Our choice for FFE
245 sequences for dynamic data acquisition was motivated by the fact that these techniques are
246 less sensitive to motion artifacts [27] and more than 5 times faster than ultrafast MRI.

247 In the work of Sheehan *et al.* [24], the displacements of three to five points on each bone were
248 calculated through Fourier integration and then converted into three-dimensional orientation
249 angles. As part of the tracking process, they identified a series of vertices, defining regions
250 on each bone of interest in the first time frame (*i.e.* three to five vertices per bone). The
251 distance between these vertices in the first time frame was considered the absolute distance
252 under the assumption that it should remain fixed throughout the movement because bones
253 are rigid. Thus, for each bone, the difference in distance between vertices in each time frame
254 relative to the absolute distance was defined as the tracking error. A potential limitation
255 of this study [24] was the out of plane accuracy of the bone motion because the accuracy
256 of cine-PC MRI is independent of the shape of the bone being tracked [6]. Another clinical
257 limitation is that subjects with musculoskeletal disease who cannot complete a large number
258 of repeated motions cannot be studied with cine-PC MRI techniques. Although the vertices
259 were well-defined from 3D high-resolution adult data in previous work of Sheehan *et al.* [24],
260 it was hard to reproduce their exact locations from developing children data for comparison
261 purposes because of the differences in bone size and topology between children and adults.
262 From another point of view, it was not sufficient to consider the distance between only some
263 vertices as system bias and thus we have considered all the bone segmentations (*i.e.* all the

264 volumetric information) for method evaluation.

265

266 The proposed method remains robust as long as the field-of-view (FOV) is well adjusted
267 (i.e. when the FOV covers either the full or nearly-full anatomy of the ankle bones throu-
268 ghout the entire joint trajectory).

269

270 We have also extended the log-euclidean framework to estimate temporal dense deforma-
271 tion fields from multiple rigid transforms. The polyrigid approach provides a way to combine
272 high resolution spatial information with temporal dynamics of joints. The output of this pro-
273 cess is a series of high-resolution anatomical images portraying the different phases of the
274 movement cycle. In this context, we proposed to compute the exponential mapping of the
275 LEPF in an efficient and elegant way using matrix diagonalization-based techniques rather
276 than using techniques involving approximation theory. The preservations of the bone shapes
277 after the polyrigid fusion were checked by computing the Jacobian maps associated to the
278 estimated deformation fields (as shown in figure 11).

279

280 To conclude, our work is the first effort to track ankle joint motion and deformation
281 from volumetric image data using intensity-based non-rigid image registration rather than
282 using explicit mechanistic models. It therefore achieves its goals without having to per-
283 form time-consuming manual segmentations. In immediate future, the proposed approach
284 will be applied to compare the ankle joint dynamics of children with spastic equinus with
285 age-matched healthy children. Since spastic equinus is typically defined as the inability to
286 dorsiflex the foot above plantigrade, with the hindfoot in neutral position and the knee in
287 extended position [13], the foot was constrained to a specific path using the fixture in this
288 work. However, this set-up is problem-specific and can be changed or removed while evalua-
289 ting the pathomechanics of other joint(s). We will also explore this method to extract fine
290 biomechanical parameters of tendon, and cartilage contact mechanics (e.g. temporal joint
291 space width) of the tibio-talar joint which is the primary joint responsible for plantarflexion
292 and dorsiflexion of the ankle. Furthermore, these techniques can be applied to other joints
293 and related musculoskeletal disorders. This suggests that anatomical dynamic MRI and de-
294 dicated image processing techniques can open a new way to study in vivo human joints.

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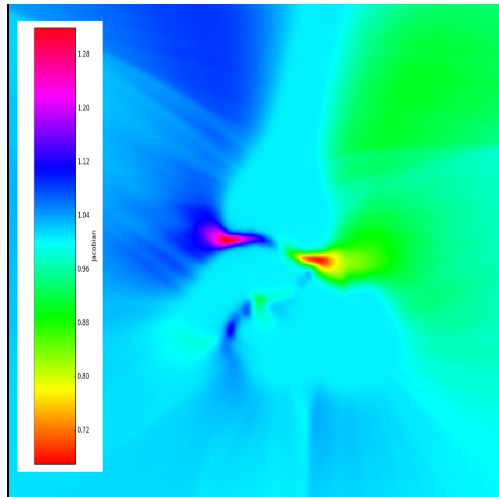


FIGURE 11 : Jacobian map of the joint deformation fields that maps D_1 to D_2 for subject 4. The Jacobian determinant $J(x)$ at a voxel x measures how the voxel volume changes after registration. It indicates a volume increase if > 1 , and a volume decrease if < 1 . The Jacobian determinant is equal to 1 inside bone segmentations (no voxel volume changes) as bones only perform linear rigid transformations (rotations and translations).

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387 **Annexe A. Supplementary Material**

388 An MRI safe orthotic fixture has been specifically designed in such way that it can be used
389 for performing either passive plantar-dorsiflexion or voluntary active ankle joint movement
390 (Figure 1). For passive acquisition, after placing the ankle joint in the fixture, each child was
391 asked to relax the lower-limb musculature and then the fixture was cyclically moved by a
392 technician at a rotation speed of 4°/s to 5°/s. The technician was given a set of headphones

Algorithm 1 Bone motion estimation

- 1 : **Input** : segmentation of bones of interest in S .
 - 2 : **Mapping estimation from S to $\{D_k\}$** :
 - Estimate rigid transforms $\{T_{S \rightarrow D_k}\}_{k=1, \dots, K}$
 - Estimate rigid transform $\{T_{S \rightarrow D_k}^i\}_{k=1, \dots, K}$ using bone mask M^i , initialized with $\{T_{S \rightarrow D_k}\}_{k=1, \dots, K}$
 - Select D_{k^*} in $\{D_k\}_{k=1, \dots, K}$ such that $k^* = \underset{k}{\operatorname{argmax}}(\prod_{i=1}^N \operatorname{Dice}(T_{S \rightarrow D_k}(M^i), T_{S \rightarrow D_k}^i(M^i)))$
 - 3 : **Motion estimation**
 - Estimate forward successive rigid transforms $\{T_{D_k \rightarrow D_{k+1}}^i\}_{k = k^*, \dots, K-1; i=1, \dots, N}$.
 - Estimate backward successive rigid transforms $\{T_{D_k \rightarrow D_{k-1}}^i\}_{k = k^*, \dots, 2; i=1, \dots, N}$.
 - 4 : **Output** : compute bone rigid transforms $\{T_{S \rightarrow D_k}^i\}_{k=1, \dots, K; i=1, \dots, N}$ by combining steps 2 and 3
-

393 through which he/she could hear a metronome. Fixture was then moved in a consistent
394 passive plantar-dorsiflexion by the technician at the beat of the metronome and using the
395 guide wires attached to the fixture. For active movement, no technician was present and
396 children were asked to perform voluntary plantar-dorsiflexion between the extreme positions
397 on the beat of the metronome. Meaning, the active motion was completely voluntary with all
398 the muscles dynamically taking part in the production of the plantar-dorsiflexion movement.

399 **Annexe B. Algorithm**

400 The overall algorithm for bone motion estimation is described in Algorithm 1 and in
401 Figure 3, using the following notations :
402 S : high-resolution static image, $\{D_k\}_{k=1, \dots, K}$: set of low-resolution dynamic images, $\{M^i\}_{i=1, \dots, N}$:
403 set of mask of bones of interest, $T_{A \rightarrow B}$: rigid transform from image A to image B , $T_{A \rightarrow B}^i$:
404 rigid transform from image A to image B for the bone i , $\operatorname{Dice}(A, B)$ is the DICE coefficient
405 which measures the overlap between segmented regions ($\operatorname{Dice}(A, B) = \frac{2|A \cap B|}{|A| + |B|}$). Rigid
406 registrations were performed using FSL-flirt [12] with correlation ratio as similarity mea-
407 sure. A voxel-wise weighting based on the segmentation masks was used when estimating
408 bone-dependent motion.

409 Code is available online at <https://github.com/rousseau/dynMRI>.