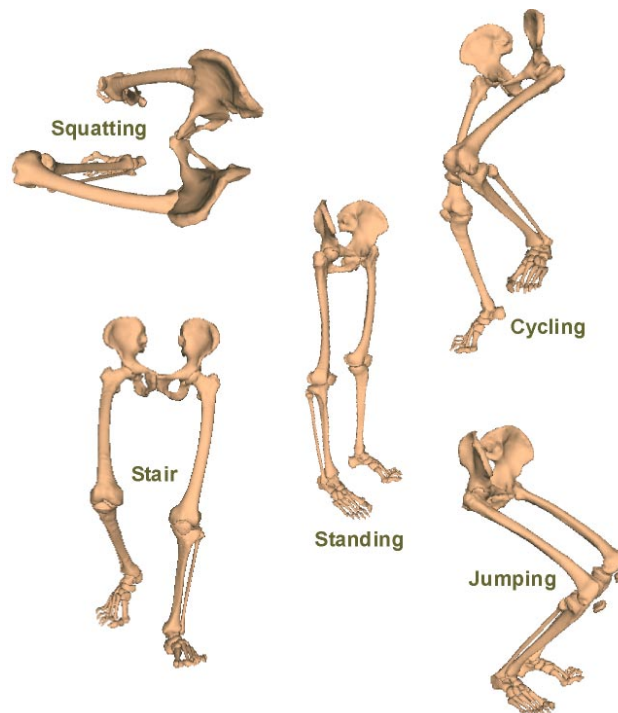


# How to use the VAKHUM database?

Version 1.0



**VAKHUM**

is an european project about

*"Virtual Animation of the Kinematics of the Human for Industrial, Educational and Research Purposes"*

VAKHUM is funded by the European Commission under the  
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## **How to use the VAKHUM database?**

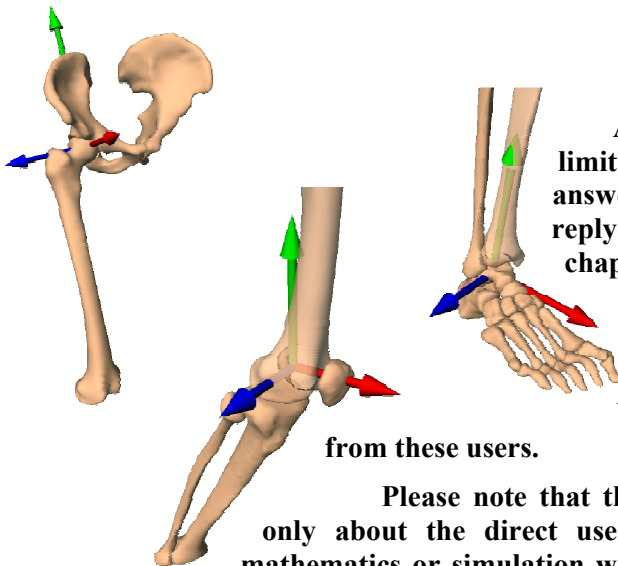
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Please, allow some time to receive an answer.

As the resources to support users are extremely limited, if the available documentation is sufficient to answer a question sent by a user, the authors will reply only by directing the user to the appropriate chapter of this document.

Some users of the VAKHUM database may consider that this document does not help them fully to understand the use of the VAKHUM database. We shall be happy to hear

from these users.

Please note that the VAKHUM consortium will answer questions only about the direct use of the database and that no help on basic mathematics or simulation will be given. For example, it is assumed that the user has the technical knowledge necessary to manipulate the data.



**VAKHUM**

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***"Virtual Animation of the Kinematics of the Human for Industrial, Educational and Research Purposes"***

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## Chapter I. VAKHUM Database Structure and Content

### 1.1 About this Document

This document is the *User's Guide* of the VAKHUM database. It contains information about the data and documents that you can find in the VAKHUM database. It also describes how to use the VAKHUM data.

**Some users of the VAKHUM database may consider that this document does not help them fully to understand the use of the VAKHUM database. We shall be happy to hear from these users.**

**Please note that the VAKHUM consortium will answer questions only about the direct use of the database and that no help on basic mathematics or simulation will be given. For example, it is assumed that the user has the technical knowledge necessary to manipulate the data.**

The indexing used for the equations in this document has been selected for clarity. We have tried to avoid using mathematical indices (e.g.  $A_i$ , where  $i = foot$ ), instead preferring self-explanatory indices, such as  $A_{foot}$ . We feel that this will make the document more understandable for inexperienced users.

### 1.2 About the Public Repository Website structure

The following structure is found in the data repository on the VAKHUM website, <http://www.ulb.ac.be/project/vakhum/>.

The two first links are self-explanatory:

- “**Doc**”: contains all documents necessary to understand and use the VAKHUM data.
- “**Data**”: contains all data.

#### The “DOC” section

The following documents are found in this section:

- **VAKHUM-0-How-To-Use:**
  - this document
- **VAKHUM-1-Data\_Collection\_Procedure.pdf**
  - VAKHUM internal report on the data collection procedure performed to obtain the morphological and kinematics data
  - this also includes validation data
  - note that no information on the registration protocols used within the VAKHUM project is given (this information is not yet public)
- **VAKHUM-2-Landmarks\_Palpation.pdf:**
  - contains the description of the anatomical landmarks used within the VAKHUM project for the creation of the anatomical frames and the registration process
  - both Virtual and Manual palpation are described
- **VAKHUM-3-Frame\_Convention.pdf:**
  - documents on the frame convention used within the VAKHUM project
- **VAKHUM-4-PGD\_File\_Structure.pdf:**
  - description of the PGD file structure (PGD is the file format used within VAKHUM for kinematics data storage).

## The “DATA” section

The following data are found in this section:

- **vakhum\_dicom:**
  - all original images, usually in several sequences, each of which is available in a separate .zip file
  - See *Chapter II. How to Visualise the Medical Imaging Datasets* for details
  
- **vakhum\_landmarks:**
  - **very useful data** that will allow you to perform complex operations on the VAKHUM data
  - .zip files containing files which names are characterised by the following strings:
    - “*...alignment*”: data to register all image data and/or 3D bone models (see *Chapter V. How to Create a Full Lower Limb Skeleton* for details)
    - “*...landmarks*”: 3D location of some particular anatomical landmarks collected directly on the 3D bone models (see *Chapter VII. How to Determine Anatomical Axes* to use these landmarks). Two separate files are given for the right and left lower limbs
  
- **vakhum\_stl, vakhum\_surf, vakhum\_vrml:**
  - three sections that contain 3D bone models in STL, SURF and VRML format respectively.
  - contain several .zip files that correspond to the same bone, but in different resolutions: **full** resolution, **medium** resolution, **small** resolution.
  - see *Chapter III. How to Visualise the 3D Bone Models* for details about the different resolutions and file formats
  - note that to create the full skeleton of the lower limb, you will also need the data available from the **vakhum\_landmarks** section (see above).
  
- **vakhum\_fem:**
  - contains a .zip file with all finite-element 3D bone models in six different resolutions and different file formats
  - see *Chapter IV. How to Choose and Use the Finite Element Models* for details.
  - warning: this is usually a huge file
  
- **vakhum\_pgd\_invivo:**
  - .zip file with all gait analysis data (in PGD format) collected on a volunteer
  - several tasks are usually available: walking, cycling, stair climbing, and so on – filenames are self-explanatory
  - note that data are not smoothed
  - see *Chapter VI. How to Create a Motion Simulation of the Kinematics of the Lower Limb Segments and Bones* for details about how to create a simulation of the lower limb segments from these data
  
- **vakhum\_pgd\_register:**
  - .zip file with all gait analysis data (in PGD format) collected on a volunteer registered to a particular morphology (also available from the VAKHUM website)
  - both registered subjects are indicated in the filename: for example “*vakhum\_subj006-025jump.pgd*” means that *subject006* has been registered to *subject025* for a **jump** task in **pgd** file format

- several tasks are usually available: walking, cycling, stair climbing, and so on – filenames are self-explanatory
- note the file contains both non-smoothed and smoothed data – the directory names are self-explanatory
- see **Chapter VI. How to Create a Motion Simulation of the Kinematics of the Lower Limb Segments and Bones** for details about how to create a simulation of the lower limb segments and bone models from these data
  
- **vakhum\_simulation:**
  - several .zip files showing the simulation result of the registration of the file available from both *vakhum\_pgd\_invivo* and *vakhum\_pgd\_register*
  - after decompression, the directory tree shows a sub-directory **HANIMsimulation** that contains several files in VRML format
  - several simulations are available and are characterised by particular strings in the filename:
    - “...*seg*”: means that this is the simulation of the lower limb segments
    - “...*bon*”: means that this is the simulation of the lower limb bone models
    - “...*sm*”: means that the simulation has been obtained after smoothing of the kinematics data
  - these simulations have been created from the VAKHUM data using the specifications from the Humanoid Animation Working Group (<http://www.h-anim.org/index.html>).

## Chapter II. How to Visualise the Medical Imaging Datasets

The image datasets available from the VAKHUM database are all in standard DICOM formats. Each image dataset is made of several sequences, each of which is separately available from the database (*Table 1*).

The user can visualise each dataset either separately or simultaneously by simply storing the images of successive sequences within the same directory (*Figure 1*).

No software for visualising medical imaging datasets is available from the VAKHUM database.



**Figure 1.** Display of a 3D femoral bone model together with the original image data source. The frontal slice has been interpolated from the stack of horizontal slices obtained after superposition of several sequences (available from the VAKHUM database).

**Important note 1:** for some subjects, several datasets have been obtained (*dataset1* and *dataset2*, see *Table 1*).

<i>dataset1 (up)</i>	<i>sequence1</i>	Iliac bone, hip joint (1 mm)
	<i>sequence2</i>	Femoral diaphysis (3mm)
	<i>sequence3</i>	Knee joint, upper part of shank (1 mm)
<i>dataset2 (low)</i>	<i>sequence1</i>	Knee joint, upper part of shank (1 mm)
	<i>sequence2</i>	Tibial diaphysis (3 mm)
	<i>sequence3</i>	Ankle joint and foot (1 mm)

**Table 1.** Example of datasets and sequences. Each dataset contains several sequences that are continuous within each other. The maximal length coverage (i.e. the distance between the first image of the first sequence and the last image of the last sequence) of a particular dataset is 1000mm.<sup>1</sup>

<sup>1</sup> This is due to the physical limitations of the medical imaging system used within the VAKHUM protocol.

Long bones can be reconstructed by using all the sequences within the relevant dataset.

If the dataset was obtained from the upper part of the lower limb (e.g. **Table 1**, *dataset1*), then data on the iliac bone, femoral bones, hip joint, and knee joint will be available.

If the dataset was obtained from the lower part of the lower limb (e.g. **Table 1**, *dataset2*), then data on the knee joint, tibial bone, fibula, ankle joint and foot bones will be available.

Note that in **Table 1** slice thickness was thinner at joint level (typically 1mm) than at diaphysis level (typically 3mm). Also, the number of sequences within each dataset varies between the subjects available from the VAKHUM database.

For some subjects, only one dataset is available. It is always similar to *dataset1* of **Table 1**.

For other subjects, both *dataset1* and *dataset2* (**Table 1**) are available. As explained previously<sup>1</sup> above, a simple display of both datasets will show unaligned bone models (**Figure 2**) – to visualise these datasets simultaneously, alignment must first be performed (see **Section 5.2 Morphology Visualisation**)



**Figure 2.** Example of bone display without alignment correction. The green bone models have been obtained from *dataset1*, while the yellow bone models were obtained from *dataset2* of the same subject. See text for explanations.

**Important note 2:** all datasets show the fiducial landmarks (i.e. aluminium balls) that were used in order to further process the data within the VAKHUM project frame. The landmarks were either directly inserted into the bones or mounted on aluminium pins that were screwed into the bones. These fiducial landmarks do not appear on the 3D models available from the VAKHUM database (see **Chapter III. How to Visualise the 3D Bone Models**).

## Chapter III. How to Visualise the 3D Bone Models

### 3.1 File Formats

The bone models are available in several formats (STL, SURF and VRML). It is up to the user to obtain or create proper filters to display or use the bone models on her/his system. Note that for the VRML format several viewers are freely available on the Internet. Bone models from different subjects and genders are available from the VAKHUM database.

### 3.2 Model Reference Frame

All 3D models are defined in the original reference frame of the medical imaging system. It means that each model can be displayed simultaneously with the corresponding image dataset without any particular processing (*Figure 1*).

### 3.3 Model Resolution

Several model resolutions are available: *full*, *medium*, *small* (*Table 2*). Different resolutions are of interest for different applications, as explained below.

#### Full

*Full* resolution shows the models obtained from segmentation with no decimation<sup>2</sup>. Because no facet reduction was applied, these models require large amounts of storage, i.e. some models have several hundred thousand facets. Computer processing or visualisation of these models can be slow because of their complexity.

This resolution is for users who want unprocessed data as input for their own data processing algorithms (e.g. decimation).

#### Small

*Small* resolution shows the models obtained after segmentation and extensive decimation. The maximum number of facets in these models is a few thousand. The decimation rate was decided by people highly experienced in the simulation field.

This resolution is for users who want data for simulation purposes (e.g. real time simulation of complex human motion). Because of the light mesh structure, several bones can be combined in a full lower limb model without overload for most computers. However, the decimation will probably have removed most of the small natural anatomical structures on the bone surface.

#### Medium

*Medium* resolution shows the models obtained after a *medium* decimation has been applied. It is a good compromise between the *full* and *small* resolutions, and aims to provide models that combine accurate 3D anatomical data with a mesh sufficiently decimated to allow comfortable 3D object manipulation on an everyday computer. The decimation rate was again decided by people highly experienced in the simulation field.

*Full* resolution models are too large to be manipulated easily during an anatomy class using normal computers. On the other hand, *small* resolution is too low to be acceptable for the study of bone anatomy. The *medium* resolution is for users who want close-to-reality bone models, but without the need to have special computer graphics hardware to display them.

---

<sup>2</sup> Decimation is the process that allows a systemic reduction in the number of facets in the model mesh.

Bone name	Full	Medium	Small
L4, L5	> 40000	8000	NA
Coccyx	> 6000	2000	NA
Sacrum	> 100000	30000	NA
Iliac bone	> 220000	85000	3000
Femur	> 200000	85000	3000
Fabela	> 1800	500	NA
Patella	> 15000	5000	1000
Tibia	> 120000	70000	3000
Fibula	> 52000	30000	2000
Talus	> 25000	8000	1500
Calcaneus	> 30000	8000	1500
Navicular	> 10000	4000	700
Cuboid	> 10000	4000	700
Cuneiforms (1 to 3)	> 4000	4000	700
Metatarsal bones (1 to 5)	> 4000	4000	700
Proximal phalanx (a)	> 3500	3000	500
Proximal phalanx (b)	> 1500	1000	300
Medium phalanx	> 1000	600	300
Distal phalanx	> 1000	300	100
Full digital ray	> 12000	4000	700
Sesamoid bone	> 1500	550	100
Trigon bone	> 2000	550	100
Foot	> 80000	15000	2000
Prosthetic hip cup	> 32500	8000	500
Prosthetic femoral component	> 35000	8000	1500
Surgical pin	> 55000	8000	NA

Table 2. Number of facets in full, medium and small resolutions for each bone available from the database. Note that the full resolution is only indicative – it is the resolution obtained after 3D reconstruction without any facet decimation. For both medium and small resolution, some 3D models available from the database may show slight differences. NA: non available.

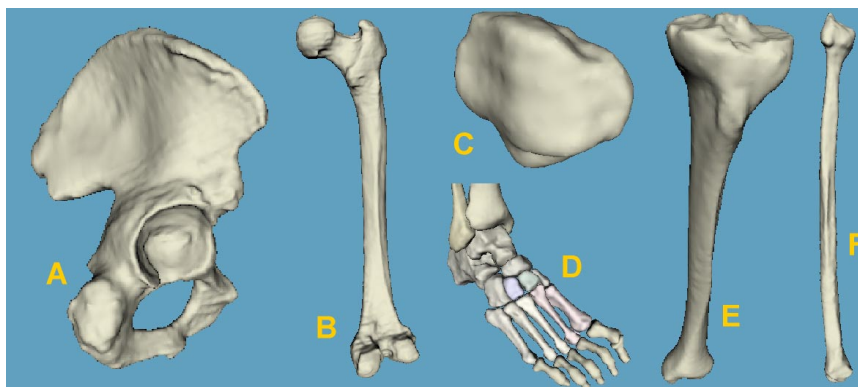
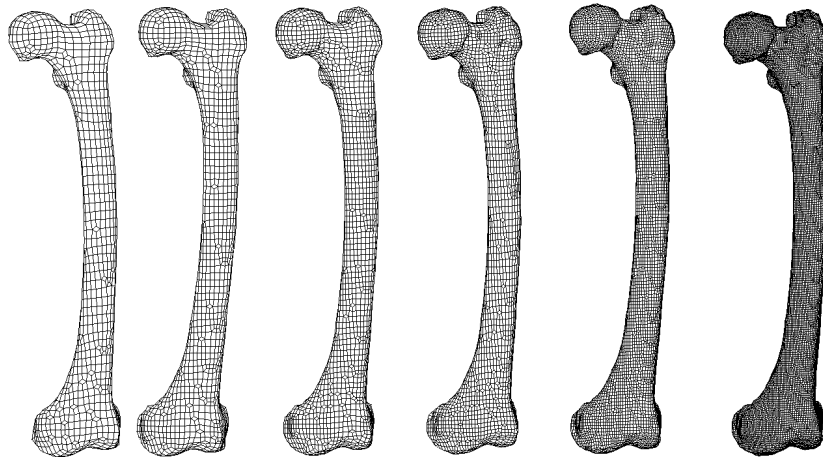


Figure 3. Examples of 3D bones available from the VAKHUM database. A: pelvic bone, B: femoral bone, C: patella, D: foot, E: tibial bone, F: fibula. For some datasets other bones are also available (see Table 2). Note that for some subjects the feet are totally segmented, for others the image dataset did not allow full segmentation.

#### Chapter IV. How to Choose and Use the Finite Element Models

Several meshes, with increasing mesh refinements, are available for each bone segment, both with and without material properties mapped on. The meshes are available in different formats.

Six levels of mesh refinement were generated for each bone segment, starting from the high resolution 3D bone model described in **Section 3.3 Model Resolution**. All of the meshes are made of linear hexahedral elements and were generated using the HEXAR (Cray Research, USA) automatic mesh generator that implements a grid-based meshing algorithm. The meshes are numbered from 1 (lowest refinement level) to 6 (highest refinement level). The six meshes of the left femur of the dataset *subj006* are shown in **Figure 4**, where the increasing level of captured morphological details is visible. The choice of the correct mesh refinement to use depends upon the particular application.

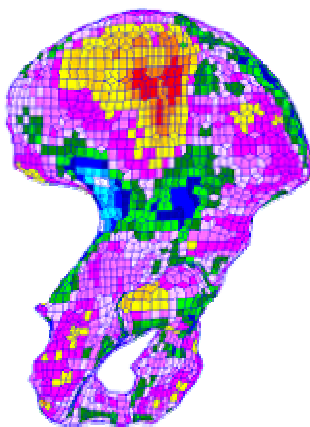


**Figure 4.** The six meshes with different refinement levels of the left femur of the *subj006* dataset.

An image of each mesh is provided in TIFF format to allow the user to judge the correct refinement for his personal needs.

The mechanical material properties were mapped on to the mesh using software developed in-house (BONEMAT\_v2), which is publicly available at <http://www.cineca.it/hosted/LTM-IOR/back2net/SW/index.html>. The number of materials assigned to each mesh is quite high, but it represents a good compromise between the accuracy of results and the complexity of the model.

The meshes with the material properties mapped on are made available in three different file formats: NEUTRAL, NASTRAN input file and ANSYS input file – see **Figure 5**.



**Figure 5.** The right pelvis of *subj006*, refinement 3, with different material properties mapped on it.

If a user is interested in generating models with fewer material properties there are two possible paths to follow. The first is to cluster manually the materials into a predefined number of material cards, using pre-processing software. Otherwise the NEUTRAL model, without material properties, is provided. Since the material mapping software is freely available from our website, each user can customise the number of materials depending upon his needs.

For subjects in which registration between the lower and upper parts of the leg is necessary, both meshes – the original unregistered ones, and the registered ones – are provided. The availability of the original meshes, which are spatially registered with the CT datasets, is necessary to allow the possibility of mapping the material properties on to the meshes using software different from that which we used.

If, on the contrary, the user has no need to change the materials, then the registered meshes are available, and ready to be used in a simulation. In the first case, it will be up to the user to register the models of the lower part of the limb with those relating to the upper part, using the roto-translation matrices explained in ***Chapter V. How to Create a Full Lower Limb Skeleton.***

## Chapter V. How to Create a Full Lower Limb Skeleton

There are three protocols to rebuild a full lower limb skeleton.

The *Final User* way does not require any computer programming skills and is thus well suited to anybody who wants simply to display the skeleton to visualise it. The other two protocols (*Morphology Visualisation* and *Kinematics Visualisation*) both require computer graphics programming skills.

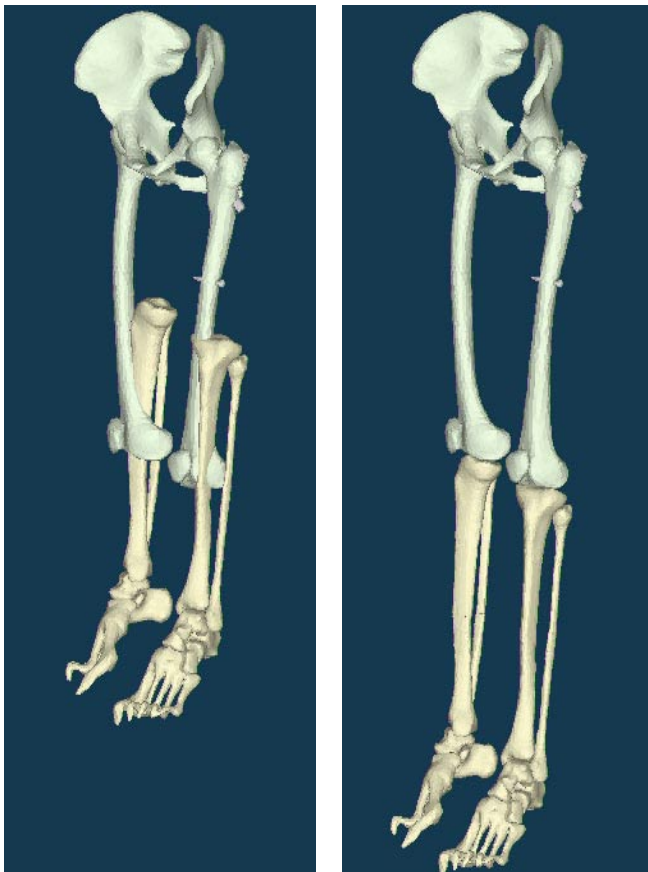
### 5.1 Final Users

This is the most straightforward way – the user merely needs to have a VRML viewer installed on her/his computer.<sup>3</sup> For some subjects, the database contains links to a VRML full model that contains all the information to allow the VRML viewer installed on your system to create the skeleton of the lower limb. Simply click on the link to build the skeleton.

### 5.2 Morphology Visualisation

This protocol is for users who want to rebuild a lower limb skeleton from several bone models available from the database.<sup>4</sup> It can be applied to most bone models, bone resolution and bone formats available from the database.

Because of the limited scanning length of the CT installation (1000mm), it has been necessary to collect two datasets for some subjects (*Figure 6*).



*Figure 6. As mentioned in Chapter II, bone models for the lower limb have been collected in two stages.*

*The first stage data collected from the upper part of the limb (i.e. iliac bone, femoral bone and patella – dataset1 or  $D_{up}$ , in green).*

*The second stage data collected from the lower part of the limb (i.e. tibial bone, fibula, foot – dataset2 or  $D_{low}$ , in yellow).*

*Obviously, plain visualisation (left image) of both  $D_{up}$  and  $D_{low}$  is not physiologically correct, and alignment must take place (right image, see text for explanation).*

*(Images were obtained from the VAKHUM dataset “subj002”, which includes surgical pins in the left femoral bone).*

<sup>3</sup> VRML viewers are freely found on the Internet; several of them are indicated on the VAKHUM website.

<sup>4</sup> Note that this section is not for users who wish to perform a motion simulation using both bone models and kinematics from the VAKHUM database. To perform a motion simulation, go to *Chapter VI. How to Create a Motion Simulation of the Kinematics of the Lower Limb Segments and Bones*.

As the  $D_{up}$  and  $D_{low}$  datasets are not aligned, if a user were to display these datasets directly from the database, the final display would look unrealistic because the 3D models have been kept **in the original medical imaging reference system**.

This problem can be easily solved using the alignment matrix  $C_{low \rightarrow up}$  found in the database for each subject dataset.<sup>5</sup> The alignment matrix  $C_{low \rightarrow up}$  contains the rotation and translation necessary to realign the above datasets:

$$C_{low \rightarrow up} = \begin{bmatrix} R_c & Tr_c \\ 0 & 1 \end{bmatrix}$$

Thus, the relationship between  $D_{up}$  and  $D_{low}$  is fully defined thanks to  $C$ . Alignment of  $D_{low}$  with  $D_{up}$  occurs according:

$$D_{low \rightarrow up} = C_{low \rightarrow up} D_{low}$$

Both datasets are now fully aligned (see **Figure 6**, right image).

Of course, if only the bones of one particular anatomical area are to be displayed (i.e., either from  $D_{up}$  **OR**  $D_{low}$ , but not from  $D_{up}$  **AND**  $D_{low}$ ), then no model alignment is necessary prior to final display.

Within the VAKHUM database, the datasets requiring an alignment are clearly indicated by an “**ALIGNMENT DATA**” section, which contains all the necessary information, including the above  $C$  matrix.

**Note:** One may wonder why the database does not include pre-aligned 3D models. The reason that we choose to keep **ALL** 3D models in the **original medical imaging frame** is simple: for some applications, some users need to superpose both original image datasets and 3D models (e.g. generation of finite elements). Also, the frame convention depends upon the users’ applications. These applications are so numerous that it is difficult to generate 3D models for each particular application frame.

---

<sup>5</sup> The full experimental method used to determine matrix  $C$  is fully described and validated in the VAKHUM public report untitled: “D3.2. Technical Report on Data Collection Procedure” (see “**VAKHUM-1-Data\_Collection\_Procedure.pdf**” file).

## Chapter VI. How to Create a Motion Simulation of the Kinematics of the Lower Limb Segments and Bones

This chapter describes the information that can be extracted and exploited from the PGD files available from the VAKHUM database.<sup>6</sup> The information included in the PGD<sup>7</sup> files allows building anatomical segments, to simulate this segment motion during particular tasks according global reference system and/or local joint frames. This chapter also explain how to simulate the 3D bone models using the PGD kinematics data, both of which are available from the VAKHUM database.

### 6.1 Generation of the Anatomical Segments

This section indicates how one can build the anatomical segments from the PGD files. Note that these segments are built from the few anatomical landmarks available from the PGD files and will not show a full bone model (the use of a bone model for motion simulation is explained in Section 6.3 Motion Simulation of the Anatomical Segments).

Initially, the anatomical segments are generated using the anatomical landmarks of each segment of the lower limb found in the CAL section of the PGD files. For example, the anatomical landmarks *IT* (i.e., Ischial Tuberosity):

$$\text{CALRIT} = \begin{bmatrix} \text{CALRIT}_x \\ \text{CALRIT}_y \\ \text{CALRIT}_z \end{bmatrix}$$

The user has two options to perform this operation, the first of which requires the use of all the available landmarks from the PGD file:

$$\begin{aligned} A_{\text{pelvic}} &= \begin{bmatrix} \text{CALIPY} & \text{CALRIT} & \text{CALRAS} & \text{CALRPS} & \dots \\ \text{CALRPI} & \text{CALRAC} & \text{CALIS2} & \text{CALLPI} & \dots \\ \text{CALLPS} & \text{CALLAS} & \text{CALLIT} & \text{CALLAC} & \dots \end{bmatrix} \\ A_{\text{rthigh}} &= \begin{bmatrix} \text{CALRFH} & \text{CALRGT} & \text{CALRLE} & \text{CALRLC} & \dots \\ \text{CALRLP} & \text{CALRMP} & \text{CALRAT} & \text{CALRMC} & \text{CALRME} \end{bmatrix} \\ A_{\text{rshank}} &= \begin{bmatrix} \text{CALRYT} & \text{CALRHF} & \text{CALRLR} & \dots \\ \text{CALRMR} & \text{CALRTT} & \text{CALRMM} & \text{CALRLM} \end{bmatrix} \\ A_{\text{rfoot}} &= \begin{bmatrix} \text{CALRCA} & \text{CALRST} & \text{CALRTN} & \text{CALRFM} & \dots \\ \text{CALRSM} & \text{CALRVM} & \text{CALRVT} & \text{CALRPT} \end{bmatrix} \\ A_{\text{lthigh}} &= \begin{bmatrix} \text{CALLFH} & \text{CALLGT} & \text{CALLLE} & \text{CALLLC} & \dots \\ \text{CALLLP} & \text{CALLMP} & \text{CALLAT} & \text{CALLMC} & \text{CALLME} \end{bmatrix} \\ A_{\text{lshank}} &= \begin{bmatrix} \text{CALLYT} & \text{CALLHF} & \text{CALLLR} & \dots \\ \text{CALLMR} & \text{CALLTT} & \text{CALLMM} & \text{CALLLM} \end{bmatrix} \\ A_{\text{lfoot}} &= \begin{bmatrix} \text{CALLCA} & \text{CALLST} & \text{CALLTN} & \text{CALLFM} & \dots \\ \text{CALLSM} & \text{CALLVM} & \text{CALLVT} & \text{CALLPT} \end{bmatrix} \end{aligned}$$

<sup>6</sup> The PGD format is a format that allows storing of kinematics data. It is strongly advised to have the related VAKHUM report “D3.2. Technical Report on Data Collection Procedure ANNEX II” (see file “*VAKHUM-4-PGD\_File\_Structure.pdf*”) available before reading the current chapter further. This report describes the PGD file structure, acronyms and conventions as used in this document.

<sup>7</sup> PGD = Preprocessed Gait Data; a special format for kinematics data.

where  $A_{pelvic}$  is the pelvic segment,  $A_{rthigh}$  is the right thigh,  $A_{rshank}$  is the right shank,  $A_{rfoot}$  is the right foot,  $A_{lthigh}$  is the left thigh,  $A_{lshank}$  is the left shank,  $A_{lfoot}$  is the left foot and “...” indicates the continuation between the column vectors.

Note that the above anatomical landmarks are ordered as column vectors, for example:

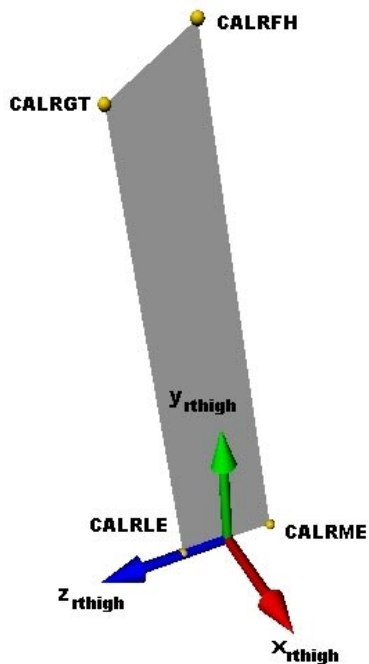
$$A_{pelvic} = \begin{bmatrix} CALIPY_x & CALRIT_x & CALRAS_x & CALLAC_x \\ CALIPY_y & CALRIT_y & CALRAS_y & \dots & CALLAC_y \\ CALIPY_z & CALRIT_z & CALRAS_z & CALLAC_z \end{bmatrix}$$

The second option to build the anatomical segment is based on a sub-set of the first option: only a limited number of the available landmarks are used (see **Figure 7** and **Figure 8**):

$$\begin{aligned} A_{pelvic} &= [CALRAS \quad CALRPS \quad CALLPI \quad CALLPS] \\ A_{rthigh} &= [CALRFH \quad CALRGT \quad CALRLE \quad CALRME] \\ A_{rshank} &= [CALRHF \quad CALRTT \quad CALRMM \quad CALRLM] \\ A_{rfoot} &= [CALRCA \quad CALRFM \quad CALRSM \quad CALRVM] \\ A_{lthigh} &= [CALLFH \quad CALLGT \quad CALLLE \quad CALLME] \\ A_{lshank} &= [CALLHF \quad CALLTT \quad CALLMM \quad CALLLM] \\ A_{lfoot} &= [CALLCA \quad CALLFM \quad CALLSM \quad CALLVM] \end{aligned}$$

The representations to be adopted is a function of the study that it is desired to carry out.

The different segments must now be aligned to each other in order to be in a so-called “reference position” that would be used to start the motion simulation.



**Figure 7. Anatomical Segment of a right thigh. The segment is built using the landmarks available from the PGD files.**

## 6.2 Reference Position of the Lower Limb

In order to orient the above segments along the *reference position* of the **same** PGD file, the URP field of the PGD file is used:<sup>8</sup>

$$\vec{A}_{\text{segment ref}} = R_{\text{URP segment}} \vec{A}_{\text{segment}} + \vec{d}_{\text{URP segment}} \quad \text{Eq. 1}$$

where  $\vec{A}_{\text{segment}}$  represents the list of points defining the segment,  $R_{\text{URP segment}}$  is the matrix of the rotation of the anatomical frame orientation from the rotation vector, and  $\vec{d}_{\text{URP segment}}$  is the position vector of the anatomical frame.

The rotation vector  $\vec{\theta}_{\text{URP segment}}$  and the position vector  $\vec{d}_{\text{URP segment}}$  are determined using the components of the URP field and the matrix of rotation  $R_{\text{URP segment}}$  by applying the following general equation<sup>9</sup>:

$$R(\theta) = \cos \theta I + \frac{\sin \theta}{\theta} A(\theta) + \frac{1 - \cos \theta}{\theta^2} \vec{\theta} \vec{\theta}^T \quad \text{Eq. 2}$$

where R is the rotation matrix,  $\vec{\theta}$  is the rotation vector and, I is the identity matrix.

$$\vec{\theta} = \begin{bmatrix} \theta_x \\ \theta_y \\ \theta_z \end{bmatrix}$$

$$\theta = \sqrt{\vec{\theta}^T \vec{\theta}}$$

$$A(\theta) = \begin{bmatrix} 0 & -\theta_z & \theta_y \\ \theta_z & 0 & -\theta_x \\ -\theta_y & \theta_x & 0 \end{bmatrix} \quad \text{Eq. 3}$$

Consider an example from a PGD file and, more particularly, the upright posture (URP) of a right (R) thigh (TH) segment (URPRTH):

From the PGD file, the following line is located:

```
!URPRTH -3 -2
1.057835 -13.833795 2.395315 -46.152181 -521.877798 98.028080
```

From this, both position vector  $\vec{d}_{\text{URPRTH}}$  and rotation vector  $\vec{\theta}_{\text{URPRTH}}$  are found:

$$\vec{d}_{\text{URPRTH}} = \begin{bmatrix} -46.152181 \\ -521.877798 \\ 98.028080 \end{bmatrix}$$

$$\vec{\theta}_{\text{URPRTH}} = \begin{bmatrix} 1.057835 \\ -13.833795 \\ 2.395315 \end{bmatrix} \left( \frac{\pi}{180} \right) = \begin{bmatrix} 0.0185 \\ -0.2414 \\ -0.0418 \end{bmatrix}$$

<sup>8</sup> Note that this section may appear as POPURP in some (non-VAKHUM) PGD files. No POPURP section exists in PGD files produced in VAKHUM, and the reference position is always given in the URP section.

<sup>9</sup> Spoor, C.W. and Veldpaus F.E. "Rigid Body Motion Calculated from Spatial Coordinates of Markers", *J.Biomech.*, Vol. 13, pp. 391-393, 1990.

The rotation matrix  $R_{URPRTH}$  is calculated using  $\bar{\theta}_{URPRTH}$  in **Equation 2** and **Equation 3**:

$$R_{URPRTH} = \begin{bmatrix} 0.9701 & -0.0436 & -0.2386 \\ 0.0392 & 0.9990 & -0.0233 \\ 0.2394 & 0.0133 & 0.9708 \end{bmatrix}$$

The *reference* position of the segment is then found from **Equation 1**.

The transformations applied to each of the anatomical segments (**Equation 1**) allow the representation of the anatomical landmarks and segments based on global reference system,  $xyz_{global}$  (**Figure 8**).

The position of global reference system,  $xyz_{global}$ , is defined for the origin of the anatomical frame of the pelvic segment according to the standards of the ISB (International Society of Biomechanics)<sup>10</sup>.

The directions of the three Cartesian axes are mutually perpendicular – one axis is vertical, and the directions of the remaining two horizontal axes are not usually contentious:

- the  $y_{axis}$  is generally vertical (parallel to the gravitational field  $\vec{g}$ ) and points upwards, and
- the  $z_{axis}$  is perpendicular to the  $y_{axis}$  and points to the right, and
- the  $x_{axis}$  is perpendicular to both  $y_{axis}$  and  $z_{axis}$  and points in the anterior direction (the direction of progression).

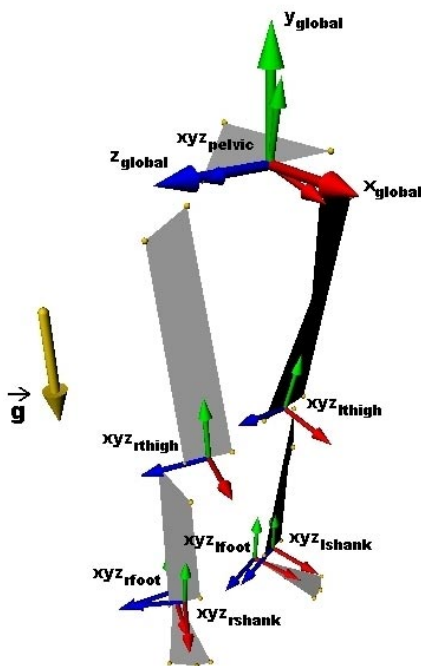


Figure 8. Anatomical segments and anatomical frames for the lower limbs

More details about the construction of reference frames are given in **Chapter VII. How to Determine Anatomical Axes**.

The previous sub-section explained how to use the information contained in a particular PGD file to create the 3D models for each anatomical segment of the lower limb and to position these segments in a *reference* position. The motion simulation of the kinematics of these segments, also contained in the same PGD file, can now take place.

<sup>10</sup> Wu G. and Cavanagh P.R. "ISB Recommendations for Standardisation in the Reporting of Data". *J.Biomech.*, Vol. 28, pp. 1257-1261, 1995.

### 6.3 Motion Simulation of the Anatomical Segments

To obtain the different positions of the anatomical segments during a determined movement in reference to the global reference system  $xyz_{\text{global}}$ , the same PGD files as above must be used. As mentioned previously, these PGD files contain data about the kinematics of the lower members in relation to the anatomical reference systems,  $xyz_{\text{segments}}$ .

The kinematics transformations are established in the DOF fields of the PGD files, which contain the six degrees of freedom for each of the anatomical segments.

Each line of the DOF fields contains a rotation vector and a translation vector that determines the kinematics position of the segment for an interval of time  $t$ .

To obtain the position  $n$  of a segment,  $\vec{A}_{\text{segments}_{\text{ref}}}$  is applied according to the following transformation:

$$\vec{A}_{\text{segments}_{\text{ref}}_n} = R_{\text{segments}_n} \vec{A}_{\text{segments}_{\text{ref}}} + \vec{d}_{\text{segments}_n} \quad \text{Eq. 4}$$

where  $\vec{A}_{\text{segments}_{\text{ref}}}$  is the segment in the reference position (found from *Equation 1*),  $\vec{A}_{\text{segments}_{\text{ref}}_n}$  is the anatomical segment in the position  $n$  of the current motion frame,  $R_{\text{segments}_n}$  is the transformation matrix of the corresponding rotation, and  $\vec{d}_{\text{segments}_n}$  is the vector of translation for the interval  $n$ .

The matrix of rotation  $R_{\text{segments}_n}$  and the vector of translation  $\vec{d}_{\text{segments}_n}$  are found from:

$$\begin{aligned} R_{\text{segments}_n} &= R_{\text{DOF segments}_n} R_{\text{URP segments}}^T \\ \vec{d}_{\text{segments}_n} &= -R_{\text{segments}_n} \vec{d}_{\text{URP segments}} + \vec{d}_{\text{DOF segments}_n} \end{aligned} \quad \text{Eq. 5}$$

As an example, consider calculating the position of the right thigh segment in a particular frame (#174, in red below):

```
!DOFRTH -3 -2;174; 0.010; 3.020
 6.112831 -7.009994 22.348749 115.525369 -485.816173 73.284135
 6.134987 -6.881068 21.554710 121.827937 -485.868031 74.007106
    ...      ...      ...      ...      ...      ...
 7.180192 -8.968958 -5.947205 1701.579097 -518.151016 69.901975
 6.644667 -9.409499 -5.690935 1714.160635 -520.214528 71.098829
```

$$\vec{d}_{\text{DOFRTH}_{174}} = \begin{bmatrix} 1714.160635 \\ -520.214528 \\ 71.098829 \end{bmatrix}$$

$$\vec{\theta}_{\text{DOFRTH}_{174}} = \begin{bmatrix} 6.644667 \\ -9.409499 \\ -5.690935 \end{bmatrix} \left( \frac{\pi}{180} \right) = \begin{bmatrix} 0.1160 \\ -0.1642 \\ -0.0993 \end{bmatrix}$$

The rotation matrix  $R_{\text{DOFRTH}_{174}}$  is calculated using *Equation 2*:

$$R_{\text{DOFRTH}_{174}} = \begin{bmatrix} 0.9817 & 0.0890 & -0.1686 \\ -0.0180 & 0.9884 & -0.1069 \\ 0.1571 & 0.1231 & 0.9799 \end{bmatrix}$$

The rotation matrix  $R_{\text{rthigh}_{174}}$  and the vector of translation,  $\vec{d}_{\text{rthigh}_{174}}$  for frame #174 are calculated from **Equation 5**:

$$R_{\text{rthigh}_{174}} = R_{\text{DOFRTH}_{174}} R_{\text{URPRTH}}^T$$

$$R_{\text{rthigh}_{174}} = \begin{bmatrix} 0.9817 & 0.0890 & -0.1686 \\ -0.01080 & 0.9884 & -0.1069 \\ 0.1571 & 0.1231 & 0.9799 \end{bmatrix} \begin{bmatrix} 0.9701 & -0.0436 & -0.2386 \\ 0.0392 & 0.9990 & -0.0233 \\ 0.2394 & 0.0133 & 0.9708 \end{bmatrix}^T$$

$$R_{\text{rthigh}_{174}} = \begin{bmatrix} 0.9887 & 0.1313 & 0.0725 \\ -0.1223 & 0.9856 & -0.1165 \\ -0.0868 & 0.1063 & 0.9905 \end{bmatrix}$$

and,

$$\vec{d}_{\text{rthigh}_{174}} = -R_{\text{rthigh}_{174}} \vec{d}_{\text{URPRTH}} + \vec{d}_{\text{DOFRTH}_{174}}$$

$$\vec{d}_{\text{rthigh}_{174}} = - \begin{bmatrix} 0.9887 & 0.1313 & 0.0725 \\ -0.1223 & 0.9856 & -0.1165 \\ -0.0868 & 0.1063 & 0.9905 \end{bmatrix} \begin{bmatrix} -46.152181 \\ -521.877798 \\ 98.028080 \end{bmatrix} + \begin{bmatrix} 1714.160635 \\ -520.214528 \\ 71.098829 \end{bmatrix}$$

$$\vec{d}_{\text{rthigh}_{174}} = \begin{bmatrix} 1821.202923 \\ -0.063823 \\ 25.479136 \end{bmatrix}$$

The final position of the anatomical segment at frame n is the found using  $R_{\text{rthigh}_{174}}$  and  $\vec{d}_{\text{rthigh}_{174}}$  in **Equation 4**.

In summary, the position of each anatomical segment will be given by:

$$\begin{aligned} \vec{A}_{\text{pelvic ref } n} &= R_{\text{pelvic } n} \vec{A}_{\text{pelvic ref}} + \vec{d}_{\text{pelvic } n} \\ \vec{A}_{\text{rthigh ref } n} &= R_{\text{rthigh } n} \vec{A}_{\text{rthigh ref}} + \vec{d}_{\text{rthigh } n} \\ \vec{A}_{\text{rshank ref } n} &= R_{\text{rshank } n} \vec{A}_{\text{rshank ref}} + \vec{d}_{\text{rshank } n} \\ \vec{A}_{\text{rfoot ref } n} &= R_{\text{rfoot } n} \vec{A}_{\text{rfoot ref}} + \vec{d}_{\text{rfoot } n} \\ \vec{A}_{\text{lthigh ref } n} &= R_{\text{lthigh } n} \vec{A}_{\text{lthigh ref}} + \vec{d}_{\text{lthigh } n} \\ \vec{A}_{\text{lshank ref } n} &= R_{\text{lshank } n} \vec{A}_{\text{lshank ref}} + \vec{d}_{\text{lshank } n} \\ \vec{A}_{\text{lfoot ref } n} &= R_{\text{lfoot } n} \vec{A}_{\text{lfoot ref}} + \vec{d}_{\text{lfoot } n} \end{aligned} \quad \text{Eq. 6}$$

where

$$\begin{aligned}
 \mathbf{R}_{\text{pelvic}_n} &= \mathbf{R}_{\text{DOFIPE}_n} \mathbf{R}_{\text{URPIPE}}^T \\
 \mathbf{R}_{\text{rthigh}_n} &= \mathbf{R}_{\text{DOFRTH}_n} \mathbf{R}_{\text{URPRTH}}^T \\
 \mathbf{R}_{\text{rshank}_n} &= \mathbf{R}_{\text{DOFRSH}_n} \mathbf{R}_{\text{URPRSH}}^T \\
 \mathbf{R}_{\text{rfoot}_n} &= \mathbf{R}_{\text{DOFRFO}_n} \mathbf{R}_{\text{URPRFO}}^T \\
 \mathbf{R}_{\text{lthigh}_n} &= \mathbf{R}_{\text{DOFLTH}_n} \mathbf{R}_{\text{URPLTH}}^T \\
 \mathbf{R}_{\text{lshank}_n} &= \mathbf{R}_{\text{DOFLSH}_n} \mathbf{R}_{\text{URPLSH}}^T \\
 \mathbf{R}_{\text{lfoot}_n} &= \mathbf{R}_{\text{DOFLFO}_n} \mathbf{R}_{\text{URPLFO}}^T
 \end{aligned}
 \tag{Eq. 7}$$

and

$$\begin{aligned}
 \vec{\mathbf{d}}_{\text{pelvic}_n} &= -\mathbf{R}_{\text{pelvic}_n} \vec{\mathbf{d}}_{\text{URPIPE}} + \vec{\mathbf{d}}_{\text{DOFIPE}} \\
 \vec{\mathbf{d}}_{\text{rthigh}_n} &= -\mathbf{R}_{\text{rthigh}_n} \vec{\mathbf{d}}_{\text{URPRTH}} + \vec{\mathbf{d}}_{\text{DOFRTH}} \\
 \vec{\mathbf{d}}_{\text{rshank}_n} &= -\mathbf{R}_{\text{rshank}_n} \vec{\mathbf{d}}_{\text{URPRSH}} + \vec{\mathbf{d}}_{\text{DOFRSH}} \\
 \vec{\mathbf{d}}_{\text{rfoot}_n} &= -\mathbf{R}_{\text{rfoot}_n} \vec{\mathbf{d}}_{\text{URPRFO}} + \vec{\mathbf{d}}_{\text{DOFRFO}} \\
 \vec{\mathbf{d}}_{\text{lthigh}_n} &= -\mathbf{R}_{\text{lthigh}_n} \vec{\mathbf{d}}_{\text{URPLTH}} + \vec{\mathbf{d}}_{\text{DOFLTH}} \\
 \vec{\mathbf{d}}_{\text{lshank}_n} &= -\mathbf{R}_{\text{lshank}_n} \vec{\mathbf{d}}_{\text{URPLSH}} + \vec{\mathbf{d}}_{\text{DOFLSH}} \\
 \vec{\mathbf{d}}_{\text{lfoot}_n} &= -\mathbf{R}_{\text{lfoot}_n} \vec{\mathbf{d}}_{\text{URPLFO}} + \vec{\mathbf{d}}_{\text{DOFLFO}}
 \end{aligned}
 \tag{Eq. 8}$$

#### 6.4 Making the Motion Simulation Using a Skeleton

Until now, we have described the simulation of particular landmarks found directly from the PGD files. No skeleton models have yet been involved. This sub-section explains how to simulate some of the skeletal models available from the database using the PGD files.

Note that the registration between the skeleton morphology and the PGD files has already been performed for you – you merely have to follow the instructions below to animate the bone morphology.

Of course, if the PGD files and bone models come from different subjects with different morphologies, then some particular registration processing has had to be applied. The registration method is not yet public, but it has been rigorously tested.

The names of the files containing the registration data are self-explanatory. For example: *VAKHUM\_subject006-025\_walking3* means that subject006 and subject025 of the VAKHUM database have been registered together for a motion of walking (third repetition).

Note that all 3D bone models found in the VAKHUM database are defined in the global medical imaging system, which is not the same as the global reference system of the kinematics data. Therefore, a preliminary alignment must occur prior to visualising the motion simulation on the bone models.

In order to obtain the representation of the object, i.e. the bone models, in the system of reference of the kinematics data, the following transformation must be applied:

$$\vec{\mathbf{A}}_s = \mathbf{R}_{\text{CT}} \vec{\mathbf{A}}_{\text{CT}} + \vec{\mathbf{d}}_{\text{CT}}
 \tag{Eq. 9}$$

where  $\mathbf{R}_{\text{CT}}$  represents the rotation matrix,  $\vec{\mathbf{A}}_{\text{CT}}$  is the 3D bone model object,  $\vec{\mathbf{d}}_{\text{CT}}$  is the translation vector, and  $\vec{\mathbf{A}}_s$  is the 3D bone model aligned with the kinematics data.

Both  $R_{CT}$  and  $\vec{d}_{CT}$  can be found from information contained in **Table 3**. The rotation matrix  $R_{CT}$  is calculated using **Equation 2**, and the orientation vector  $\vec{\theta}_{CT}$  is found from **Table 3** as follows (based on *subject006* of the table).

The translation vector  $\vec{d}_{CT}$  is found:

$$\vec{d}_{CT} = \begin{bmatrix} 184.717 \\ -1483 \\ -220.116 \end{bmatrix}$$

Then,  $\vec{\theta}_{CT}$  is obtained:

$$\vec{\theta}_{CT} = \begin{bmatrix} 69.2822 \\ -69.2822 \\ 69.2822 \end{bmatrix}$$

The rotation matrix  $R_{CT}$  is determined by using  $\vec{\theta}_{CT}$  in **Equation 2**:

$$R_{CT} = \begin{bmatrix} -0.00000226384129 & -0.99999999999487 & 0.00000226384642 \\ -0.00000226384642 & -0.00000226384129 & -0.99999999999487 \\ 0.99999999999487 & -0.00000226384642 & -0.00000226384129 \end{bmatrix}$$

**Equation 9** allows the final alignment of the 3D bone model to its new position to be performed:

$$\vec{A}_s = \begin{bmatrix} -44.3969 & -52.5178 & -48.3449 & \dots & -95.9725 & -91.2495 \\ 87.0092 & 85.6192 & 86.9992 & \dots & -119.2810 & -121.1510 \\ -88.2720 & -89.3230 & -84.0240 & \dots & -58.6975 & -48.1205 \end{bmatrix}$$

The aligned 3D bone model  $\vec{A}_s$  is now ready for the motion simulation by substituting it in **Equation 4** or **Equation 9**.

		Subject001	Subject003	Subject004	Subject006
Pelvis	(mm)	183.807 43.8118 -251.58	-38.8379 -1493.09 0.166665	198.403 -1539.54 -194.274	184.717 -1483 -220.116
	(deg)	69.2822 -69.2822 69.2822	69.2818 -69.2818 69.2818	-138.5640 138.5645 -138.5640	69.2822 -69.2822 69.2822
Right Thigh	(mm)	183.807 43.8118 -251.58	-38.8379 -1493.09 0.166665	198.403 -1539.54 -194.274	184.717 -1483 -220.116
	(deg)	69.2822 -69.2822 69.2822	69.2818 -69.2818 69.2818	-138.5640 138.5645 -138.5640	69.2822 -69.2822 69.2822
Right Patella	(mm)	189.617 41.2839 -274.856	-38.8379 -1493.09 0.166665	198.403 -1539.54 -194.274	184.717 -1483 -220.116
	(deg)	67.7399 -68.0803 69.2986	69.2818 -69.2818 69.2818	-138.5640 138.5645 -138.5640	69.2822 -69.2822 69.2822
Right Shank	(mm)	184.025 -426.889 -293.725	-58.4976 -2002.78 51.2774	237.283 -1990.36 -140.588	195.047 -1994.72 -257.861
	(deg)	67.7399 -68.0803 69.2986	69.1598 -67.6876 69.4598	69.0718 -67.8416 71.0794	-137.9453 139.2437 -135.8641
Right Foot	(mm)	184.025 -426.889 -293.725	-58.4976 -2002.78 51.2774	237.283 -1990.36 -140.588	195.047 -1994.72 -257.861
	(deg)	67.7399 -68.0803 69.2986	69.1598 -67.6876 69.4598	69.0718 -67.8416 71.0794	-137.9453 139.2437 -135.8641
Left Thigh	(mm)	183.807 43.8118 -251.58	-38.8379 -1493.09 0.166665	198.403 -1539.54 -194.274	184.717 -1483 -220.116
	(deg)	69.2822 -69.2822 69.2822	69.2818 -69.2818 69.2818	-138.5640 138.5645 -138.5640	69.2822 -69.2822 69.2822
Left Patella	(mm)	189.617 41.2839 -274.856	-38.8379 -1493.09 0.166665	198.403 -1539.54 -194.274	184.717 -1483 -220.116
	(deg)	67.7399 -68.0803 69.2986	69.2818 -69.2818 69.2818	-138.5640 138.5645 -138.5640	69.2822 -69.2822 69.2822
Left Shank	(mm)	184.025 -426.889 -293.725	-63.7875 -2000.31 58.3247	214.967 -1991.23 -152	197.323 -1993.07 -264.074
	(deg)	67.7399 -68.0803 69.2986	68.7063 -67.6977 69.5141	68.7720 -68.7886 70.6317	70.7688 -70.5744 68.8756
Left Foot	(mm)	184.025 -426.889 -293.725	-63.7875 -2000.31 58.3247	214.967 -1991.23 -152	197.323 -1993.07 -264.074
	(deg)	67.7399 -68.0803 69.2986	68.7063 -67.6977 69.5141	68.7720 -68.7886 70.6317	70.7688 -70.5744 68.8756

Table 3.  $\bar{\theta}_{CT}$  and  $\bar{d}_{CT}$  values of different VAKHUM datasets. The *Pelvic* segment includes both left and right pelvic bones, the *Thigh* segment includes the homolateral femoral bone, the *Patella* segment includes the homolateral patella, the *Shank* segment includes the homolateral tibia bone and fibula, the *Foot* segment includes all bones of the foot.

## Chapter VII. How to Determine Anatomical Axes

### 7.1 Introduction.

Interpolating anatomical axes, or anatomical frames (AFs), from the VAKHUM database is relatively straightforward and is explained in this section. This section is also useful for a better understanding of the PGD file structure.

The orientation of the anatomical axes as described in this section is according to **Annex I “Local Anatomical Frames”** of the VAKHUM internal report D3.2 (see *VAKHUM-3-Frame\_Convention.pdf* file). This annex describes the orientation of the AFs for the hip, knee and ankle joints. AF definition is strictly based on the 3D location of well-determined anatomical landmarks (ALs). A full description of the ALs used within the VAKHUM project is found in the report “**Lower Limb Anatomical Landmark Definition and Identification within Different Experimental Contexts**” (see *VAKHUM-2-Landmarks\_Palpation.pdf*).

Within the VAKHUM project, two different protocols were applied for AL collection: *manual palpation* during stereophotogrammetry experiments, and *virtual palpation* on 3D models obtained from medical imaging. The ALs used by both protocols defined the ALs in different frames (due to technical reasons).

To provide uniformity and to allow results from both protocols to be compared, AL coordinates have to be recalculated in the local AFs. Reprocessing of the data frames is explained in the two following sub-sections.

#### **Manual palpation (motion analysis experiments).**

AL location was performed manually during the motion analysis experiments. The 3D location of the ALs was defined in technical frames (TFs) rigidly attached to each limb segment for which the kinematics data was collected, i.e. pelvis, thigh, shank and foot.

One must keep in mind that particular ALs characterise each limb segment. These ALs are defined in local TFs in the VAKHUM kinematics data files, which have PGD format. For example, **Table 4** shows ALs defined in local TFs as can be found in a typical PGD file.

The method to obtain the 3D location of the same ALs redefined into AFs is given below (see **Section 7.2 Method to Interpolate AFs**). **Table 5** shows the result of this method on the ALs of **Table 4**.

#### **Virtual palpation (medical imaging).**

The same ALs have been located on medical imaging directly on the 3D bone models. Here the location of all ALs is defined in the same global reference frame (GF), i.e. the frame of the CT installation. **Table 6** shows typical values the user can find in the VAKHUM database.

The method to obtain the 3D location of the same ALs redefined into AFs is given below (see **Section 7.2 Method to Interpolate AFs**). **Table 7** shows the results of this method on the ALs of **Table 6**.

In some cases, a user may need to compare the AL location and AF orientation between datasets obtained from the manual and virtual palpation protocols. For this, reordering of **Table 7** is necessary – see **Table 8**.

Now, all AL coordinates are defined in AFs in all data sources and comparison is possible.<sup>11</sup>

The method to create the AFs is explained in the following section.

### 7.2 Method to Interpolate AFs.

This section explains the mathematical background to the creation of AFs. Note that only some particular ALs from the VAKHUM data files are required in order to create the AFs.

The full list of ALs can be found from the report entitled “**Lower Limb Anatomical Landmark Definition and Identification within Different Experimental Contexts**” (see *VAKHUM-2-Landmarks\_Palpation.pdf*).

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<sup>11</sup> Note that the bone models (e.g. vertexes) can be processed in the same way as the ALs.

This way simulated motion can be applied on the bone models as well.

From this list, a subset is necessary to create the AFs; this list is found in **Annex I “Local Anatomical Frames”** of the VAKHUM internal report D3.2 (see *VAKHUM-3-Frame\_Convention.pdf* file).

The method to create AFs presented here uses 5 ALs.

Take  $\mathbf{P}_i$  ( $i = 1, \dots, 5$ ) as 5 radius-vectors (i.e. the 3D location of the selected ALs), defined in the local frame (e.g. TFs for motion analysis data or a common global frame for medical imaging data – see above) coordinates.

From  $\mathbf{P}_1, \mathbf{P}_2, \mathbf{P}_3$ , we can define a plane (if  $\mathbf{P}_1, \mathbf{P}_2, \mathbf{P}_3$  are not co-linear) and its unit normal vector  $\mathbf{X}$  according to:

$$\begin{aligned} A &= \|P_2 - P_1\|; \\ B &= \|P_3 - P_2\|; \\ X &= A \times B; \end{aligned} \quad \text{Eq. 10}$$

where  $A$  and  $B$  are normalised vectors (e.g.  $\|A\| = A/|A|$ ).

Then, from  $\mathbf{P}_4, \mathbf{P}_5$ , (these points can be equal to  $\mathbf{P}_1, \mathbf{P}_2, \mathbf{P}_3$ ) we can define:

$$\begin{aligned} R &= \|P_5 - P_4\|; \\ Y &= X \times R; \\ Z &= X \times Y; \end{aligned} \quad \text{Eq. 11}$$

Finally, a rotation matrix  $Rot$  can be expressed from the column vectors  $X, Y, Z$ :

$$Rot_{15} = [X \quad Y \quad Z]; \quad \text{Eq. 12}$$

Note that the sequence of  $\mathbf{P}_i$  points has to be selected (see recommendations below) in order to obtain a final set of unit vectors coincident with the AFs defined in the above VAKHUM report.

In practice, the ALs necessary to obtain each AFs are the following.

### **Pelvic AF**

The pelvic landmarks used to create the pelvic AF are (see **Table 5** and **Table 8**, these ALs are indicated in **bold**):

- **RAS** : right anterior superior iliac spine
- **LAS** : left anterior superior iliac spine
- **RPS** : right posterior superior iliac spine
- **LPS** : left posterior superior iliac spine.

A *quasi-transverse pelvic plane* is found by using **RAS**, **LAS** and the midpoint (**MSA**) between **RPS** and **LPS** in **Equation 10**. The unit vector normal to this plane points proximally and is labelled  $\mathbf{Y}_p$ .

A *quasi-coronal pelvic plane* is orthogonal to the *quasi-transverse pelvic plane* and contains both **RAS** and **LAS**. The unit vector normal to this plane points in the anterior direction and is labelled  $\mathbf{X}_p$ .

The third axis  $\mathbf{Z}_p$  is given by  $Z_p = X_p \times Y_p$ ;

The midpoint between **RAS** and **LAS** defines the origin of pelvic segment AF.

### **Femur AFs**

The femur landmarks used to create the femur AF are (see **Table 5** and **Table 8**, these ALs are indicated in **bold**):

- **FH**: centre of the femoral head
- **LE**: lateral epicondyle
- **ME**: medial epicondyle.

A *quasi-coronal femur plane* is found by using **LE**, **ME** and **FH** in **Equation 10**. The unit vector normal to this plane points in the anterior direction and is labelled **X<sub>T</sub>**.

A *quasi-sagittal femur plane* is orthogonal to the *quasi-coronal femur plane* and contains **MI** (midway between **ME**, **LE**) and **FH**. The unit vector normal to this plane points Laterally and Medially for Right and Left sides, respectively, and will be **Z<sub>T</sub>**.

The third axis **Y<sub>T</sub>** is given by  $Y_T = Z_T \times X_T$ ;

The midpoints **MI** define the origins of the anatomical frames of the Thigh segments.

### **Tibia/Fibula AFs**

The tibia/fibula landmarks used to create the tibia/fibula AFs are (see **Table 5** and **Table 8**, these ALs are indicated in **bold**):

- **HF**: apex of the head of the fibula
- **TT**: prominence of the tibial tuberosity
- **LM**: distal apex of the lateral malleolus
- **MM**: distal apex of the medial malleolus.

A *quasi-coronal tibia/fibula plane* is found by using **LM**, **MM** and **HF** in **Equation 10**. The unit vector normal to this plane points in the anterior direction and is labelled **X<sub>S</sub>**.

A *quasi-sagittal tibia/fibula plane* is orthogonal to the *quasi-coronal tibia/fibula plane* and contains **MI** (midpoint between **LM** and **MM**) and **TT**. The unit vector normal to this plane points Laterally and Medially for Right and Left sides, respectively, and will be **Z<sub>S</sub>**.

The third axis **Y<sub>S</sub>** is given by  $Y_S = Z_S \times X_S$ ;

The middle points **MI** define the origins of the anatomical frames of the Shank segments.

### **Foot AFs**

The foot landmarks used to create the pelvic AF are (see **Table 5** and **Table 8**, these ALs are indicated in **bold**):

- **CA** : upper ridge of the calcaneus
- **FM** : dorsal aspect of first metatarsal head
- **SM** : dorsal aspect of second metatarsal head
- **VM** : dorsal aspect of fifth metatarsal head.

A *quasi-transverse foot plane* is found by using **VM**, **FM** and **CA** in **Equations 11** and **12**. The unit vector normal to this plane points proximally and is labelled **Y<sub>F</sub>**.

A *quasi-sagittal foot plane* is orthogonal to the *quasi-transverse foot plane* and contains both **SM** and **CA**. The unit vector normal to this plane points Laterally and Medially for Right and Left sides, respectively, and will be **Z<sub>F</sub>**.

The third axis **X<sub>F</sub>** is given by  $X_F = Y_F \times Z_F$ ;

The **CA** points define the origins of the Foot segment AFs.

### 7.3 Summary

In summary, the above segment frames can be built using the following landmarks from **Tables 3, 4** and **7**.

The table below indicates the landmarks ( $AL_i$ ) that can be used in **Equations 11** and **12** as  $P_i$ :

N	Acronym	$AL_1$	$AL_2$	$AL_3$	$AL_4$	$AL_5$	Right side ( $Rot_+$ ) pre- multiplying ( $Rot_{AF} = Rot_{15} * Rot_+$ )
1	IPELVI	5	6	9	5	6	$Rot_Z(-90^\circ)$
2	RTHIGH	16	15	23	17	23	$Rot_X(-90^\circ)$
3	RSHANK	30	29	25	31	24	$Rot_X(-90^\circ)$
4	RFOOT_	40	38	35	39	35	$Rot_X(-90^\circ) * Rot_Z(-90^\circ)$
5	LTHIGH	47	48	55	49	55	$Rot_X(-90^\circ)$
6	LSHANK	61	62	57	63	56	$Rot_X(-90^\circ)$
7	LFOOT_	70	72	67	71	67	$Rot_X(-90^\circ) * Rot_Z(-90^\circ)$

( $Rot_{15}$  is defined in **Equation 12**).

For each segment (given by its acronym), the necessary ALs are given by their index in **Tables 3, 4** and **7**. Examples of anatomical frames can be visualised in **Figure 8** (page 18) and **Figure 9** (below).

Note that an additional rotation has to be applied to each frame for it to be in alignment with the frame described in the report, *VAKHUM-1-Data\_Collection\_Procedure.pdf*. The last column of the above table gives the amplitude and the orientation of this final alignment.

In **Tables 3, 4** and **7**, the column “S” indicates the *status* of the markers: 1 = obtained after measurement; 0 = average value from two previous rows; 2 = coordinate of the marker in UpRight Position (URP) calculated in neighbour AFs (e.g. for the relative translation calculation).

For motion analysis data, we suggest using the centre of the acetabulum (AC) instead of the centre of the femoral head (FH) of the thigh segment (THIGH), because the accuracy for the determination of AC is higher than that for FH.

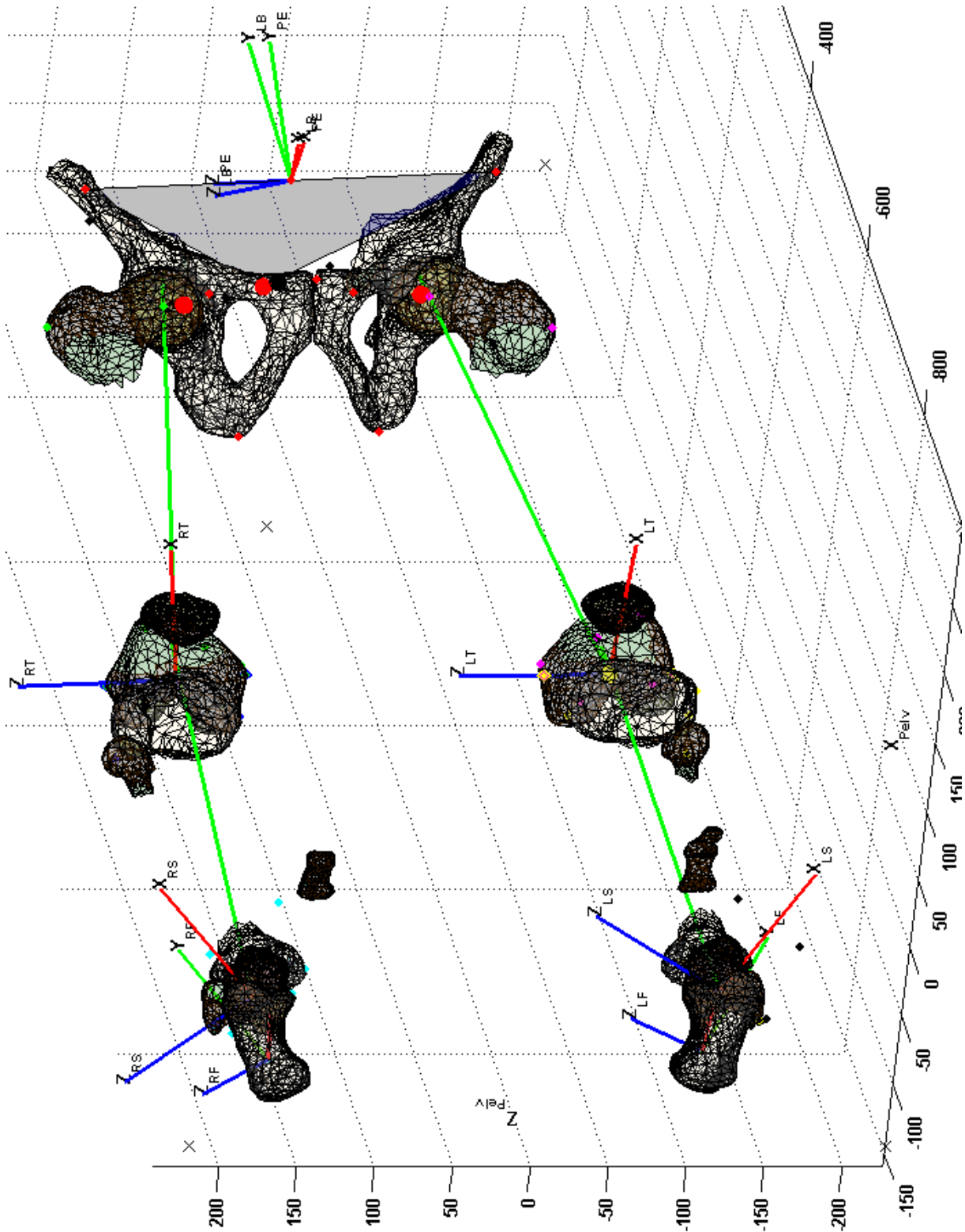


Figure 9. Example of anatomical frames displayed with joint segments (hip, knee and ankle).

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N	B	S	Acr	X	Y	Z	31	3	0	RMI	318.6	5.15	104.5	62	6	1	LLM	304	81.6	28.6
1	1	1	IS2	-88.5	-67.6	257.4	32	3	2	RME	-102.488	28.09939	137.6058	63	6	0	LMI	306.9	94.75	49.1
2	1	1	IPY	31.5	91.2	198.1	33	3	2	RLE	-119.045	-2.83102	46.73406	64	6	2	LME	-107.919	153.9436	133.2656
3	1	1	RIT	95.6	-46.4	290.5	34	3	0	RMI	-110.766	12.63418	92.16993	65	6	2	LLE	-114.592	112.0049	54.42641
4	1	1	LIT	110.4	-41.5	118.7	35	4	1	RCA	119.4	121.6	84.2	66	6	0	LMI	-111.256	132.9743	93.84598
5	1	1	RAS	-42.9	68.4	316.9	36	4	1	RST	96.1	57.2	113.7	67	7	1	LCA	83.4	-19.8	77.1
6	1	1	LAS	-61.2	65.6	68.8	37	4	1	RTN	100	41.2	113.1	68	7	1	LST	68.4	55.5	107.6
7	1	1	RPS	-72.3	-68.6	276.5	38	4	1	RFM	73.5	-67.9	94.7	69	7	1	LTN	75.1	78	113.3
8	1	1	LPS	-84.1	-77.8	164.8	39	4	1	RSM	79.1	-57	70.4	70	7	1	LFM	74.5	159.7	105.9
9	1	0	MSA	-78.2	-73.2	220.65	40	4	1	RVM	97.3	-26.8	29.7	71	7	1	LSM	81.9	156.6	83.6
10	1	1	RPI	-45	-90	251.6	41	4	1	RVT	111.6	30.4	36.1	72	7	1	LVM	101.2	137.9	19
11	1	1	LPI	-52.2	-88	176.5	42	4	1	RPT	97.8	64.6	60.9	73	7	1	LVT	93.7	68.9	40.3
12	1	1	RAC	18.3	7	278.1	43	4	2	RMM	84.72474	75.78652	121.7618	74	7	1	LPT	69.9	44.8	47
13	1	1	LAC	5.1	5	99.5	44	4	2	RLM	94.23334	90.35805	83.20504	75	7	2	LMM	41.99642	21.00036	122.5699
14	2	1	RGT	-86.5	77.8	62.3	45	4	0	RMI	89.47904	83.07229	102.4834	76	7	2	LLM	41.59353	14.56881	73.94066
15	2	1	RME	289	25.9	119.7	46	5	1	LGT	-118.2	47.7	46.3	77	7	0	LMI	41.79497	17.78458	98.25528
16	2	1	RLE	271.5	52.7	27.7	47	5	1	LME	247.4	-2.2	120.8							
17	2	0	RMI	280.25	39.3	73.7	48	5	1	LLE	251.1	-37.3	38.5							
18	2	1	RLP	253	11.8	56.3	49	5	0	LMI	249.25	-19.75	79.65							
19	2	1	RMP	269.2	0.3	94.5	50	5	1	LLP	234.5	25.5	77.8							
20	2	1	RAT	255.9	12	128.6	51	5	1	LMP	228.4	39.2	107.1							
21	2	1	RLC	305.6	45.1	58.4	52	5	1	LAT	226.7	15.8	132.3							
22	2	1	RMC	312.1	23.2	112.2	53	5	1	LLC	269.6	-24.6	102.4							
23	2	2	RAC	-168.261	56.86219	150.5486	54	5	1	LMC	272.8	-11.1	133.3							
24	3	1	RTT	-37.4	-3.8	101.5	55	5	2	LAC	-205.081	68.39083	114.1483							
25	3	1	RHF	-70	34.1	50.2	56	6	1	LTT	-41.8	154.9	68.8							
26	3	1	RMR	-69.9	47.9	144.7	57	6	1	LHF	-92.7	91.9	62.2							
27	3	1	RLR	-82.5	20.4	52.4	58	6	1	LMR	-83.7	148.9	135.7							
28	3	1	RYT	-53.1	8.7	70.5	59	6	1	LLR	-106.6	113.7	55							
29	3	1	RMM	311.6	-0.3	123.7	60	6	1	LYT	-87.4	144.2	54.5							
30	3	1	RLM	325.6	10.6	85.3	61	6	1	LMM	309.8	107.9	69.6							

Table 4. Local TFs (subject A, 7 bodies or segments)

N : Anatomical Landmark Number.

B : Body (or segment) number: 1 = pelvis, 2 = right thigh, 3 = right shank, 4 = right foot, 5 = left thigh, 6 = left shank, 7 = left foot.

S : Status of the current marker.

Acr : AL acronym.

X,Y,Z : AL 3D location (in mm) in TFs.



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N	Name	B	X	Y	Z
1	RAS	1	-4.8861	-2.52	131.9385
2	RPS	1	-123.186	66.63	26.723
3	RIT	1	-140.646	-78.12	33.0561
4	RPY	1	-32.19	-58.83	-5.38691
5	RPP	1	-34.139	-69.99	14.3054
6	RIC	1	-25.4372	45.62	147.5355
7	RPI	1	-118.689	41.01	45.7024
8	RAC	1	-72.9424	-30.2967	66.38365
9	RGT	2	-79.7939	-45.48	156.3405
10	RAT	2	-96.4924	-430.11	100.0602
11	RME	2	-95.7406	-443.06	99.455
12	RLE	2	-108.593	-435.33	185.7345
13	RMP	2	-70.7861	-450.59	130.1045
14	RLP	2	-66.3496	-435.56	165.9625
15	RMC	2	-101.84	-471.39	119.9075
16	RLC	2	-104.554	-463.26	171.5415
17	RFH	2	-72.3012	-33.4183	80.01842
18	RTT	3	-70.2986	-502.409	169.9894
19	RMR	3	-105.429	-478.471	108.7179
20	RLR	3	-111.592	-467.43	186.1011
21	RYT	3	-91.6117	-484.386	188.2637
22	RMM	3	-73.372	-833.35	145.4027
23	RHF	3	-135.153	-480.351	185.1093
24	RLM	3	-111.74	-846.69	190.0648
25	RCA	4	-133.73	-848.728	154.7185
26	RST	4	-80.3244	-857.212	147.2007
27	RPT	4	-101.186	-871.112	185.3926
28	RTN	4	-59.2036	-862.772	141.8274
29	RFM	4	28.54703	-907.349	157.8635
30	RSM	4	23.25695	-918.249	177.6349
31	RVM	4	-9.02902	-927.699	220.1553
32	RVT	4	-75.2732	-907.785	193.9899
33	RPA	5	-56.1171	-465.39	147.3205
34	RPM	5	-49.4213	-447.4	122.4585
35	RPL	5	-56.083	-434.39	169.6575
36	RP1	5	-55.4872	-434.3	169.4875
37	RP2	5	-48.2612	-445	122.0795
38	RP3	5	-57.1194	-421.48	142.5065
39	RP4	5	-52.5887	-464.14	151.3735
40	LAS	1	4.8861	2.52	-131.939
41	LPS	1	-117.648	75.39	-43.3171
42	LIT	1	-140.417	-72.32	-58.3786
43	LPY	1	-31.4406	-58.75	-10.2657
44	LPP	1	-32.2976	-71.51	-29.4378
45	LIC	1	-13.6752	64.14	-148.359
46	LPI	1	-109.252	45.03	-59.9536
47	LAC	1	-68.7127	-24.2483	-86.5065
48	LGT	6	-78.2549	-49.1	-167.396
49	LAT	6	-96.3442	-429.29	-92.5601
50	LME	6	-94.2545	-446.27	-91.3605
51	LLE	6	-98.6746	-437.08	-176.819
52	LMP	6	-66.2664	-447.18	-122.346
53	LLP	6	-56.954	-434.46	-151.36
54	LMC	6	-98.0301	-471.27	-110.653
55	LLC	6	-90.6967	-463.39	-157.218
56	LFH	6	-68.4653	-27.525	-91.3268
57	LTT	7	-58.6972	-508.445	-161.919
58	LMR	7	-100.867	-483.724	-100.599
59	LLR	7	-107.307	-473.337	-180.542
60	LYT	7	-81.5628	-487.092	-180.374
61	LMM	7	-70.8157	-835.176	-105.05
62	LHF	7	-126.086	-488.817	-178.333
63	LLM	7	-102.649	-852.934	-156.403
64	LCA	8	-127.187	-849.824	-123.051
65	LST	8	-75.97	-860.175	-105.239
66	LPT	8	-91.4659	-877.546	-145.505
67	LTN	8	-53.4525	-867.776	-98.8903
68	LFM	8	31.07751	-909.945	-94.9806
69	LSM	8	29.66303	-924.767	-115.447
70	LVM	8	1.751501	-936.619	-155.616
71	LVT	8	-64.117	-915.378	-145.343
72	LPA	9	-49.6112	-464.54	-139.086
73	LPM	9	-44.1558	-446.12	-111.563
74	LPL	9	-48.9148	-430.2	-156.877
75	LP1	9	-43.0722	-446.56	-111.898
76	LP2	9	-49.1999	-440.12	-158.144
77	LP3	9	-43.5087	-421.76	-135.484
78	LP4	9	-49.5637	-464.24	-141.178

**Table 6. Global Frame (subject B; 9 bodies or segments).**

**N : Anatomical Landmark Number.**

**B : Body (or segment) number: 1 = pelvis, 2 = right thigh, 3 = right shank, 4 = right foot, 5 = right patella, 6= left thigh, 7 = left shank, 8 = left foot, 9 = left patella.**

**Acr : AL acronym.**

**X,Y,Z : AL 3D location (in mm) in segmental GF.**

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N	Name	B	X	Y	Z												
1	RAS	1	0	0	132.053	31	RVM	4	153.3797	0	50.4326	62	LHF	7	0	357.2178	-49.0365
2	RPS	1	-139.333	-3.94322	29.98633	32	RVT	4	81.73302	-14.6469	39.39974	63	LLM	7	0	-7.8408	-30.4955
3	RIT	1	-80.8942	-137.313	39.72227	33	RPA	5	-11.3819	-23.47	-1.5883	64	LCA	8	0	0	0
4	RPY	1	1.947351	-67.1787	-3.06851	34	RPM	5	-1.77154	-4.02462	-24.3064	65	LST	8	51.42306	2.405336	19.93689
5	RPP	1	6.360341	-77.0904	16.89181	35	RPL	5	-0.58073	2.053539	24.71427	66	LPT	8	43.1889	4.188276	-25.8047
6	RIC	1	-41.7576	31.64557	147.4782	36	RP1	5	0	2.004945	24.48543	67	LTN	8	75.26949	1.906538	25.95513
7	RPI	1	-122.054	-23.0827	49.27181	37	RP2	5	0	-2.00495	-24.4854	68	LFM	8	169.7901	0	24.92918
8	RAC	1	-46.0363	-60.6739	69.6032	38	RP3	5	0	19.19374	0	69	LSM	8	173.9967	-1.19809	0
9	RGT	2	4.758413	387.6235	73.66394	39	RP4	5	-7.33032	-23.9429	2.126553	70	LVM	8	152.1934	0	-45.3453
10	RAT	2	-1.28898	15.83256	-40.8851	40	LAS	1	0	0	-132.053	71	LVT	8	84.01743	-14.3185	-38.8354
11	RME	2	0	3.214117	-43.6685	41	LPS	1	-140.557	3.943219	-40.3651	72	LPA	9	-0.21244	-21.3732	-4.6025
12	RLE	2	0	-3.21412	43.66852	42	LIT	1	-85.6691	-135.417	-51.7523	73	LPM	9	-1.16673	-3.0192	23.48299
13	RMP	2	29.6497	-7.05691	-18.4848	43	LPY	1	2.444149	-66.9024	-7.97232	74	LPL	9	-1.12332	13.17034	-21.9851
14	RLP	2	38.72009	2.629423	18.32939	44	LPP	1	7.744759	-79.0086	-26.8526	75	LP1	9	0	-3.31782	23.31138
15	RMC	2	-1.52658	-28.2626	-27.3903	45	LIC	1	-47.5851	43.14377	-148.948	76	LP2	9	0	3.317819	-23.3114
16	RLC	2	3.214254	-28.2946	24.73506	46	LPI	1	-118.307	-18.5628	-56.7185	77	LP3	9	0	21.74429	0
17	RFH	2	0	411.6582	0	47	LAC	1	-48.8558	-58.7022	-83.4263	78	LP4	9	0.105181	-21.0252	-6.66325
18	RTT	3	37.33083	336.2854	0	48	LGT	6	-4.00832	387.4276	-73.755						
19	RMR	3	-28.0744	364.8423	-21.6341	49	LAT	6	-3.0544	16.55561	39.9334						
20	RLR	3	19.03274	370.8088	40.76277	50	LME	6	0	-0.03339	43.03214						
21	RYT	3	34.46022	353.4107	28.48742	51	LLE	6	0	0.033389	-43.0321						
22	RMM	3	0	7.816203	-29.1565	52	LMP	6	29.74512	-2.23384	13.79829						
23	RHF	3	0	358.3838	55.13075	53	LLP	6	39.93043	8.041955	-15.8833						
24	RLM	3	0	-7.8162	29.15648	54	LMC	6	-1.10648	-27.0754	26.33066						
25	RCA	4	0	0	0	55	LLC	6	8.424249	-23.5346	-20.3684						
26	RST	4	50.86916	5.220145	-19.1246	56	LFH	6	0	417.2923	0						
27	RPT	4	42.58754	4.664524	25.79944	57	LTT	7	47.8502	334.8183	0						
28	RTN	4	71.52424	4.342087	-27.9834	58	LMR	7	-19.9241	360.0398	30.33297						
29	RFM	4	171.0276	0	-23.0173	59	LLR	7	17.41518	372.0233	-40.3948						
30	RSM	4	173.2055	-1.77736	0	60	LYT	7	38.80269	357.3198	-27.0404						
						61	LMM	7	0	7.840805	30.49553						

**Table 7. Segmental Local AFs (subject B, 9 bodies or segments)**

Table 7 is derived from Table 6 (see text).

**N : Anatomical Landmark Number.**

**B : Body (or segment) number: 1 = pelvis, 2 = right thigh, 3 = right shank, 4 = right foot, 5 = right patella, 6= left thigh, 7 = left shank, 8 = left foot, 9 = left patella.**

**Ac : AL acronym.**

**X,Y,Z : AL 3D location (in mm) in segmental GF.**

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N	B	S	Name	X	Y	Z	31	3	0	RMI	0	0	0	62	6	1	LLM	0	-7.83955	-30.4956
1	1	1	IS2	0	0	0	32	3	2	RME	-25.7785	397.5432	-32.8064	63	6	0	LMI	0	0	0
2	1	1	IPY	0	0	0	33	3	2	RLE	22.13136	399.7543	40.46598	64	6	2	LME	-19.8826	393.8426	42.24266
3	1	1	RIT	-80.8942	-137.313	39.72227	34	3	0	RMI	-1.82354	398.6487	3.829782	65	6	2	LLE	21.88854	404.5561	-32.2385
4	1	1	LIT	-85.6691	-135.417	-51.7523	35	4	1	RCA	0	0	0	66	6	0	LMI	1.002949	399.1993	5.002058
5	1	1	RAS	0	0	132.053	36	4	1	RST	50.8683	5.21996	-19.1239	67	7	1	LCA	0	0	0
6	1	1	LAS	0	0	-132.053	37	4	1	RTN	71.52303	4.341932	-27.9825	68	7	1	LST	51.42313	2.40523	19.93649
7	1	1	RPS	-139.333	-3.94322	29.98633	38	4	1	RFM	171.0266	0	-23.0166	69	7	1	LTN	75.26961	1.906453	25.95464
8	1	1	LPS	-140.557	3.943219	-40.3651	39	4	1	RSM	173.2055	-1.7773	0	70	7	1	LFM	169.79	0	24.92875
9	1	0	MSA	-139.945	0	-5.1894	40	4	1	RVM	153.3817	0	50.4313	71	7	1	LSM	173.9963	-1.19804	0
10	1	1	RPI	-122.054	-23.0827	49.27181	41	4	1	RVT	81.73479	-14.6463	39.39818	72	7	1	LVM	152.1924	0	-45.3446
11	1	1	LPI	-118.307	-18.5628	-56.7185	42	4	1	RPT	42.58854	4.664358	25.79893	73	7	1	LVT	84.01723	-14.3179	-38.8344
12	1	1	RAC	-46.0363	-60.6739	69.6032	43	4	2	RMM	47.57221	26.53183	-31.6072	74	7	1	LPT	43.18825	4.18809	-25.8044
13	1	1	LAC	-48.8558	-58.7022	-83.4263	44	4	2	RLM	24.03867	24.21145	23.93802	75	7	2	LMM	45.45389	23.35916	33.23324
14	2	1	RGT	4.758413	387.6235	73.66394	45	4	0	RMI	35.80544	25.37164	-3.83461	76	7	2	LLM	22.16815	24.37296	-25.2689
15	2	1	RME	0	3.214117	-43.6685	46	5	1	LGT	-4.00832	387.4276	-73.755	77	7	0	LMI	33.81102	23.86606	3.982166
16	2	1	RLE	0	-3.21412	43.66852	47	5	1	LME	0	-0.03339	43.03214							
17	2	0	RMI	0	0	0	48	5	1	LLE	0	0.033389	-43.0321							
18	2	1	RLP	38.72009	2.629423	18.32939	49	5	0	LMI	0	0	0							
19	2	1	RMP	29.6497	-7.05691	-18.4848	50	5	1	LLP	39.93043	8.041955	-15.8833							
20	2	1	RAT	-1.28898	15.83256	-40.8851	51	5	1	LMP	29.74512	-2.23384	13.79829							
21	2	1	RLC	3.214254	-28.2946	24.73506	52	5	1	LAT	-3.0544	16.55561	39.9334							
22	2	1	RMC	-1.52658	-28.2626	-27.3903	53	5	1	LLC	8.424249	-23.5346	-20.3684							
23	2	1	RFH	0	411.6582	0	54	5	1	LMC	-1.10648	-27.0754	26.33066							
24	3	1	RTT	37.33077	336.2738	0	55	5	1	LFH	0	417.2923	0							
25	3	1	RHF	0	358.3752	55.12831	56	6	1	LTT	47.84849	334.8068	0							
26	3	1	RMR	-28.0744	364.8322	-21.6346	57	6	1	LHF	0	357.2093	-49.0367							
27	3	1	RLR	19.03271	370.7984	40.76109	58	6	1	LMR	-19.9234	360.0293	30.33292							
28	3	1	RYT	34.46016	353.3997	28.48643	59	6	1	LLR	17.41455	372.0134	-40.3949							
29	3	1	RMM	0	7.815024	-29.1556	60	6	1	LYT	38.8013	357.3089	-27.0404							
30	3	1	RLM	0	-7.81502	29.15557	61	6	1	LMM	0	7.839546	30.49558							

**Table 8. Reordered Segmental Local AFs (subject B, 7 bodies or segments)**

Table 8 is derived from Table 7, which has been reordered to be compared with Table 5 (see text).

**N : Anatomical Landmark Number.**

**B : Body (or segment) number: 1 = pelvis, 2 = right thigh, 3 = right shank, 4 = right foot, 5 = left thigh, 6 = left shank, 7 = left foot.**

**S : Status of the current marker.**

**Acr : AL acronym.**

**X,Y,Z : AL 3D location (in mm) in segmental AFs**