



HAL
open science

Fusion of anthropometric data and principal component analysis of the bones for generating a personalized skeleton: case of the lower limb

Christophe Lecomte, Xuguang Wang

► To cite this version:

Christophe Lecomte, Xuguang Wang. Fusion of anthropometric data and principal component analysis of the bones for generating a personalized skeleton: case of the lower limb. 5th International Digital Human Modeling Symposium, Jun 2017, BONN, Germany. 14 p. hal-01769913

HAL Id: hal-01769913

<https://hal.science/hal-01769913>

Submitted on 18 Apr 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Lecomte et al.:

Fusion of anthropometric data and principal component analysis of the bones for generating a personalized skeleton: case of the lower limb

Lecomte, C.¹, Wang, X.²

¹ University of Southampton, Computational and Engineering Design Group,
United Kingdom

² Université de Lyon, IFSTTAR, France

Abstract

An approach is presented and evaluated here to provide realistic internal and external dimensions of Human Body Models for a broad range of predictor values, such as, for example, to estimate the dimensions of a slightly overweight 11 year old of height 1m40. The difficulty due to lack of sufficient internal and external data is alleviated by combining widely available anthropometric measurements with more sparse databases of surface meshes of bones. Assuming that the external anthropometric measurements are estimated from the predictors through a regression, the link with the internal shape dimensions is made through the subset of target “skeletal” measurements that can be closely estimated from skeletal landmarks. The matching of internal dimensions then proceeds as follows. First the set of surface meshes of bones is aligned and a Principal Component Analysis (PCA) model of their variance compared to their mean shape is evaluated. This is done by aligning the bones, body part by body part, in such a way that the effect of posture is removed, and by evaluating the variance for the whole skeleton, so that the covariance of shapes between different bones is captured. Any subject sampled from this PCA model consists in a set of bones loosely positioned compared to each other, for particular values of the Principal Component (PC) modal magnitudes or scores. In a second step, values of these modal magnitudes are estimated in such a way that the corresponding sampled subject skeleton has dimensions that estimate closely the target skeletal anthropometric measurements. In this last step, a direct kinematic approach and a sequential quadratic programming method are used to reposition the sampled bones in an appropriate posture and to evaluate the most appropriate PC scores. The whole approach is successfully applied and evaluated on a three segment model of the lower limb.

Key words:

Internal-external, Anthropometric measurements. PCA model, skeleton mesh, lower limb

1 Introduction

Accurate geometric and mechanical models of human bodies for a wide range of types of occupants and other road users are required for vehicle crash simulation. However, while the shape of human body parts can be obtained from images of medical scans, the amount of such data available to represent any chosen human population is limited due to two main reasons. First, medical scans of a full body may not be publicly available for a wide range of the population - this is a particularly acute problem for children, and, second, the process of segmentation into body parts is currently so time consuming that a large database may only contain data concerning shapes for a few tens of partial bodies.

Due to their complexity and cost, it is not realistic to generate a full finite element human body model (HBM) that include material properties for each subject. The strategy chosen in the EU funded PIPER project (PIPER, 2017) consists of deforming one of the very few existing HBMs to match some dimensional targets. As part of that project, the work presented here consists of generating personalised target skeletal shapes that are accurately representative of a wide range of predictors within the human population.

Information from two resources is combined here in order to reach this goal. First, publicly available databases are used to estimate the anthropometric dimensions of a target subject or population. Since these measurements have been made in relatively large numbers and for a wide range of the population, estimated anthropometric dimensions can be trusted to be realistic. For example, a slightly overweight 13 year old female passenger can be sampled from a female population regression using predictors such as age and body mass index (BMI). However anthropometric measurements only represent limited information such as length and breadth of body parts. The internal skeleton remains difficult to be predicted from external measurements. One way to alleviate this issue is to use principal component (PC) analysis of the bone shape data which can be used as a second source of information.

The objective of the paper is to present such an approach of fusion of anthropometric data and principal component analysis of the bones that consists in generating a realistic personalised skeleton to match sampled external body dimensions. Here this is illustrated for the lower limb. The methods used are presented in section 2, and the application to the lower limb in section 3. This is followed by discussion and conclusion in section 4.

2 Methods

2.1 PC model of the skeleton

In the present work, the PC model of the skeleton is built from bone surface meshes segmented with the Anatoreg tools (MOREAU et al., 2016), following a semi-automatic segmentation approach adopted within the PIPER project. With data having been generated this way, the meshes of the bones are already in correspondence, meaning that they have the same number and connectivity of nodes. Anthropometric features on the same bone from different subjects can be estimated using the same nodes for all the subjects. In order to evaluate the mean shape mean and the variance of a group of bones, the bones of interest are individually aligned between all the subjects via generalized Procrustes analysis, so that the sum of all squares of distance between equivalent nodes is minimized. Grouping some bones together, such as the tibia and the fibula, allows to bypass the modelling of their relative articulation. Alignments are reached by two steps, as follows: each group of bones is first centered so that the average spatial coordinates of its mesh nodes, for any particular subject, is at the origin. These groups of bones are then aligned by generalized Procrustes (iterating one to one Procrustes of one subject's bones from the current group to the average of the corresponding bones of all other subjects).

After alignment, principal component analysis is performed by considering the mean and covariance matrices for all the aligned bones considered together, and extracting the main modes of the covariance matrix. A single covariance matrix, \mathbf{C} , is thus evaluated for all vertices coordinates of all bones, independent of whether they share the same group, or not. The modes or eigenvectors of this matrix with non-zero eigenvalues are the modes or principal components of shape variation. They are then normalized. Expressed in the basis of these modes, the modal magnitudes or PC scores, $\mathbf{c} = [c_1 \ c_2 \ \dots \ c_m]^T$, of the difference of the aligned meshes compared to the mean mesh differ for each subject. The variance of these modal magnitudes among the subjects is equal to the eigenvalues of the covariance matrix, \mathbf{C} , while the standard deviation, σ_j , of each modal magnitude, $j = 1, \dots, m$, is defined as the square root of its variance divided by the number m of non-zero PC scores.

The mean, modes, and standard deviation define a statistical shape model, from which sampled skeleton can be drawn, for example by estimating that the modal magnitudes are normally distributed. Due to the translations and rotations that occur during alignment, the resulting mean bones and any sampled bones from the statistical model are generally in a loose posture, as illustrated in Fig 2.1, in the sense that the relative location and orientation of the bones is relatively random and is not corresponding to a particular realistic human posture. The mean or sampled bones must therefore be assembled or positioned in a particular posture, based on positioning landmarks. This is done by using the direct kinematic model discussed in the next section.

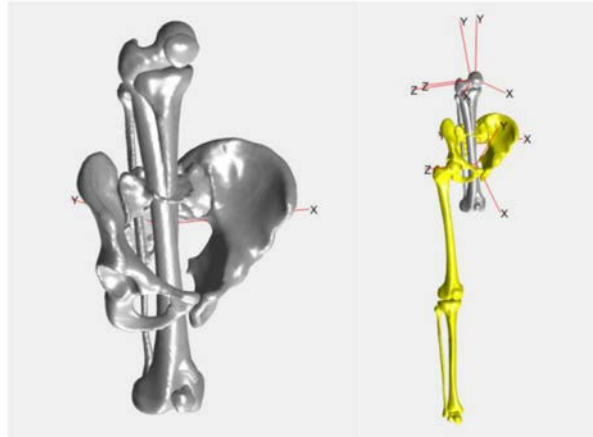


Fig 2.1 Illustration of sampled bones, before (grey) and after (yellow) articulation.

2.2 Articulated skeleton and its repositioning

The articulation of the sampled bones is necessary not only because the bones of the sampled skeletons are in a loose position, but also because most of the anthropometric dimensions are measured in a reference standing or sitting posture. For each value of the PC scores, the corresponding sampled skeletons are, therefore, assembled and articulated so that identical standing and sitting reference postures can be imposed, as illustrated in Fig 2.2. Here, this is done through a direct kinematic model whose joint and bone coordinate systems are mainly based on the ISB recommendations (WU et al., 2002, WU et al. 2005). Anthropometric dimensions can then be evaluated and compared to the target set of anthropometric dimensions, using landmarks on the bones similarly as for an actual human subject. The PC scores may then be searched as explained in section 2.4, so that the estimated skeletal anthropometric measurements approach or match the target anthropometric dimensions.

In practice, the landmarks used to measure the dimensions, as well as those used to define the coordinate systems are identified beforehand and integrated in the PC model. The details about the chosen skeletal anthropometric dimensions and landmarks for the right lower limb are described in the next section.

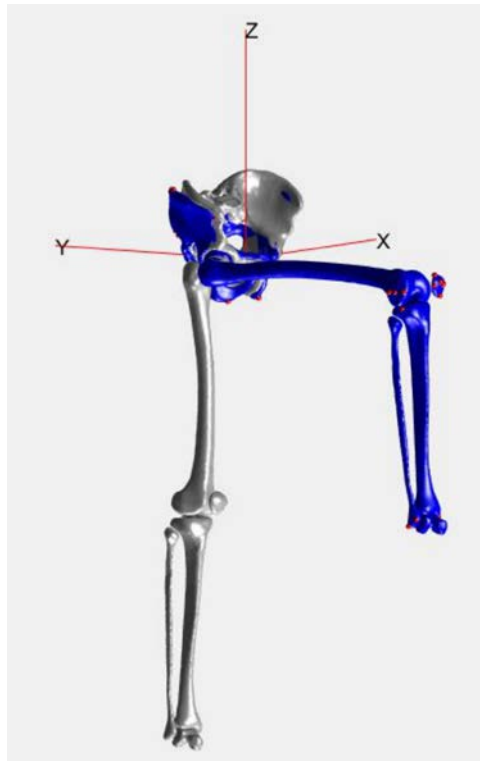


Fig 2.2 Illustration of the lower limb bone segments articulated in standing (in grey) and seated (in blue) positions

2.3 Skeletal anthropometric dimensions

As mentioned, the “skeletal measurements” are those among the external anthropometric measurements that can, in principle, be evaluated accurately on the

skeleton. For example, the stature of a standing subject could be estimated from the head vertex as far as a correct standing posture is defined, or the bispinous breadth is the width separating the right and left anterior spinous landmarks on the pelvis bone.

For the ANSUR anthropometric database (GORDON et al., 1989), selected candidate skeletal measurements for the right lower limb are presented in Table 2.1, together with the formulae to evaluate them. The skeletal landmark used in these formulae are themselves described in Table 2.2.

The postures are also reported in Table 2.1 for each measurement. Those are related to the general orientation of the subject body for which the lateral, vertical, and frontal directions are denoted respectively $\mathbf{d}_{lateral}$, $\mathbf{d}_{vertical}$, and $\mathbf{d}_{frontal}$. Since the foot bone meshes are not used, the lateral malleolar height is subtracted from measurements including the foot. For example “Crotch Height minus Lateral Malleolar Height” refers to the difference between the crotch and lateral malleolar heights.

Table 2.1 Skeletal anthropometric measurements selected from the ANSUR database and their estimation for the right lower limb. The numbers in parentheses are the measurement numbers in the ANSUR report (GORDON et al., 1989). The formulae, and posture of reference used to evaluate the measurements on a sampled subject's skeleton are also reported. The operations $abs(\cdot)$, $norm(\cdot)$, $dot(\cdot, \cdot)$ indicate absolute value, two-norm, and inner product.

Skeletal Measurements	(No)	Posture	Formula
Bimalleolar Breadth	(13)	Standing	$abs(dot(\mathbf{d}_{lateral}, TMM_R - FIML_R))$
Bispinous Breadth	(14)	Standing	$norm(ASIS_R - ASIS_L)$
Crotch Height minus Lateral Malleolar Height	(38) & (75)	Standing	$abs(dot(\mathbf{d}_{vertical}, (ISTL_R - FIML_R)))$
Iliocristale Height minus Lateral Malleolar Height	(67)	Standing	$abs(dot(\mathbf{d}_{vertical}, IC_R - FIML_R))$
Knee Height, midpatella minus Lateral Malleolar Height	(72) & (75)	Standing	$abs(dot(\mathbf{d}_{vertical}, (PCE_R - FIML_R)))$
Lateral Femoral Epicondyle Height minus Lateral Malleolar Height	(74) & (75)	Standing	$abs(dot(\mathbf{d}_{vertical}, (FLE_R - FIML_R)))$
Trochanterion Height minus Lateral Malleolar Height	(107) & (75)	Standing	$abs(dot(\mathbf{d}_{vertical}, (FTRION_R - FIML_R)))$
Buttock-Knee Length	(26)	Seated	$abs(dot(\mathbf{d}_{frontal}, (PSP_R - PASA_R)))$
Buttock-Popliteal Length	(27)	Seated	$abs(dot(\mathbf{d}_{frontal}, (PSP_R - TPOPS_R)))$
Knee Height, Sitting minus Lateral Malleolar Height	(73) & (75)	Seated	$abs(dot(\mathbf{d}_{vertical}, (PSUP_R - FIML_R)))$
Popliteal Height minus Lateral Malleolar Height	(86) & (75)	Seated	$abs(dot(\mathbf{d}_{vertical}, (TPOPS_R - FIML_R)))$

Table 2.2 List of skeletal landmarks used to estimate the ANSUR anthropometric measurements described in Table 1.

Landmark	Body part	Description
TMM_R	(Tibia_R)	Most medial point of the right tibial malleolus
TPOPS_R	(Tibia_R)	Tibia point at the dorsal juncture of the right calf and thigh when sitting erect
ASIS_R	(Hip_R)	See(van Sint Jan,2007) p.106
ASIS_L	(Hip_L)	See(van Sint Jan,2007) p.106
ISTL_R	(Hip_R)	Lowest point of the right ilium in standing posture
ISTL_L	(Hip_L)	Lowest point of the left ilium in standing posture
ISTL_M	(Pelvis)	Average of ISTL_R & ISTL_L
ICR_R	(Hip_R)	Right iliocristale, the highest palpable point of the right iliac crest
FIML_R	(Fibula_R)	Most lateral point on the right fibular malleolus
FLE_R	(Femur_R)	Lateral-femoral-epicondyle landmark, Lateral point of the right femoral epicondyle (knee pivot point).
FTRION_R	(Femur_R)	Trochanterion, the superior point, of the greater trochanter of the right femur of a standing subject.
PSP_R	(Pelvis, Hip_R)	Most posterior point of right pelvis ilium in sitting posture
PASA_R	(Patella_R)	Most anterior point of right patella in sitting posture
PSUP_R	(Patella_R)	The superior point of the right patella. (kneecap).
PCE_R	(Patella_R)	Right midpatella, The anterior point halfway between the top and bottom of the right patella (the kneecap).
PME_R	(Patella_R)	Center of medial edge of right patella
PLE_R	(Patella_R)	Center of lateral edge of right patella
PAX_R	(Patella_R)	Apex of right patella

2.4 Matching PC scores to target anthropometric dimensions

The main step of the fusion presented here consists in matching those available target skeletal anthropometric measurements, $\mathbf{a}^{(skel)}$, to their estimation obtained from the PCA models.

The objective is thus to choose the PC scores or modal magnitudes, $\mathbf{c} = [c_1 \ c_2 \ \dots \ c_m]^T$, so that, the corresponding skeletal model when repositioned in adequate posture, has estimated skeletal dimensions, $\tilde{\mathbf{a}}^{(skel)} = [\tilde{a}_1 \ \tilde{a}_2 \ \dots \ \tilde{a}_s]^T$ that match closely their target values.

In loose posture, and for a specific value set of PC scores \mathbf{c} , the coordinates of the bones are the coefficients of the vector $\tilde{\mathbf{s}}_{(loose)}$, or simply $\tilde{\mathbf{s}} = \bar{\mathbf{t}} + \mathbf{M}\mathbf{c}$, where $\bar{\mathbf{t}}$ is the vector of mean coordinates and where each column of \mathbf{M} contains the coefficients of a PC of shape variation. The direct kinematic operations (translations and rotations of the bones or groups of bones) allow to reposition the skeleton in standing or sitting postures, with coordinates $\tilde{\mathbf{s}}_{(standing)}$ and $\tilde{\mathbf{s}}_{(sitting)}$. The skeletal measurements $\tilde{\mathbf{a}}_{(standing)}^{(skel)}$ and $\tilde{\mathbf{a}}_{(sitting)}^{(skel)}$ can then be evaluated through the location of landmarks on

the skeleton placed respectively in standing and sitting postures (see section 2.2 and Table 3.1). The estimated full set of skeletal measurements, for particular values of \mathbf{c} , is therefore $\tilde{\mathbf{a}}^{(skel)} = \begin{bmatrix} \tilde{\mathbf{a}}_{(standing)}^{(skel)T} & \tilde{\mathbf{a}}_{(sitting)}^{(skel)T} \end{bmatrix}^T$.

An optimisation approach is proposed that consists in iterating on the PC scores, so that the corresponding Euclidian distance of the estimated and target is minimised, so the optimization problem reads as:

Find \mathbf{c} that minimizes $(\tilde{\mathbf{a}}^{(skel)} - \tilde{\mathbf{a}}^{(skel)T})(\tilde{\mathbf{a}}^{(skel)} - \tilde{\mathbf{a}}^{(skel)T})$ or equivalently, find \mathbf{c} that minimises $d(\mathbf{c}) = \sqrt{(\tilde{\mathbf{a}}^{(skel)} - \tilde{\mathbf{a}}^{(skel)T})(\tilde{\mathbf{a}}^{(skel)} - \tilde{\mathbf{a}}^{(skel)T})/s}$.

Several points are worth noting. First, the solution of this optimisation problem may not be unique if there are more PC scores to determine than the number of skeletal anthropometric measurements that one desires to match, i.e. if $m > s$. In order to remediate that, only the first $m_{opti} \leq s$ PC scores with highest standard deviation, σ_j , for $j=1, \dots, m_{opti}$, are allowed to change, while the other values are forced to be zero, $c_{m_{opti}+1} = \dots = c_m = 0$. This is equivalent to working with the modes that are responsible for the most variance in the available shapes of bones, i.e. segmented surface meshes used to generate the PCA. Second, with this approach, information about the statistical distribution of the PC scores found in this available shape data is not really used, in the sense that a value of a PC score c_j that is large relative to its standard deviation σ_j would be as likely as a smaller one. One knows however that larger relative values were less likely in the available data. To preserve plausibility of the PC scores, their relative values, c_j/σ_j are limited between -3 and 3 .

With these choices, a constraint Sequential Quadratic Programming (SQP) algorithm (NOCEDAL, 2006), as implemented in Matlab, is used to solve the constrained nonlinear minimisation problem:

Minimise

$$d(\mathbf{c}) = \sqrt{(\tilde{\mathbf{a}}^{(skel)} - \tilde{\mathbf{a}}^{(skel)T})(\tilde{\mathbf{a}}^{(skel)} - \tilde{\mathbf{a}}^{(skel)T})/s} \quad (2.1)$$

$$\text{for } [c_1 \ c_2 \ \dots \ c_{m_{opti}}]^T \text{ in } \mathbb{R}^{m_{opti}}, \quad (2.2)$$

$$\text{and } c_{m_{opti}+1} = \dots = c_m = 0, \quad (2.3)$$

$$\text{subject to } -3 \leq c_j \leq 3, \text{ for } j = 1, \dots, m_{opti}. \quad (2.3)$$

3 Application to the lower limb

The proposed fusion approach is now applied to the lower limb composed of three segments: pelvis, thigh, and lower leg (tibia, fibula, patella, and talus).

3.1 Data

The PC model of the six right lower limb bones was generated from the surface meshes of 22 subjects whose lower limb and thorax bones were segmented using Anatoreg (MOREAU et al., 2016). Altogether, the six meshes contain 88079 nodes (52109 for the Pelvis, and other 16899, 920, 11888, 3937 and 2326 respectively for the right femur, Patella, Tibia, Fibula and Talus). This resulted in the mean of the aligned three segments and in the $m=21$ modes of variance further described in section 3.2.

The meshes of a 23rd “LTE678” subject, segmented by the same approach and in correspondence with - but not included within - the set of 22 other subjects were also available. The bones of this subject “left-out” of the PCA model were used in the assessment of the behaviour of the fusion optimization approach, as described in section 3.3. This represents actual situations in which one would like to fit anthropometric measurements that cannot necessarily be exactly matched by samples from the PCA model. Nine skeletal anthropometric dimensions from the ANSUR database are considered. They are those described in Table 2.1, except the two popliteal measurements.

3.2 PCA of the lower limb bones

The modes, and mean, of the shape models are constructed from the 22 sets of six surface meshes. In the alignment, as well as in the articulation, the four bones below the knee are kept together in a single segment. Each of the pelvis and femur bones describes a single articulated segments. The values of the corresponding standard deviation, σ_j , $j = 1, \dots, = 21$ are presented in Fig 3.1. This corresponds to 80% of the aligned meshes variance being covered by 7 modes, 90% by 11 modes, and 95% by 14 modes.

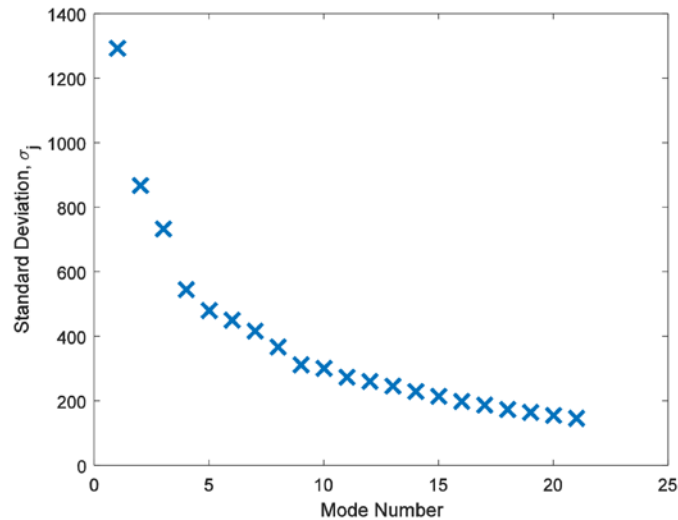


Fig 3.1 Standard deviation of the PC modes of the six bones/three segments of the Lower Limb model.

3.3 Assessment

The proposed fusion approach is now assessed. The nine LTE678 skeletal anthropometric dimensions are first evaluated. Their “exact” values are presented in Table 3.1 and compared to the corresponding values evaluated on the PCA mean subject. One can see that the lower limb (iliocristale) height of the LTE678 differs from that of the mean subject by about 7 cm.

This difference cannot be exactly reconciled by seeking an approximation of the LTE678 in the PCA model, since its shapes were not one of the 22 subjects used in the PCA model. The misfit of the LTE678 compared to the PCA models can be measured by first projecting the actual LTE678 meshes into the PCA space and by then evaluating the distance between the original and projected meshes.

Table 3.1 Anthropometric dimensions in [mm] of the LTE678 model, of its approximations though fusion, using 5 and 7 PCs (“F(5)” and “F(7)”), and those of the mean PCA model (“Mean”)

Anthro. dimension	LTE678	F(5)	F(7)	Mean
Bimalleolar Breadth	57.54	60.8	58.8	60.8
Bispinous Breadth	241.58	243.1	241.0	245.7
Crotch Ht – MH.	692.07	691.2	687.8	748.3
Iliocr. Ht – MH.	887.12	895.0	889.2	954.8
Knee Ht - MH	380.26	372.7	376.4	402.5
F. Epic. Ht - MH	377.53	382.1	381.2	410.5
Troch. Ht – MH	754.65	758.0	760.3	821.7
Buttock-Knee Lth	548.88	541.0	546.3	579.4
Knee Ht – MH	403.56	397.0	399.1	426.4

The projection can be seen as the best match of the LTE678 subject in the PCA model. It can be evaluated by the algorithmic steps described in section 2.4. Most

noticeable is that one takes into consideration alignment and averaging that were used to generate the PCA models. For each mesh or group of meshes, the first step consists in the alignment of the shape with its current approximation within the PCA model, starting with the mean meshes. The mean PCA shape is then subtracted before projection in the space spanned by the modes (the LTE678 pelvis mesh is first aligned with the PCA mean pelvis mesh, etc.). The approach appears to converge quickly and to provide good approximation with a single iteration. The mean nodal distances between the aligned meshes of the projected meshes and those of LTE678 equals 3.8 [mm], and the minimal and maximal nodal distances are 0.1 and 13.6 [mm].

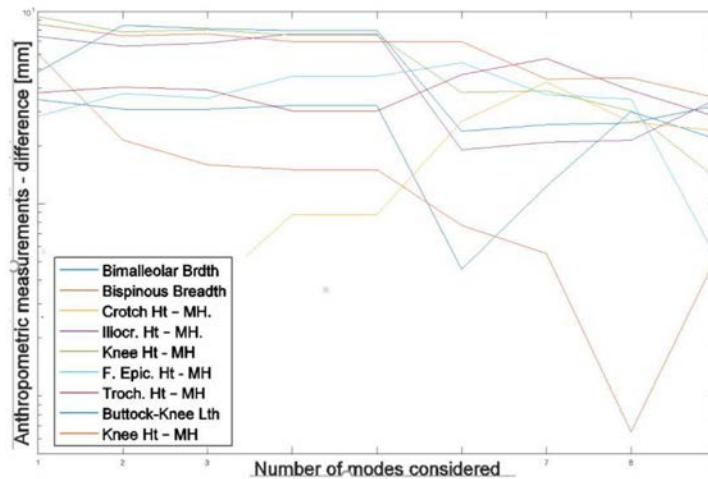


Fig 3.2 Evolution, for a varying number of PCs, of the distance between the LTE678 anthropometric dimensions and their approximation through fusion.

For the lower limb problem considered here, the optimization phase of the fusion approach takes the order of a couple minutes on a laptop. The distances between the exact LTE678 anthropometric dimensions and their approximation through fusion, using from $m_{opti} = 1$ to 9 PC scores, are presented in Figure 3.2. One can see that, by using a single PC, all differences are about 1 [cm] and that these differences decrease by about one order of magnitude, when more PCs are considered. However, since there is necessarily a misfit between the LTE678 subject and the PCA model, increasing the quality of the match of the anthropometric dimensions may be at the cost of creating shapes that are unlikely and for which there exists excessive nodal distance between the original LTE678 meshes and their approximation. A moderate number, m_{opti} , of PCs compared to the number, m , of target skeletal anthropometric dimensions is therefore recommended.

The comparison of the original and approximated versions of the three lower limb segments are presented in Fig 3.5 for $m_{opti} = 7$ non-zero PC scores. The approximated shapes appear to be of reasonable quality for the purpose of crash simulation. One may nevertheless notice that some distances exist, for example, at the level of the patella. The mean and maximal differences between nodal distance of the approximations of the LTE678 meshes through fusion and either their through projection or the exact meshes are presented in Fig 3.3. Based on these metrics only, it appears that using the five first PCs provide the best approximations. Further study would be worth as the quality of the approximations might be improved by

using a larger dataset to generate the PCA model, more or better selected skeletal anthropometric dimensions. The jump in distances at $m_{opti} = 6$ might be due to the fact that an unlikely shape is being considered. This might be controlled by a better criteria in the selection of the PC scores. As a reminder, any of their values in the relative range $\sigma_j = [-3,3]$ is equally allowed, while larger absolute values should be less likely based on the shape data statistics. This assumption seems to be confirmed by the values of the PC score values presented in for $m_{opti} = 1$ to 9. Looking at such plots (see Fig 3.4) also give an indication of the optimum value of m_{opti} that may be recommended. It appears nevertheless, as seen in Fig 3.5, that even results with $\sigma_j = 3$ may provide reasonable models.

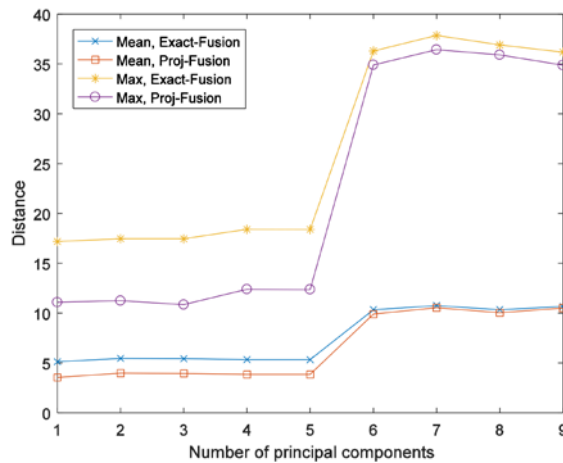


Fig 3.3 Mean and maximum nodal distances between the fusion and the exact and projected LTE678 meshes.

Additional bias may need to be considered, when dealing with anthropometric measurements coming from the ANSUR data, for example the fact that skeletal measurements are not exactly measured on the bones, and the difference between the actual human postures and their simulated versions.

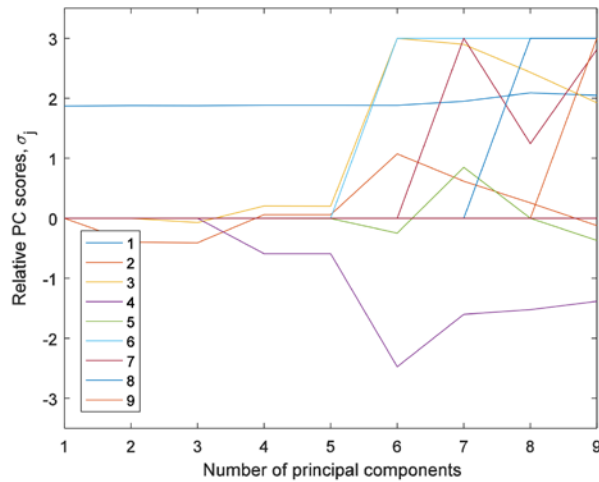


Fig 3.4 Relative PC scores for varying number of non-zero scores allowed.

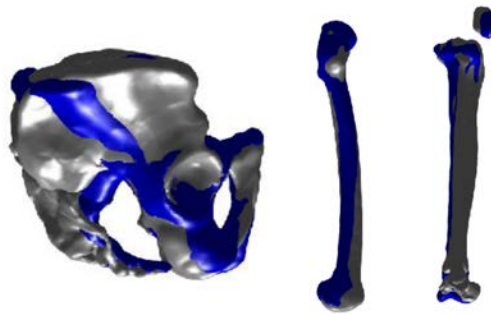


Fig 3.5 Comparison of the LTE678 Pelvis, Femur, and Leg meshes and their approximation through fusion, using 7 non-zero PC scores (in grey and blue).

4 Discussion and conclusions

The proposed fusion approach to combine external anthropometric dimensions of human body models with their internal skeletal dimensions has been successfully applied on the lower limb. The number of PC scores should be appropriately chosen, to make sure that their values stay likely. Other aspects may be worth studying, such as the effect of the quality of skeletal anthropometric measurements, and of the kinematic model used to reposition the skeleton standing and seated postures.

Acknowledgement

The work presented in this paper has been funded by the EU PIPER project, under the European Union Seventh Framework Programme ([FP7/2007-2013]), grant agreement n°605544. The authors are grateful for the data from CEESAR, that has been segmented using Anatoreg from Anatoscope, and thank in particular Erwan

Jolivet and Baptiste Moreau for this, as well as Atul Bhaskar for edition of the manuscript.

List of references

Gordon, C. C.; Blackwell, C. L.; Bradtmiller, B.; Parham, J. L.; Barrientos, P.; Paquette, S. P.; Corner, B. D.; Carson, J. M.; Venezia, J. C.; Rockwell, B. M.: 2012 Anthropometric Survey of US Army Personnel: Methods and

Summary Statistics: DTIC Document. Natick/TR-89-044. US Army Natick Research Development and Engineering Center, Natick, MA. Available from the National Technical Information Service website, <http://www.ntis.gov>.

Moreau, B.; Dicko, A.-H.; Mailliez, P.; Portejoie, P.; Lecomte, C.; Bah, M.; Grenier, T.; Jolivet, E.; Petit, P.; Fréchède, B.: A segmentation pipeline for the creation of statistical shape models in the PIPER project. In: Proceedings of the 22nd Congress of the European Society of Biomechanics. Lyon, France (2016)

Nocedal, J.; Wright, S.: Sequential quadratic programming (pp. 529-562), in: Numerical optimization: Springer Science & Business Media., Springer New York , 2006

Piper Project, EU PIPER project, under the European Union Seventh Framework Programme ([FP7/2007-2013]), grant agreement n°605544, www.piper-project.eu, 2104-2017. This has been followed up by the open source PIPER project, www.piper-project.org, 2017.

van Sint Jan, S.: Color atlas of skeletal landmark definitions: guidelines for reproducible manual and virtual palpations: Elsevier Health Sciences., 2007

Wu, G.; Siegler, S.; Allard, P.; Kirtley, C.; Leardini, A.; Rosenbaum, D.; Whittle, M.; D'Lima, D. D.; Cristofolini, L.; Witte, H.: ISB recommendation on definitions of joint coordinate system of various joints for the reporting of human joint motion—part I: ankle, hip, and spine. In: Journal of biomechanics 35 (2002), Nr. 4, S. 543--548

Wu, G; Van der Helm, F. C. T.; Veeger, H. E. J. D.; Makhsous, M.; Van Roy, P.; Anglin, C.; Nagels, J.; Karduna, A. R.; McQuade, K.; Wang, X.; Werner, F. W.; Buchholz, B.: ISB recommendation on definitions of joint coordinate systems of various joints for the reporting of human joint motion—Part II: shoulder, elbow, wrist and hand. In: Journal of biomechanics 38 (2005), Nr. 5, S. 981—992.