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Development and validation of a generic 3D model of the distal femur

Dr. Beat Schmutz
Institute of Health and Biomedical Innovation
Queensland University of Technology
60 Musk Avenue
Kelvin Grove Brisbane, QLD 4059
Australia

Ph: +61 7 3138 6291
Fax: +61 7 3138 6030
E-mail: b.schmutz@qut.edu.au

A/Prof. Karen J. Reynolds
School of Informatics & Engineering
Flinders University
GPO Box 2100
Adelaide SA 5001, Australia

Tel: +61 8 8201 5190
Fax: +61 8 8201 3618
E-mail: karen.reynolds@flinders.edu.au

Dr. John P. Slavotinek
Division of Medical Imaging
Flinders Medical Centre
Bedford Park SA 5042, Australia

Tel: +61 8 8204 4154
Fax: +61 8 8374 1731
E-mail: john.slavotinek@flinders.edu.au

Abstract

The development and validation of a virtual generic 3D model of the distal femur using computer graphical methods is presented. The synthesis of the generic model requires the following steps: acquisition of bony 3D morphology using standard CT (computed tomography) imaging; alignment of 3D models reconstructed from CT images with a common coordinate system; computer graphical sectioning of the models; extraction of bone contours from the image sections; combining and averaging of extracted contours; and 3D reconstruction of the averaged contours.

The generic models reconstructed from the averaged contours of six cadaver femora were validated by comparing their surface geometry on a point to point basis with that of the CT reconstructed reference models. The mean errors ranged from 0.99 - 2.5 mm and were in agreement with the qualitative assessment of the models.

Keywords

1 Introduction

Today a vast amount of literature exists on the anatomy and function of the knee joint (for reviews see [1-3]). Despite this, controversy still exists regarding the exact shape of the femoral condyles [4,5]. It is the geometry of the articulating surfaces of the knee joint that contributes significantly to the movement pattern of the joint [5-7]. Therefore the 3D morphology of the distal femur is of particular importance to the design of knee replacement components. Although total knee replacement (TKR) surgery generally enjoys a high success rate, with the increasing activity demand of patients there is a need to improve the function and longevity of knee implants [8]. Given that knee function and movement pattern of the femur are related to morphology, the capacity to quantify morphology of the distal femur may assist design of joint replacement components.

The 3D morphology of the distal femur has been quantified using various data acquisition methods. Wismans *et al*. [9] developed a dial gauge to measure 50 – 100 points on each condyle of one cadaver specimen. Martelli *et al*. [10] used a FARO arm electrogoniometer (accuracy 0.3 mm) to digitise the articulating surfaces of the distal femur of six cadaver specimens. Ghosh [11] developed a close-range photogrammetric 3D mapping system (accuracy 0.2 mm) for the perspective diagramming of the knee joint. Huiskes *et al*. [12] used an analytical stereophotogrammetric method (accuracy 0.2 mm) to measure the 3D articular geometry of a pair of knee joints. Siu *et al*. [13] manually digitised the bone outlines from transverse CT scan images of five cadaver specimens. In their study Siu and colleagues employed a calibration frame to standardise positioning of the resected cadaver specimens during CT imaging.

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All of the above studies were based on relatively small data sets of 1-6 cadaver specimens. However, larger data sets are required in order to construct an average shape of the condylar articulating surfaces representative of a larger population sample.

None of these data acquisition methods is particularly well suited for such a task as they either require dissection of the joint and/or rely on specialist equipment that is generally not present in hospitals. This study proposes a simpler data acquisition method which makes use of CT images that have been acquired without a calibration frame. The significant advantage of this approach is that it enables the development of a generic model of the femur using existing (or newly acquired) CT scan image data from a range of hospitals. Hence, a potentially greater and more age diverse source of image data would be accessible.

The purpose of this study was to provide a quantitative answer to the question: 'How well does a generic 3D model resemble a particular model of the distal femur?' The method used to quantify the difference between two models was based on calculating the disparity between the surface geometry of two models on a point to point basis. To the best knowledge of the authors, such a comparison (on a point to point basis) between a generic model and individual femur models has not yet been reported in the literature.

2 Materials and Methods

2.1 Image data acquisition & 3D model reconstruction

CT scan data was obtained from the distal femur of nine intact embalmed human cadaver lower limbs, made available by the Department of Anatomy & Histology of the School of Medicine, Flinders University, South Australia. The average age of the specimens was 80 years (range 72 - 89). Only right knees were available from five male and four female donors.

Each leg was positioned in the centre of the scan field to minimise beam hardening and partial volume effect [14]. This was achieved by aligning the longitudinal axis of the leg with the scanning axis. The images were acquired in a helical mode with a CT scanner (HiSpeed CT/i, General Electric Medical Systems) at the Flinders Medical Centre, Adelaide, operating at 120 kV, 150 mA, with a pitch of 1.5:1 and a gantry rotation time of 0.8 seconds. With all slices overlapping by 50% the effective slice spacing was 0.5 mm for the condylar region and 1.5 mm for the diaphysis. From each femur about 155 transverse image slices with a pixel size of 0.33 mm were obtained. The image data were transferred to a PC (Pentium III, 1 GHz, 256 MB RAM) where 3D models of the distal femora were reconstructed with an accuracy of 0.5 mm using Mimics 7.30 software (Materialise, Leuven, Belgium) [15]. After their reconstruction the 3D models were saved in DXF-file format such that they could be imported as polygon mesh objects into IDL 5.5 (Research Systems Inc, Boulder, USA) for further processing.

A visual inspection of the reconstructed models revealed that two of the models were not suitable to be included in the data set used to develop a generic model of the femur. One of the models displayed significant marginal osteophytes (a manifestation of osteoarthrosis, a common degenerative condition), and the other exhibited a deep 'groove' on the anterior aspect of the condyles most likely an impression due to

movement of the patella. However, the models were still used for a comparison between the developed generic model and femur models.

2.2 Alignment of the 3D models

Alignment of the models with a common coordinate system was performed using a method adapted from Kwak *et al*. [16]. This was achieved by adjusting the position of the models until the posterior aspects of the condyles appeared superimposed in the lateral/medial view (Fig. 1). A circle (of variable radius) was then visually fitted to the profile of the condyle.

[Insert figure 1 about here]

The x-axis of the coordinate system was defined as the line passing through the medial and lateral circle centres as seen in Figure 2. The midpoint between the circle centres on the medial/lateral condyles was taken as the origin of the coordinate system. The model was rotated about the x-axis until the diaphysial axis was parallel, in the yz-plane, with the z-axis. The y-axis was orthogonal to both the x- and z-axes.

[Insert figure 2 about here]

After alignment the models were scaled uniformly to the average condylar width of the femur models. The circle centres on the medial and lateral condyles were taken as

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measuring positions for determining the width of the femur. The distance between these points does not necessarily correspond to the maximum width of the femur.

2.3 Repeatability study on the alignment method

A repeatability study was conducted to quantify the variability involved in aligning a model with the common coordinate system. A randomly chosen model was aligned with the coordinate system by following the method developed in this study. The following values were recorded: the medial/lateral circle centres in data coordinates, the distance between the circle centres on the medial/lateral condyles, and the angle through which the model was rotated about the x-axis. The alignment was repeated five times with the same model and the measurements were recorded. For each set of measurements the average, standard deviation and worst case error were calculated.

2.4 Computerised re-sectioning of the models & contour extraction

The aligned and scaled models were computer graphically sectioned in planes orthogonal to the z-axis. The models were sectioned at 1 mm intervals. The range on the z-axis over which the models were sectioned spanned from 90 mm (proximal) to -28 mm (distal) generating 119 image slices for each model. The external bone contour was automatically extracted from each image slice using a border tracing algorithm [17].

2.5 Combining and averaging of the extracted contours

In order to determine the average outline of the bone the extracted contours were combined for each plane of section. Although the models have been aligned with a common coordinate system, their contours in the shaft region when displayed together were not closely superimposed as Figure 3a clearly shows.

[Insert figure 3a & 3c about here]

The most likely explanation for this lack of shaft alignment is due to differences in the angle between the bone's diaphysial axis and the line connecting the circle centres on the medial and lateral condyles (x-axis) as seen in Figure 3b.

To obtain a better alignment for the contours prior to averaging the contours were translated such that their centroids were aligned at a common point (Fig. 3c). The average of all the centroid positions was chosen as the common point for the alignment of the contours. The average outline was determined by employing a graphical method which lent itself to automation [15].

2.6 Reconstruction of the averaged contours

The generic 3D model was reconstructed from the average contour outlines by firstly creating a volume (3D) array from the images of the average contour outlines. Then a list of vertices and polygons describing the contour surface was generated. Finally, the minimum amount of spatial smoothing was performed on the polygon mesh in order to preserve the local morphology.

Due to the limited amount of image data it was necessary to take one femur model (for validation) out of the data set of the available seven models and use the remaining six for the development of the generic model. Using the approach of 'take one out' removed any bias of the generic model towards the reference model since the latter was excluded from the dataset used to generate the former. Furthermore, this approach enabled using all seven CT image reconstructed models as reference models.

2.7 Validation of the generic model

The method used in this study to quantify the difference between two models was based on calculating the disparity between the surface geometry of two models on a point to point basis. The disparity function was based on Besl & McKay's [18] Iterative Closest Point (ICP) algorithm which calculates the Euclidean distance between a given point and its nearest neighbour on a geometric entity. The definition of the disparity function was adapted from Besl & McKay [18] and is presented in the appendix. The mean error obtained by using Equation (3) is a measure of the overall similarity (disparity) between two models. A low value indicates a high similarity whereas a high value indicates greater disparity. The disadvantage of such an approach is that the error is non-directional, i.e. it provides no reference to the location at which two models differ. To provide some means of reducing the model space over which the error was calculated the models were clipped proximally by a plane orthogonal to the z-axis and set at a distance equal to half of the model's condylar width away from the origin. In this way the overall difference between the models in the condylar region could be quantified in a way not affected by variations in the angle between the bone's long axis and the line

connecting the circle centres on the medial and lateral condyles (x-axis) as seen in Figure 3b. The mean error between the models was also calculated for the full length (clipped at condylar width above origin) of the models.

Prior to quantifying the difference between a generic and a reference model the generic model was scaled to the average (of three repeats) measurement of the condylar width of the reference model. Then the two models were brought into optimal alignment. The 'gross' alignment was achieved by aligning the models relative to the common coordinate system. The alignment of the models was then iteratively 'fine' tuned by transforming (translations and rotations) one model until the disparity function (Eqn. 2) converged at a minimum.

The development and validation of the generic models was performed on a PC (Pentium 4, 2.4 GHz, 512 MB RAM) using customised graphical user interfaces developed in IDL 5.5 (Research Systems Inc, Boulder, USA).

3 Results

3.1 Repeatability of the alignment method

Repeatability of fitting circles to the medial/lateral profiles of the condyles was good, the variation in the obtained circle coordinate positions being less than 1 mm (Table 1). The y-component of the circle centres showed the greatest variability with a SD of 0.30 and 0.32 and a maximal difference between positions of 0.77 mm and 0.89 mm for the lateral and the medial condyles, respectively.

[Insert table 1 about here]

The x-coordinates of the circle centres were fairly constant with a SD of 0.13 and 0.02, and a maximal difference between positions of 0.11 mm and 0.05 mm for the lateral and the medial condyle, respectively. This was also reflected by the low variation in the distance between the circle centres of 0.13 SD and 0.34 mm as the largest difference in measurements which is equivalent to a percentage error of 0.4%. The angle through which the model was rotated about the x-axis had a standard deviation of 0.11, with a relatively low maximum difference between the measurements of 0.26°.

3.2 Interspecimen variability

For a qualitative assessment of how and where the morphology of the femur models differed, the models were aligned with the common coordinate system, scaled to the average width of the data set and then displayed as different coloured polygon meshes in the same view (Fig. 3b).

[Insert figure 3b about here]

The most obvious differences between the models are the variations in the angle between the diaphysial axis and the axis joining the circle centres on the medial and lateral condyles (x-axis). The differences in the condylar region appeared to be random and relate to the local characteristic morphologies of the individual models. The

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different lengths of the models are a result of scaling the individual models up or down to the average width of the data set.

The largest interspecimen variability between the aligned contours was in the order of 13 mm and caused by an osteophyte on the lateral aspect of the medial condyle. The largest variability not caused by an osteophyte was 9 mm and occurred on the anterior aspect of the medial condyle.

3.3 Resulting generic model

The generic model that has been developed from the data of seven femora is shown in Figure 4.

[Insert figure 4 about here]

3.4 Comparing reference models to the generic model

Error values between generic and femur models are provided for resection of the bone shaft half the condylar width above the origin (Table 2) and full condylar width above the origin (Table 3). Greatest maximum errors were recorded for femur 7 from an individual with a groove on the anterior aspect of the condyles, whereas the greatest mean errors were recorded from an individual with prominent osteophytes (femur 2).

[Insert table 2 about here]

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[Insert table 3 about here]

4 Discussion

4.1 Repeatability study on the alignment of the models with the coordinate system

A repeatability study has demonstrated that the accuracy of the method for aligning the reconstructed femur models with a common coordinate system prior to sectioning was sufficient for the purpose of this project. The variations resulting from the alignment of the model with the common coordinate system were either overshadowed by the interspecimen variability of the bone contours, or were too small to have any noticeable effect on the cross sectional dimension of the bone [15]. The only comparable study [13] did not provide results regarding the repeatability of the alignment method used.

4.2 Resulting generic model

The developed generic model (Fig. 4) exhibits the characteristic shape of the distal femur. The maximal interspecimen variability of 13 mm between the contours was considerably higher than the 5 mm observed in the study by Siu *et al.* [13] who considered that their five knees were representative of a 'normal' population. Studies by Noble *et al.* [19,20] reported that the interspecimen variability in the morphology of bones is increased by aging. The maximum variability in the bone contours in our study was caused by an osteophyte on the lateral aspect of the medial condyle. Therefore, it is most likely that the larger interspecimen variability of the knees used in this study was

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due to the effect of aging as the average age of the knees was 20 years higher than that in the study by Siu *et al.* [13].

By visual comparison, the generic model of this study contains more local variations on the surface compared to Siu's [13] model which is of smoother appearance. This difference is most likely a combination of two factors: one is the narrower spacing (0.5 mm compared to 3 mm in Siu's [13] study) of the CT image slices; the other is the minimal amount of smoothing performed on this model which was done in an effort to preserve as much local surface detail as possible. Depending on the requirements of future applications of the model further smoothing would be possible.

The model of the femur developed by Martelli *et al.* [10] based on the data of six cadaveric knees can be considered as a reductionistic approach as the condyles were represented by ellipsoids interconnected by a crossbar. Therefore, the visual appearance of the generic model developed by Martelli significantly differs from the one presented in this study. Comparison with other models [9,11,12] reported in the literature was not conducted as those models were based on data sets of one to two femora.

The accuracy of the CT-based data acquisition method used in this study is slightly lower compared to the methods used in similar studies [10-12]. However, considering that the average outline of the combined contours was obtained it is questionable whether a more accurate acquisition method would improve the result in any meaningful way.

4.3 Comparing individual models to the generic models

There was a considerable spread in the average error values between the different femur and generic models which ranged from 0.94 to 2.52 mm for the models that were clipped at half of their condylar width (Table 2). For the longer models (clipped at their condylar width) the average errors ranged from 0.99 to 2.52 mm (Table 3). As expected, the average errors were lower for the models that did not display any bony outgrowths (osteophytes) at the joint margins such as the models of femur 3, 5, 8 and 9. The highest average errors of 2.19 and 2.52 mm were obtained for the two models (Femur 2 & 7) that based on visual judgement, were excluded from the data set used to develop the generic model. This indicates that the method of using the principle of 'nearest neighbour' for quantifying the difference between two 3D models was in agreement with the qualitative assessment of the models based on their visual appearance.

For the cases when the differences between the models with the longer shafts were calculated the average error slightly decreased for two models (4 & 5) remained the same for one (model 2) and slightly increased for six models. The greatest change of 0.05 mm in the average error was obtained for femur 3 and is equivalent to a 5% increase of the value calculated for the shorter version of the model. This indicates that although the variations in the angle between the diaphysial axis and the axis through the condyles (x-axis of coordinate system) did affect the resulting average error, the extent was not significant.

The minimum and maximum error values for both the short and the long versions of the models did not appear to bear any relation to the average error, since

higher min/max values did not necessary result in higher average error values and vice versa (see Table 2 & 3).

A visual comparison of the aligned models has shown that in no two cases were the local morphological differences between a femur and generic model the same even if the average error was similar such as for Femur 5 and Femur 9. This appears to be a reflection of local morphological differences between individual bones.

Compared to studies involving CT image 3D reconstructions, the average errors between generic and individual models of the femur are comparable to the higher end of the range [21-24] of errors reported in the literature. This indicates that the generic model developed in this study represents the morphology of a particular femur (from the available dataset) reasonably well. Provided that the particular femur is considered normal, i.e. does not contain a significant number of osteophytes or any other deformities. However, it is important to note that the generic models used in this study were both generated and validated based on image data from older specimens (average age 80 years). Therefore, it is not known how representative the developed generic model would be of a particular femur model generated from a younger (55 years) subject.

In relation to the potential clinical relevance of the method of quantifying the difference between two 3D models, osteophytes are routinely assessed visually with regard to small, moderate or large size but do not necessarily relate strongly to clinical symptoms as their size is only one of the features of degenerative joint disease. Thus, it is not likely that the developed method of comparing two 3D models will be applied in this particular clinical setting. Other potential clinical applications have not yet been identified.

5 Conclusion

In this study, computer graphical methods were developed for the construction of a generic 3D model of the distal femur based on CT-scan image data.

The advantage of this method of generating a generic model over other methods [9-13] is that no specimens have to be dissected since the 3D data of the joint can be acquired using standard CT imaging without the need for a calibration frame. Furthermore, although more expensive than CT, MR (magnetic resonance imaging) could potentially be used for the acquisition of data from patients/subjects without exposing them to medically unjustified radiation. This method is therefore very appealing as a technique applicable to the future development of generic models based on larger and more age diverse data sets.

The resulting generic 3D model contained more local variations in the surface of the condylar region compared to Siu's [13] model which is most likely the result of different imaging and reconstruction parameters used in this study. The general morphology of the two models is comparable.

The differences between the generic model and a particular model of the femur was quantified by means of an average error metric which was based on calculating the Euclidean distances from points on the surface of one model to their nearest neighbours on the other model. The considerable range of 0.99 - 2.5 mm in the obtained average error values appears to be a reflection of the degree of bony outgrowths at the joint margins of some models, since all the models with no outgrowths had lower error values. This indicates that the method of using the principle of 'nearest neighbour' for

quantifying the difference between two 3D models was in agreement with the qualitative assessment of the models based on their visual appearance.

The generic model represents the morphology of a particular femur (from the available dataset) reasonably well, provided that the particular femur is considered normal. Due to the limited and aged data set further studies will be required to develop a generic model which is representative of a larger population sample.

Acknowledgement

Appendix

The Euclidean distance $d(p_1, p_2)$ between two points $p_1 = (x_1, y_1, z_1)$ and $p_2 = (x_2, y_2, z_2)$ is $d(p_1, p_2) = \| p_1 - p_2 \|$. Let A be the point set of vertex coordinates (x, y, z) of the generic model denoted as $A = \{a_i\}$ for $i = 1, ..., n$. Let B be the point set of vertex coordinates of the femur model denoted as $B = \{b_j\}$ for $j = 1, ..., m$. Then the minimum Euclidean distance from point b_j on the femur model to its closest neighbour a_i on the generic model is given by

$$d_{\min}\left(b_j, A\right) = \min_{i \in \{1, ..., n\}} d\left(b_j, a_i\right). \tag{1}$$

The disparity function (*D*) is then defined as the sum of all the distance values from every point (vertex) on the femur model (set *B*) to the closest point on the generic model (set *A*), which can be written as:

$$D = \sum_{j=0}^{m} d_{\min}\left(b_j, A\right).$$
$$(2)$$

To provide a more meaningful comparison between the models the average error appeared to be more appropriate than the total error, since not all models had the same number of vertices. Therefore, the sum in Equation (2) was divided by the number of points in the vertex data set of the femur model to obtain the mean error (*ME*) as follows

$$ME = \frac{1}{m} \sum_{j=0}^{m} d_{\min}\left(b_j, A\right).$$
$$(3)$$

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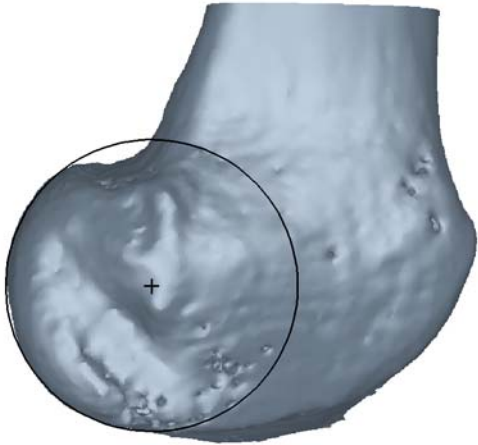Development and validation of a generic 3D model of the distal femur

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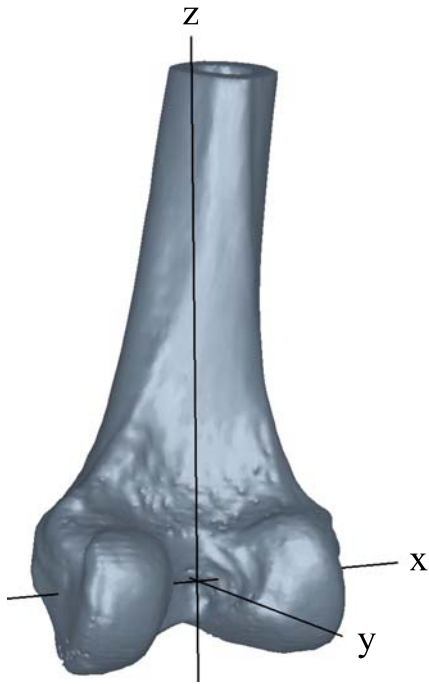FIGURE 1 Circle fitted (visually) to the contour of the lateral condyle.

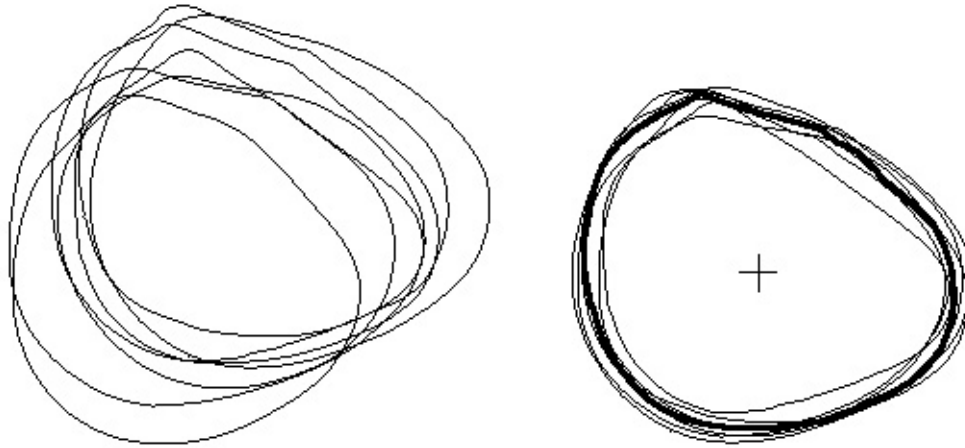FIGURE 2 Femur model aligned with the coordinate system.

FIGURE 3 (a) Combined contours of aligned models. (c) Contours aligned with the average of their centroids (average contour in bold).
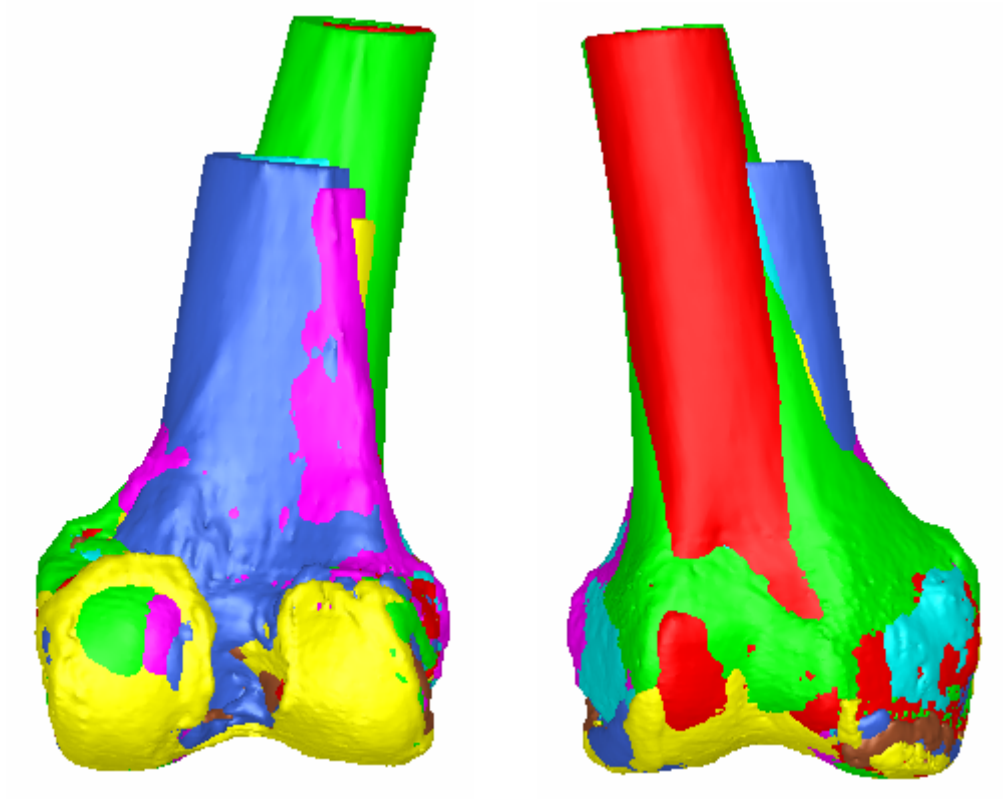
FIGURE 3 (b) Posterior (left) and anterior (right) views of the seven femur models
aligned, scaled and displayed in different colours.

FIGURE 4 Posterior (left) and anterior (right) views of the generic model generated from the averaged contour data of seven femora.

TABLE 1 Tabulated results of the repeatability study for alignment of a randomly chosen model with the common coordinate system.

	Lateral Circle Centre (mm)			Medial Circle Centre (mm)			Distance	Angle
	x	y	z	x	y	z	(mm)	(Deg)
	-44.68	8.08	-38.80	42.65	12.60	-44.10	87.60	3.84
	-44.61	8.23	-38.93	42.66	12.59	-44.06	87.53	3.77
	-44.69	7.98	-38.83	42.61	12.64	-44.28	87.60	4.00
	-44.94	7.46	-38.43	42.60	12.26	-44.30	87.87	3.75
	-44.72	7.76	-38.90	42.62	13.14	-44.18	87.67	3.95
Average	-44.73	7.90	-38.78	42.63	12.65	-44.18	87.65	3.86
SD	0.13	0.30	0.20	0.02	0.32	0.11	0.13	0.11
Max Error	0.11	0.77	0.49	0.05	0.89	0.24	0.34	0.26

TABLE 2 Table of error values between femur models and generic models for which the bone shaft was resected at a distance equal to half of their condylar width above the origin.

Femur No.	min Error (mm)	max Error (mm)	mean Error (mm)
1	0.05	5.83	1.50
2	0.06	8.30	2.52
3	0.04	3.92	0.94
4	0.04	9.82	1.76
5	0.06	4.33	1.18
6	0.06	7.21	1.46
7	0.04	10.49	2.19
8	0.04	5.43	1.34
9	0.05	3.83	1.11

TABLE 3 Table of error values between femur models and generic models for which the bone shaft was resected at a distance equal to their condylar width above the origin.

Femur No.	min Error (mm)	max Error (mm)	mean Error (mm)
1	0.07	6.09	1.54
2	0.07	8.55	2.52
3	0.02	4.29	0.99
4	0.04	9.64	1.74
5	0.04	4.37	1.17
6	0.04	7.73	1.49
7	0.07	10.43	2.21
8	0.08	5.45	1.36
9	0.05	3.95	1.14

Development and validation of a generic 3D model of the distal femur

B. SCHMUTZ *et al*.

List of figure captions:

FIGURE 1 Circle fitted (visually) to the contour of the lateral condyle.

FIGURE 2 Femur model aligned with the coordinate system.

FIGURE 3 (a) Combined contours of aligned models. (c) Contours aligned with the average of their centroids (average contour in bold).

FIGURE 3 (b) Posterior (left) and anterior (right) views of the seven femur models aligned, scaled and displayed in different colours.

FIGURE 4 Posterior (left) and anterior (right) views of the generic model generated from the averaged contour data of seven femora.