

Software System for Creation of Human Femur Customized Polygonal Models

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Abstract. Geometrically accurate and anatomically correct three-dimensional geometric models of human bones or bone sections are essential for successful pre-operative planning in orthopedic surgery. For such purposes, 3D polygonal models of bones are usually created based on Computer Tomography (CT) or Magnetic Resonance Imaging (MRI) data. In cases where there is no CT or MRI scan, or part of bone is missing, such three-dimensional polygonal models are difficult to create. In these situations predictive bone models are commonly used. In this paper, the authors describe the developed a software system for creation of Human Bones Customized Polygonal models (HBCP) which is based on the use of the predictive parametric bone model. The software system enables creation of patient-specific polygonal models of bones, by using only a limited number of parameter values. Parameter values can be acquired from volumetric medical imaging methods (CT, MRI), or from two-dimensional imaging methods (i.e. X-ray). This paper introduces the new approach to the process of creation of human bones geometrical models which are based on the anatomical landmark points. Testing of the HBCP for the cases of femur bone samples has shown that created bone and bone region models are characterized by a good level of anatomical and morphometric accuracy compared to the results presented in similar researches.

Keywords: femur, parametric model, reverse engineering, software system, polygonal model

1. Introduction

In orthopedic surgery, but also in all other sub-branches of surgery, where there is the need for preoperative planning or creation of customized implants and fixators, there is a specific requirement to know the exact geometrical model of the human bone. Therefore, it is very important to create the

geometry of the bone quickly and as accurately as possible. With such models, it is possible to build customized bone implants and fixators using rapid prototyping technologies or performing preoperative planning procedures in adequate applications. But sometimes there is no CT or MRI scan, or part of the bone is missing, so it is not possible to create a model.

The aim of the presented research is to create such a software system which will enable the creation of anatomically correct, topologically accurate and geometrically precise human bone polygonal models, even in the cases when part of the bone is missing or only a single X-ray image is available. The software system is composed of two main components: the parametric points bone model and MedApp software. Both components have been created by the authors of this paper.

The parametric points model is a predictive model consisting of parametric functions. These functions describe the relations between morphometric parameters and coordinates of the points on the bone surface. Morphometric parameters are used as arguments of parametric functions, and they represent measurements (i.e. Femoral Head Radius) which can be acquired from medical images (i.e. CT, MRI, or X-ray) for each human bone. MedApp is a software for the simulation of orthopedic interventions, and it enables the application of the parametric points models of the human bones.

The paper is organized is following:

Section 2 introduces the related work in the field of geometrical modeling of human bones. Section 3 presents Software system components and structure, while the workflow of the Software system is presented and described in Section 4. The creation of parametric model and the analysis of geometrical deviations of created geometrical models are presented in Section 5. The structure and components of MedApp software are presented in Section 6. Quality testing algorithms which improve the overall geometrical quality of the developed models are presented in Section 7. The final Section 8 is the conclusion, with references to the future work.

2. Related Work

In order to create geometrical models of human bones (especially of the long bones) and to apply them in preoperative planning, a lot of different techniques are used, as presented in papers [1-12].

The classification and analysis of 3D modeling methods for the creation of the human bones geometrical models are presented in [3] by Filippi *et al.* The mentioned paper describes the study and the development of a script for a commercial software package (3ds Max) able to reconfigure the template model of a femur (deformable by Free Form Deformation method - FFD), starting from two orthogonal images representing the specific patient's anatomy. This study provides an outstanding contribution to the research field. The only possible problem can be a semi-automatic image segmentation

which is sometimes hard to achieve due to the previously known issues with the X-ray images (superposition, inaccurate patient positioning, artifacts, etc.).

In [4] by Gunay *et al.* the authors present a cost- and time-effective computational method for generating a 3D bone shape from multiple X-ray images. Starting with a predefined 3D template bone shape, which is clinically normal and scaled to an average size, their method scales and deforms the template shape until the deformed shape gives an image similar to an input X-ray image when projected onto a two-dimensional (2D) plane. The hierarchical free form deformation method is used to scale and deform the template bone. That research provided a good example of 3D template bone shape creation and application in preoperative planning, although it faces the same possible problem with X-ray image(s) as in [3].

The 3D reconstruction process, which is based on human bones anatomical properties, is presented in [5] by Lee *et al.* The purpose of that study is to create 3D model of the human femur, by using multiple X-ray images and anatomical properties of the femur. For the 3D reconstruction, the 2D shape and specific parameters of the bone were first measured from X-ray images. Then, the corresponding CT model was modified performing axial scaling, shearing transformation and radial scaling. This research provides an excellent view on mathematical approaches and modeling procedures in defining the adaptable model geometry.

Three-dimensional (3D) representations of complex geometric shapes, especially when they are reconstructed from MRI and CT data, often result in large polygon meshes which require substantial storage for their handling as presented in [6] by Sheng *et al.* To reduce the number of polygons a small set of coefficients of the patchwise partial differential equation (PDE) function representation was used. This approach can be used to reduce the number of polygons in the model created over CT dataset, while the overall geometry of the input model is preserved.

The Finite Element Analysis of the human femur led to the creation of various types of geometric mesh models. The aim of the research presented in the paper [7] by Viceconti *et al.* was to comparatively evaluate five methods for automating mesh generation (AMG), when used to mesh the human femur. Testing of the methods included the application of the standardized femur model which was created on the basis of the CT dataset acquired by scanning the composite femur model. This composite femur model was used as a substitution for cadaveric femur specimens in the process of FEA, as described in the paper [8] by Cristofolini *et al.* and it is commercially available (Mod. 3103, Pacific Research Labs, USA).

The use of multiple regression and quadric surfaces for femur geometry prediction is presented in [9] by Sholukha *et al.* The given paper provides a complete presentation of mathematical and statistical methods application in determining geometrical and anatomical characteristics of human bones and anatomical elements, such as: Joint Centers (JC), Trochanter region, Condyles on various human bones, etc. However, quadric surfaces cannot completely describe the complex topology of human bones (e.g. combs,

prominences, notches, parts of condyles, crests and so on), so the application of this model can be limited.

In [10] by Matthews *et al.* authors are trying to create composite bone model with a possible bone part adaptation and replacement from the generic database of bone models. In [11] by Sourina et al. the authors suggest the application of the standard bone fracture models database and its implementation for planning orthopedic surgeries (PC application). Another approach for the surface model creation was proposed by another research team as presented in [12] by Au et al. They introduce a semi-automatic non-uniform rational B-spline (NURBS) technique to construct knee joint bones geometry from CT images using a combination of edge extraction and CAD surface generation. Papers [11,12] propose the use of bone models databases for creation of bone models, which is the approach used in this study as well, but in a different way. The bones database is used once for parametric function creation, and there is no need for a later use (only for testing purposes and a possible correction of parametric functions).

In relation to the models and methods described in the papers [1-12] this kind of an approach adds a new value to the researches in the field of creation of human bones geometrical models and their application in preoperative planning /simulation in orthopedics. The HBCP model is highly usable in cases when bones lack a certain segment (a bone destructed by tumor, osteoporosis or by other disease processes), or only a single X-ray image is available. In given cases it is possible to create an overall HBCP model based on the parameters available from the adequate image. If it is impossible to measure all the parameters, parametrical functions with the number of available parameters can be used. Also, the created MedApp software which enables the HBCP model creation and application is pretty straightforward (very important for preoperative procedures) and can provide an adequate simulation of orthopedic interventions to medical experts.

3. Software system structure and components

The developed software system prototype enables the creation of the polygonal human femur model based on the input data from one or more X-ray images of a certain patient, Fig. 1. The system is based on the application of the pre-created generic parametric points model (described in Section 5), which is the most important component of the software system. This model is based on anatomical points defined on B-spline curves created on the envelope surface of the input training set of bone samples (input femur models). It can be considered as the cloud of points model because it consists of spatially distributed points. Such a model can be used in any CAD application as presented in Fig. 1, and in this research CATIA was used.

The parametric points model contains parametric functions which define the geometrical position of anatomical points. Each coordinate of every anatomical point (X,Y,Z) is defined by the use of parametric functions.

Exchanging the values of morphometric parameters, acquired from X-ray images, CT or MRI patient's scans, the generic parametric model is transformed into a subject specific points bone model. With the application of adequate techniques and features in CATIA or in MedApp software, the model is transformed into the bone polygonal model. Parameters can be read from medical images manually, or through the adequate software (e.g. Mimics, Vitrea - DICOM). MedApp software contains a module which enables measuring of parameters from digital X-ray images by manually selecting adequate points.

The use of B-spline curve enables the creation of geometrical femur models with a high geometrical and topological/morphological precision, as presented in this paper. B-splines curves were defined in CATIA generative shape module and they are absolutely applicable for the use in the generic shape design of free form surfaces (human bones can be described as such), within this module.

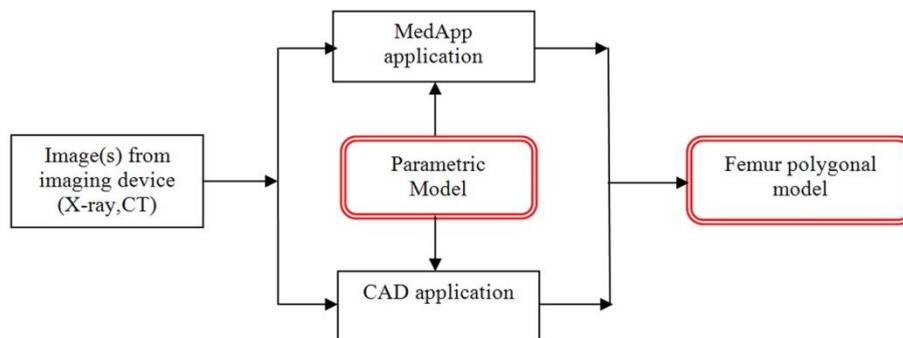


Fig. 1. The basic schema of femur polygonal model creation process

The software prototype for the simulation of orthopedic operations (MedApp) is the second important component of the system, and it enables manipulation and modification of geometrical models of bones and implants. All the necessary algorithms for polygonal model creation are implemented in MedApp software, such as: reading the parametrical values from X-ray images, application of parametric functions, the creation of coordinate points, the creation and optimization of the polygonal model and so on.

4. The system workflow

The developed system contains several processes which must be performed in order to generate a valid polygonal model for the human femur, as presented in Fig. 2.

Process of creating the polygonal model of the femur model starts with the acquisition of patient specific X-ray images. Although it is possible to obtain bone geometry data and parameters values using other procedures of

medical imaging, X-ray imaging is used due to the following reasons: less radiation, easier availability, facilitated implementation in medical application (MedApp), etc. X-ray images are then forwarded to the application for orthopedic operations simulation (MedApp), which contains a module enabling basic 2D images processing. Based on generally known algorithms for image processing (which are implemented in MedApp), it is possible to additionally process an image and improve its quality (contrast, light, etc.). After processing the image, the user manually selects points on the X-ray, and the application calculates the parameters values. The current system is based on the application of the measurement etalon, which is used to determine the scaling factor for the measures read from X-ray images. This etalon is a 10 cm long metal bar which is placed along the patient's thigh during the capture of the X-ray image. This is a very complicated process and therefore other solutions are being developed. One of these solutions is to implement automatic segmentation algorithms (contours recognition) [13] by Shubhangi et al., and [14] by Tian TP.; therefore, a complete automatic parameters values detection will be enabled by their implementation afterwards. Of course, the user will still be able to manually correct certain values if it is noticed that they are irregularly determined.

The next step is to create the adjusted point model of the femur. Defined parameters are automatically forwarded to a 3D application module implemented with an algorithm that enables the creation of points coordinates based on parametrical functions predefined for a certain bone or a bone region.

The example of defined parametrical functions is given in (11). As a result from the program code, points coordinates of the geometrical human femur model are defined. The points are possible to record as an ordinary text file in which the coordinates are separated by a comma (CSV), a tabulator (ACS - CATIA) or a blank character. This set of data can be treated as a cloud of points. It is also possible to create an MS Excel file with values of coordinates of points. The cloud of points is the basis for the human femur polygonal model creation process.

The polygonal model can be created in two different ways, and they are:

- Application of CAD software (in this case CATIA was used). The polygonal model is created by the application of adequate software modules (shape modules) and features (mesh creation, mesh optimization).
- Application of MedApp software (or other specialized software). The polygonal model is created by the use of mesh classes, which are included in managed DirectX API, or with the use of X3D technology.

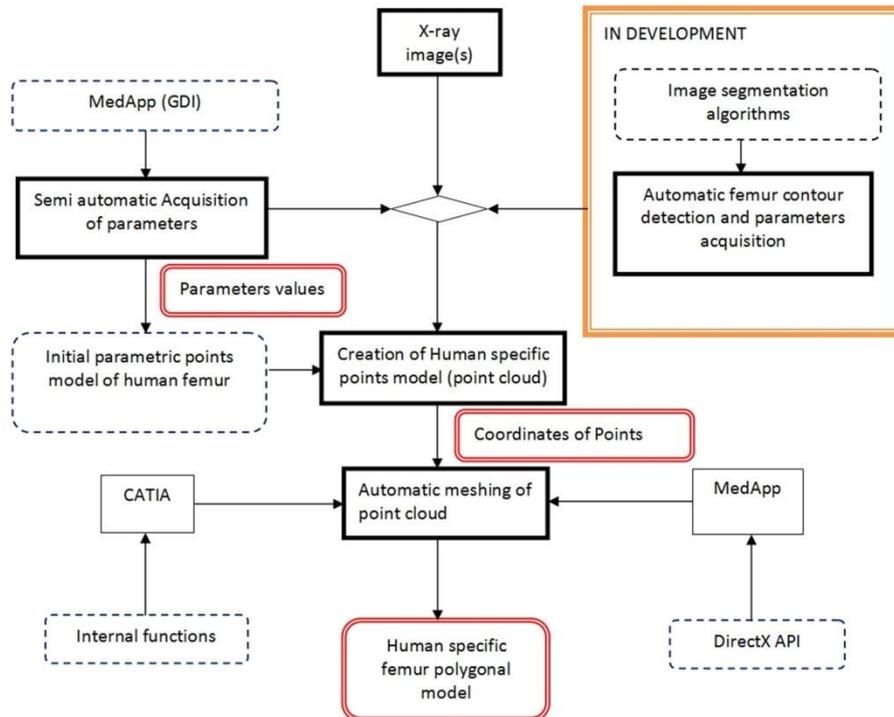


Fig. 2. System for creating subject specific polygonal model of human femur

5. The parametric model creation process

For the geometry analysis of the human femur, twenty (20) femur samples were scanned (input training set). The samples were made by 64-sliceCT (MSCT) (Aquillion 64, Toshiba, Japan), according to the standard protocol recording: Radiation of 120 kVp, Current of 150 mA, rotation time of 0.5 s, and thickness of 0.5 mm. The samples came from Serbian adults, intentionally including different gender and age: four female samples, both right and left, age 25 - 67, six male samples, both right and left, age 22 - 72, of different height and weight. It was assumed that this diverse set of samples could present quite a diverse morphology of the very same bone.

The whole process of parametric model creation is described in the previous paper of the same authors [15] by Vitkovic et al. In this paper, a short review will be presented with remarks about the applied changes.

The process of parametrical model creation is presented in Fig. 3 and it consists of five major steps as following:

P1. Definition of the anatomical model of the specific human bone

The anatomical model defines the morphology of a specific bone or region. The anatomical model is based on anatomical landmarks of a certain human bone, commonly known in medical literature (condyles, crests, prominences, etc.). This model describes relations between anatomical landmarks and their position on the polygonal model. In other words, the position of any anatomical landmark is defined on the polygonal model.

P2. Creation of Referential Geometrical Entities (RGEs)

After defining the anatomical model, creation of the basic model geometry is introduced. Initial preparatory processes are thoroughly presented in [16] by Stojkovic et al. and [17] by Trajanovic et al., demonstrating the application of the following operations: CT scanning of the part of the human body or dry samples (in this case femur); Preprocessing of raw data (scans) and their transformation into STL format; Importing the scanned model in STL format into CAD application (for example CATIA) and its further preprocessing; Cleaning the cloud of points; Tessellation and Healing the tessellated model. All of these processes are described in more detail in the papers [16, 17].

At the end of the preparatory processes, the polygonal geometrical bone model is created. The above mentioned processes are the so-called preparatory processes for a very important procedure of referential geometry defining. Referential geometrical entities - RGEs (planes, lines, axis, points, and so) are defined on the polygonal human bone model in accordance with its anatomical and morphological features.

P3. Construction of the skeleton model

The next step is examination of the polygonal bone model in order to create geometrical entities which will serve as the basis for creation of the points model. Geometrical entities are mainly spline curves (B-spline) and they are defined to follow the bone geometry and topology in the best way possible, and in accordance with the anatomical bone model.

In [15] by Vitkovic et al. the authors define spline curves which follow the rotational shape of the distal femur, and in that way the morphology (form or shape) of the bone is preserved. B-spline curves created on the femur polygonal model are presented in the Fig. 4a, where it can be seen that they follow the topology and morphology of the bone. These spline curves are created by the cross section of adequate planes and the femur polygonal model. The set of spline curves defined over whole polygonal bone model is called the skeleton model.

The spline curve presented in Fig. 4b is created on the distal femur polygonal model in CATIA Generative Shape module, and highlighted in Fig. 4a. Anatomical points are defined on each created spline curve manually, and presented in Fig. 4b. As it can be seen from the Fig. 4b, anatomical points are created in accordance with the anatomical model (anatomical landmarks). The spline curve is split into a number of anatomical sections (seven in this example) and on each section the adequate points are defined as presented in Fig. 4c: Middle Point (MP), Left Extremum Point (LEP), and Right

Extremum Point (REC). This procedure is performed over each defined spline curve on each anatomical feature, like: femoral neck, trochanteric region, femoral shaft, etc.

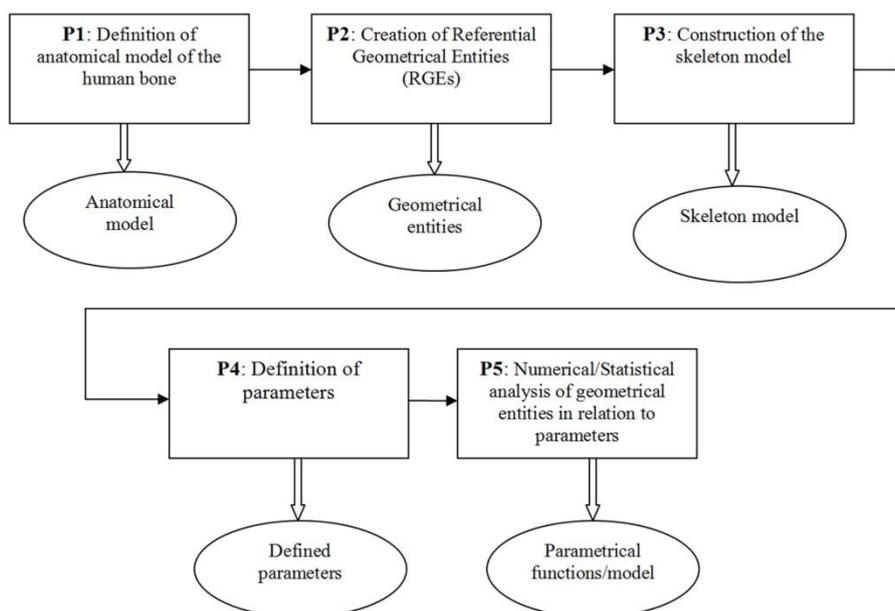


Fig. 3. The procedures of anatomical-morphological boundaries method. The results of each procedure application are presented below (certain type of model, parameter, function, etc.).

As mentioned in the previous section, spline curves can describe smooth surfaces (i.e. free form surfaces) in a very accurate way. Their application is limited when there are sharp edges on the model, or when transition with C1 or C2 continuity is impossible.

For the femur bone this is most evident in the positions where anatomical regions are connected, e.g. femoral neck to trochanteric region or femoral head, femoral body to trochanteric region or distal femur, etc. In such cases additional landmark points should be added to the region of interest, as it is done with the connection between femur neck and trochanteric region, and presented in Fig. 5. These additional points are not part of any defined spline curve (though they can be if necessary), yet, they are points which are used as additional vertex points for the creation of the polygonal model. How these points are defined depends on anatomical regions which are connected together. In the case presented in Fig. 5. these points are defined as points of cross section curve created by the intersection of the femoral neck surface model and the trochanter region surface model.

The possible drawback of this approach can be a large deviation of coordinates values of landmark points on different femur bone samples. The authors are trying to find the adequate mathematical relation between the additional points and the already defined anatomical points on different femur samples, so it can be implemented in the parametric model.

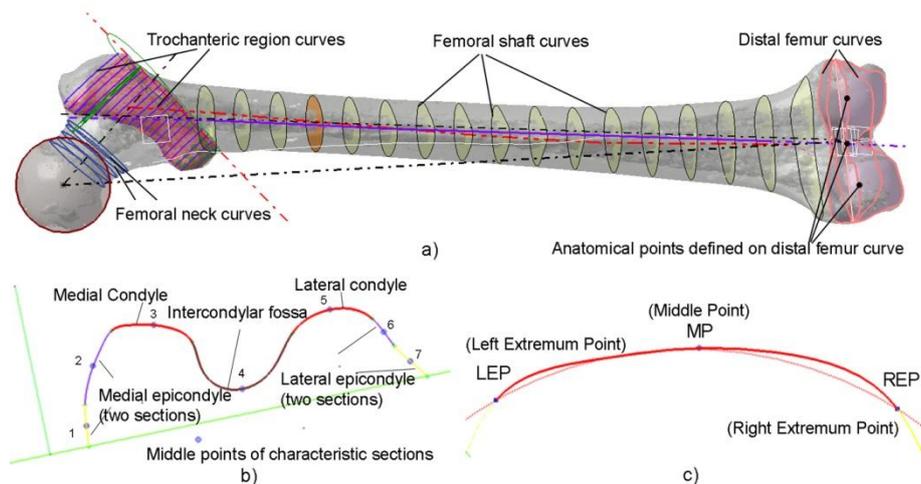


Fig. 4. Creation of anatomical points model a) B-spline curves created on the femur polygonal model, b) Seven sections of the first basic spline curve, c) First basic spline curve sections and its interpolation .

The result of the application of the procedure is a set of anatomical points which can be treated as the cloud of points defined over the polygonal femur model.

P4. Definition of parameters

In P4 process, parameter (dimension) defining is done in relation to created RGEs. Parameters are defined separately for each human bone in relation to its anatomical and morphological features and are mainly related to clear and easily noticeable geometrical entities on a bone, which is what RGEs represent.

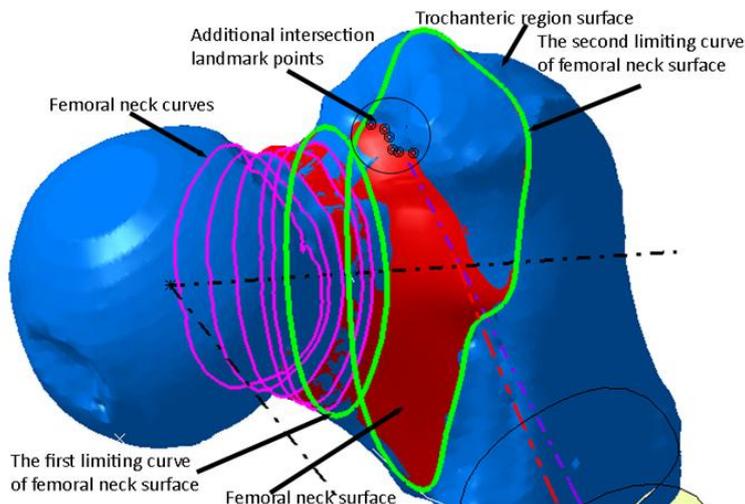


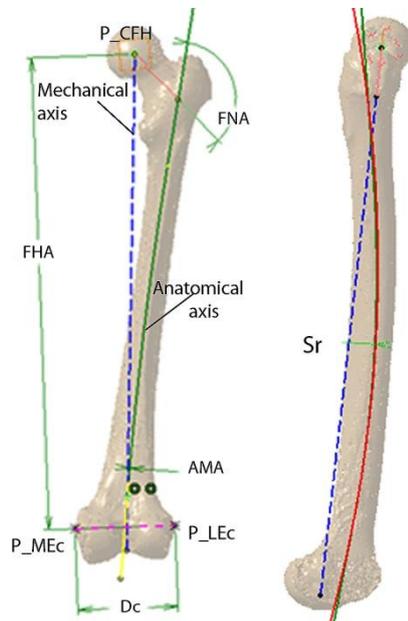
Fig. 5. Additional landmark points defined on femoral neck surface model

Those parameters can be: the femoral head radius, the angle between the anatomical and mechanical axis of femur, the angle between the mechanical axes of femur and tibia, and so on. In a recently published paper [15] by Vitkovic et al. only two parameters were chosen, but in this research additional four parameters were included, because the geometrical accuracy for some of the testing bone models was not high. The parameters and their definitions are presented in Fig. 6.

P5. Numerical/Statistical analysis of geometrical entities in relation to parameters

In order to successfully carry out the process of statistical analysis (P5), it is necessary to define the same anatomical points and parameters on certain number of polygonal models of the same human bones that belong to different patients. After that, it is necessary to measure the coordinate of points and parameters values on the each model separately and to create corresponding vectors.

The coordinate system is set for each individual bone input model. The origin point of the coordinate system can be any point which can be defined on the bone polygonal model for all femur specimens. This means that the position of the coordinate origin can be definitely determined on each polygonal model of an individual bone sample. After the initial analysis of femur specimen's polygonal models, the femoral head center was chosen as the origin of the coordinate system.



RGEs:
 P_LEc – The point of the lateral epicondyle – the most prominent point on the lateral epicondyle,
 P_MEc – The point of the medial epicondyle – the most prominent point on the medial epicondyle,
 P_CFH – Femoral Head Center

Parameters:
 FHR – Femoral Head Radius
 FNA – Femoral Neck Angle
 FHA – Distance between P_CFH and line connecting P_MEc and P_LEc
 Dc – Distance between P_MEc and P_LEc
 AMA – Angle between Anatomical and Mechanical Axis in Anterior Posterior view
 Sr – Shaft radius in Lateral–Medial view

Fig. 6. Six parameters and basic RGEs (points) defined on the femur polygonal model

The planes of the coordinate system are: Anterior Posterior (AP) plane, Lateral Medial (LM) plane, and the plane normal to these two planes. The creation of AP and LM planes is in more detail described in [16] by Stojkovic et al. It is important to mention that more than one coordinate system can be created for each bone. There can be one main absolute coordinate system, and several local for each bone region. For example, there can be one local coordinate system set at the extreme point of the lateral condyle of the distal femur.

This system is relative to the absolute coordinate system (in this case the main coordinate system, located at the femoral head center), and all points can be defined in relation to it. The absolute coordinate of a distal femur point can be calculated in relation to the main coordinate system.

Defined vectors are used as input data for the statistical analysis, which included the application of multiple linear regression which is described in [18] by Brown et al. As a result of regression application, parameter functions that give linear functional dependence between coordinates of points and parameters are created. At the end of the process, the parametric points model of a specific human bone is created. The model is composed of points whose coordinates are represented by parametric functions. If the source of parameters is an X-ray image, then one of the stated requirements, referring to less patient's radiation exposure (compared to CT for example), may be satisfied.

5.1. Example of parametric functions creation

As stated before, parametric functions are created for corresponding coordinates of points. Parametric functions define dependence between parameters (p1,p2,...pn) and coordinates (X, Y, Z) of model points, and they are presented in (1).

$$X = f_1(p_1, p_2, \dots, p_n), Y = f_2(p_1, p_2, \dots, p_n), Z = f_3(p_1, p_2, \dots, p_n) \quad (1)$$

In this example, for the creation of parametric functions ten femur samples were chosen from twenty existing ones and the analysis was performed.

In the data analysis process, multiple linear regression was chosen as the statistical function. Each of the parametric function is represented by the equation presented in (2).

$$X = b_0 + b_1 p_1 + \dots + b_n p_n \quad (2)$$

$$Y = b_0 + b_1 p_1 + \dots + b_n p_n$$

$$Z = b_0 + b_1 p_1 + \dots + b_n p_n$$

Coefficients b_0, b_1, \dots, b_n are the result of multiple linear regression application on the input data set presented in (3) for coordinate X (it is similar for Y and for Z)

$$P_1, P_2, P_3, \dots, P_n = X_i \quad (3)$$

$$\frac{p_{11}, p_{12}, p_{13}, \dots, p_{1n}}{p_{21}, p_{22}, p_{23}, \dots, p_{2n}} = X_{1i}$$

$$p_{21}, p_{22}, p_{23}, \dots, p_{2n} = X_{2i}$$

$$p_{31}, p_{32}, p_{33}, \dots, p_{3n} = X_{3i}$$

....

$$p_{m1}, p_{m2}, p_{m3}, \dots, p_{mn} = X_{mi}$$

$P_{i,j}$ are parameters values for each of the bone in the training set of bone samples. X_i is a value of coordinate for adequate anatomical points. For example, relation (3) for X coordinate of point 1 in Fig. 4b. is presented in (4).

$$P_1(\text{DC}) \quad P_2(\text{FNA}) \quad P_3(\text{FHA}) = X_1 \quad (4)$$

$$81.383 \quad 127.456 \quad 386.675 = 12.149 \quad X_{11}$$

$$82.297 \quad 125.67 \quad 391.734 = 12.149 \quad X_{21}$$

The error estimation is defined as the difference between the fitted function (X) and the sample function (X1) and it is presented in (5)

$$E = X1 - X \tag{5}$$

Multiple linear regression was chosen because of the sample data variation. The example of data variation is presented in Fig. 7 and Fig. 8.

Fig. 7 shows the dependence of X coordinate of the first point on the first curve (presented in Fig. 4c., point 1) in relation to the distance between femoral condyles. The linear approximation function of the dataset is presented in (6).

$$Xf11 = 0.029Dci + 8.9 \tag{6}$$

Fig. 8. shows the dependence of X coordinate of the first point on the first curve in relation to the distance between the center of the femur head and the line connecting the extreme points of femoral condyles. The linear approximation function of the dataset is presented in (7).

$$Xf11 = 0.004FHAi + 9.9 \tag{7}$$

Deviation from the medial line (linear approximation) lies within narrow boundaries - for Dc and FHA maximum 2mm, so the conclusion is that in certain volume (space), linear approximation might be done, and that is exactly what multiple linear regression provides.

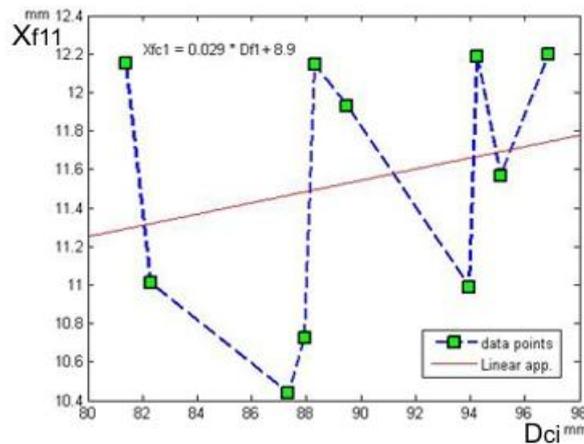


Fig 7. Xf11 coordinate of Point 1 (, f - Femur, Curve 1, Point 1) in relation to Dci (Distance between P_MEc and P_LEc)

The algorithm applied in linear multiplied regression is generally known in statistical analysis. In the paper [18] by Brown et al., a concrete example of multiple linear regression is given. In our example it is necessary to define corresponding vectors of entry values of coordinates of points as well as parameters values (for three parameters - Dc, FNA, FHA). In (8), vectors of values prepared for processing in MatLab application are shown.

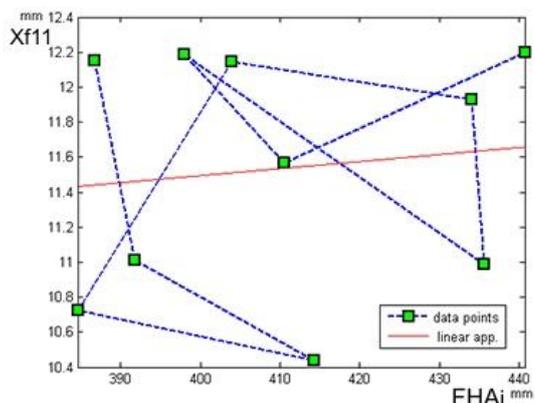


Fig. 8. Xf11 coordinate of Point 1 (, f - Femur, Curve 1, Point 1) in relation to FHAi (Distance between P_CFH and line connecting P_MEc and P_LEc)

$$\begin{aligned}
 Xcoord &= [12.149 \ 11.010 \ 10.44 \ 10.726 \ 12.148 \ 11.931 \ 10.99 \\
 &\quad 12.184 \ 11.567 \ 12.2]'; \\
 Dc &= [81.383 \ 82.297 \ 87.34 \ 87.932 \ 88.301 \ 89.493 \ 93.961 \ 94.257 \\
 &\quad 95.112 \ 96.88]'; \\
 FNA &= [127.456 \ 125.67 \ 129.45 \ 127.67 \ 130.56 \ 129.1 \ 128.7 \ 126.2 \\
 &\quad 129.5 \ 128.015]'; \\
 FHA &= [386.675 \ 391.734 \ 414.253 \ 384.577 \ 403.927 \ 434.057 \\
 &\quad 435.555 \ 397.939 \ 410.45 \ 440.713]';
 \end{aligned}
 \tag{8}$$

As it can be seen in (4), there are values defined for three parameters and values for X coordinate of the first point on the first curve, for ten femurs. After conveying the analysis in MatLab, vector of coefficients (B) and vector of errors (E) are acquired, and they are presented in (9)

$$\begin{aligned}
 B &= [11.4509 \ 0.0325 \ -0.0007 \ -0.0197] \\
 E &= [0.8522 \ -0.3480 \ -0.9907 \ -0.7811 \ 0.7003 \ 0.4381 \ -
 \end{aligned}
 \tag{9}$$

$$0.6550 \quad 0.4521 \quad -0.1183 \quad 0.4504]$$

Vector E shows the deviations from original values for each of the ten femurs, for the corresponding coordinate of point. It may be seen that deviation values are less than one millimeter, which is more than acceptable (compared to results presented in [9] by Sholukha et al.).

In the next Section (Analysis) middle values for the coordinate of points and vector of errors are presented in order to present the general accuracy of the created functions.

The parametric function for the presented example is shown in (10) and may be used in determining X coordinate of the given point for the human femur of a different patient.

$$X_{f11} = 11.4509 - 0.0325D_c - 0.0007FNA - 0.0197FHA \quad (10)$$

In (7), the example of the parametric function (for six parameters and ten femur samples) for X, Y, Z coordinate of point 1 is given.

It is important to remark that the process of creating the parametric model of a certain human bone is carried out only once, and the model may be used unlimited number of times for creating the model of the same bone belonging to different patients. For each following human bone only the reading of the corresponding parameters should be done, and the model will adjust automatically.

$$\begin{aligned} X_{f11} &= 9.168 + 0.033 \cdot D_{ci} - 0.033 \cdot FHA_i + 0.041 \cdot FNA_i \\ &\quad + 0.002 \cdot AMA_i + 0.055 \cdot S_{fi} - 0.033 \cdot FHR_i \\ Y_{f11} &= 16.706 + 0.097 \cdot D_{ci} - 0.046 \cdot FHA_i - 0.062 \cdot FNA_i \\ &\quad - 0.004 \cdot AMA_i + 0.078 \cdot S_{fi} - 0.014 \cdot FHR_i \\ Z_{f11} &= 12.213 + 0.021 \cdot D_{ci} - 0.013 \cdot FHA_i - 0.078 \cdot FNA_i \\ &\quad - 0.001 \cdot AMA_i + 0.039 \cdot S_{fi} - 0.056 \cdot FHR_i \end{aligned} \quad (11)$$

5.2. Geometrical deviations analysis of created polygonal models

The measurement of parameters values was performed on the generated femur models, and the obtained values were compared to parameters values measured on the input (original) models. The analysis results are given in Table 1. and as it can be seen, deviations of parameters are within completely satisfying limitations.

Deviations of coordinate values for adequate points on the points model, in relation to real values acquired on input femur models are presented in Table

2. Deviation values are calculated for a corresponding point on the femur model for X, Y, Z coordinates.

The chosen points are those with the maximal value for the corresponding coordinate. For maximal deviation it is Y coordinate (7.34 mm) of point 2 on femur 8. Maximal deviation values are maximal values of error for the corresponding coordinate.

Table 1. Parameters values in error analysis

Parameters	min $\Delta P_{i,n}$	max $\Delta P_{i,n}$	Mean	St. Deviation
P1 (FHA) [mm]	0.90	4.50	2.20	1.32
P2(FNA) [°]	0.50°	2.10°	1.30°	1.1°
P3 (FHR) [mm]	0.30	1.40	0.90	0.85
P4 (Sr) [mm]	3.10	11.50	6.1	2.1
P5 (AMA) [°]	0.50°	2.08°	1.07°	1.06°
P6 (Dc) [mm]	1.10	3.90	2.50	1.21

i - femur parameter, $i=1,6$; n - femur sample, $n = 1,20$

The average value is counted over the maximal set of values. The set of values is determined by taking the points with maximal deviation values on a single femur. For example, for Point 2, deviations of point coordinate values on each single femur (out of twenty) are determined along with the average value.

Table 2. Deviations of points coordinate values and mean model error for twenty femur samples [mm]

Controlled point coordinate	Maximum deviation (Femur 8, Point 2), distal region	Average value of maximum deviation	Values of mean coordinate error (EX,EY,EZ)
X	2.3	1.01	1.98
Y	7.34	1.23	2.21
Z	2.9	1.4	2.63

The maximal deviation of 7.34 mm for Y coordinate on femur 8 is relatively big (but less than 23 mm deviation presented in [9] by Sholukha et al.), and the reason is osteoporosis, which disabled the correct measurement of coordinate values for the corresponding point, on the given bone. For this reason, quality algorithms are applied and their purpose is to check and correct this kind of errors. They do not correct parametric functions (which are corrected during the test period), but they control the point position based on the defined rules. Quality algorithms will be explained in Section 6.

In the region where osteoporosis is spread over, this point has the greatest deviation compared not only to all twenty femur models, but also in general as

the point with the greatest dimensional deviation from all the points on the whole set of parametric models. By observing the average value of deviation, it may be concluded that parametric functions are completely satisfactory and that they can be used for creating a parametric model with required accuracy.

The results presented in the Table 2 for model mean errors of coordinates of points are in good range, which is confirmed by orthopedic surgeons. The values in the table were calculated as the mean error value for every coordinate of each anatomical point, for twenty femur samples. This means that the mean error was calculated for the adequate coordinate of every point on individual bone points model (for all coordinates - X,Y,Z), as presented in (12). The next step was to calculate the average mean error for all twenty samples, which is presented in (13).

$$Ex1_{avg} = (Ex1 + Ex2 + \dots + Exn) / n \quad (12)$$

$Ex1_{avg}$ - Mean Error value for X coordinate of point 1, calculated over mean errors values of point 1 for all individual points bone models ($n = 20$).

$$EX = (Ex1_{avg} + Ex2_{avg} + \dots + Exk_{avg}) / k \quad (13)$$

EX - Mean Error value for X coordinate for all points ($k = 226$), calculated over mean errors values for all individual points bone model. EX, EY and EZ values are presented in Table 2.

6. The Structure of MedApp software

Software system for preoperative planning in orthopedic surgery should provide a complete simulation of the orthopedic operation. The complete simulation of the operation involves the analysis of all the necessary factors that affect the proper surgical procedure. For the successful implementation of the software system, it is necessary to create a number of software modules that perform a variety of functions, which are defined in accordance with the requirements provided by medical experts. For that purpose MedApp software is created. For the development of MedApp software, programming language C# was chosen, because it allows the creation of both Windows (Desktop) and Web applications. In addition, C# has a high capability of working with computer graphics, controllable via managed DirectX for 3D graphics, and basic internal classes for working with 2D graphics.

One of the basic requirements is the possibility that the MedApp application accepts input data originating from different input resources. Input resources are medical devices for the medical data acquisition, which can be X-ray, CT or MRI scanners and the like. Based on the recommendations that have been acquired in cooperation with medical experts, it was concluded that the initial version of the application should provide the ability to work with input data acquired from X-ray and CT scanner. Therefore MedApp software is created as a modular software package, as shown in Fig. 9.

The modularity of MedApp is reflected in its capability to work with input data coming from a CT scanner (first module) or X-ray (second module). The first module includes API (Application Programming Interface) for the manipulation with medical data in DICOM (Digital Imaging and Communications in Medicine) standard. The second module includes standard algorithms applied for the extraction of medical data from the X-ray images (segmentation, edge recognition, etc.). Application modules are not completely independent, because in some cases is necessary to combine the inputs from multiple sources (i.e. X-ray and CT). These two modules are closely related to 2D module and 3D module of MedApp software.

2D MedApp module includes basic manipulations with 2D images which are: transformations (rotation, scaling, translation), the application of the basic filters (increase the color, blur and sharpness adjustment, etc.), measuring the distance on the images, etc. The code is written in C# using the GDI+ (Graphics Device Interface) API. On the basis of the already obtained 3D model of the femur (not parametric, but the classic volume model), an analysis of the possibilities of working with 3D graphics and the use of various open-source software solutions was performed. For the desktop module managed DirectX was selected as API for the creation of 3D content. Managed DirectX was chosen because it can be easily controlled by the C# internal classes.

Web module of MedApp was created by the use of X3D ISO standard. X3D is the standard based on the VRML (Virtual Reality Modeling Language) that allows creation of 3D content which can be displayed in any compatible browser (IE, Mozilla, Chrome are supported). It is supported by the HTML5 specification which is important for the future development.

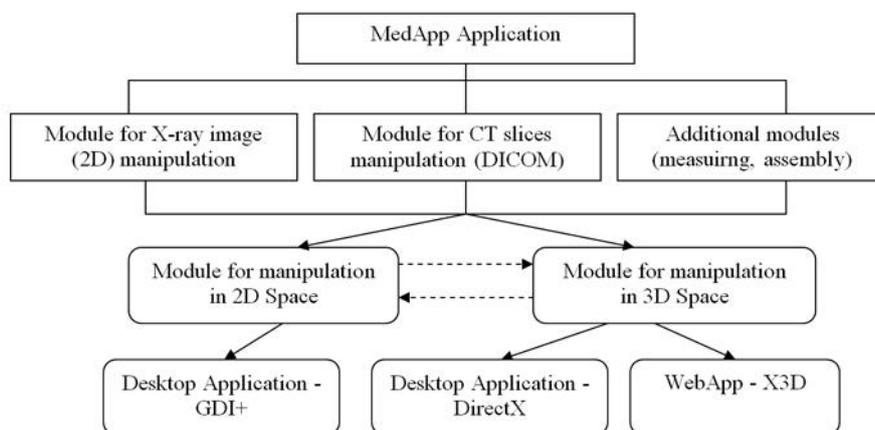


Fig. 9. The basic scheme of the MedApp software structure

Also, X3D is a variant of the XML language adapted to work with 3D graphics so it is possible to create an X3D file directly from C#. In Fig. 10 3D

shaded polygonal models of femur and fixator created in X3Dom format are presented.

It should be noted that the current version of MedApp software is a prototype version and that the potential shortcomings will be corrected through the implementation and testing of the application by the medical experts and software engineers. Some of the testing processes will include: correctness of applied algorithms, the various possibilities of applied technologies, the possibility of application of different programming languages (i.e. Java), the level of quality of the geometrical models, etc.

The structure of the MedApp and principles of its functioning are described in a more detailed manner in [19] by Trajanovic et al.

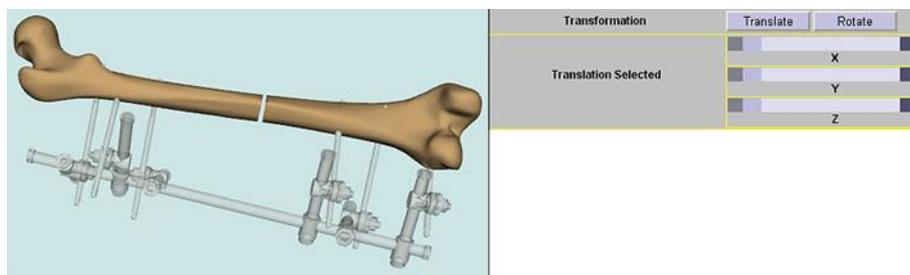


Fig. 10. 3D shaded polygonal models of femur and fixator in X3D format, displayed in Google Chrome browser

7. Implementation of the quality testing algorithms

A very important aspect of the complete process of polygonal model creation is quality control of the acquired model from geometrical, topological and morphometrical aspects. At this point, one method is already developed and implemented, the second one is in the process of being tested and the third method of quality control is in the development process.

The first method is based on a completely statistic approach and its accuracy depends on the number of tested femur samples. As already mentioned in the section on materials, the number of femurs used in this method is twenty (20) samples. Providing and applying more femur samples of different origin (age, sex, regional belonging), in order to improve the method quality, is in process. The procedure is presented in Fig. 11.

The authors strived to minimize the possibility of error occurrence in the created method by creating an algorithm which follows deviations of certain points at coordinates and if necessary corrects the positions of certain points. A possible position of a certain point is defined by setting a boundary function of the point position through a statistical method applied to a certain number of femurs. The requested condition is that the calculated point is positioned inside or at the border of the surface the boundary function includes. The first

step of this process is to determine the femur coordinates points values on each separate femur. In order to accelerate the process, the authors have created VBA (Visual Basic for Application) code in CATIA software which enables the selection of points at the input model, and with a simple click all the points coordinates are exported to an Excel file (Fig. 11a). In MS Excel file, the boundary function for each coordinate of each anatomical point is determined by using coordinates of anatomical points (X,Y,Z). The process is very simple and is reduced to defining of a closed curve that includes in its surface (as well as on its region borders) all the coordinate points values (Fig.11b).

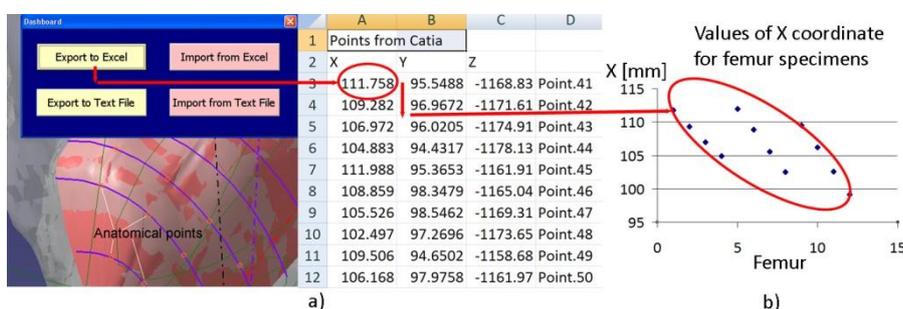


Fig. 11. Formation of the boundary overall function for a certain number of points defined in CATIA application, **a)** Form for points export from CATIA application, **b)** Example of creating a comprehensive boundary function (ellipse).

Well-known functions from basic geometry are selected as boundary functions, thus circle and ellipse functions are currently in use. These functions proved themselves to be dominant and completely applicable during the process of coordinates points values scattering analysis.

The second method is based on the manual approach for points positions modification. The user can manually move the points (using the mouse or keyboard), thus modifying the model. This is a commonly known method of Free-Form Deformation (FFD) over control points and as such, it is widely used and described in literature.

The last mathematical/statistical method is under development, and it refers to points coordinate values control on the points assembly level of the determined anatomical region (e.g. trochanteric region). Since morphometric characteristics for certain anatomical area are known [9,20], it is possible to create boundary conditions at the level of polygonal model geometry and in accordance with boundary values of adequate morphometric parameters. According to this, the authors are currently working on the algorithm which will enable modification of certain points position according to geometrical and morphometric boundary conditions of the adequate anatomical region.

8. Conclusion

The presented method for the creation of the parametric points model of the human bone(s) is based on a variable number of parameters, acquired from medical images (CT, MRI, X-ray). Considering anatomical and morphological properties of the human bone, this method enables the creation of geometrically accurate and anatomically correct models. The proposed method is not restricted to the human femur only (the human femur is the first test bone), but it can be extended to other bones and joint surfaces in the human body. The resulting model(s) of the human bone(s) can be used for various purposes: learning processes, implant manufacturing, production of bone presentation models, CAD/CAM, FEM (Finite Element Method) analysis, etc.

The authors are aware that, at the moment, the number of the used femur models is insufficient for a final claim regarding the model precision. To make such a claim, more femur samples are needed. Another possible drawback of the method is the number of parameters the parametrical model is based on. Six parameters are currently in use, achieving satisfying results; however, the authors believe that the use of more parameters will make the model far more precise. Therefore, the authors are currently working on implementation of morphometric measures presented in paper [9] by Sholukha et al. The analysis of over 36 morphometric parameters is performed, out of which a certain number will be used for further improvement of parametric functions, thus improving the model quality as well. Besides the number of samples and parameters, this method will also be verified by the use of different statistical/numerical methods, human femurs from different geographical regions, various age groups, etc. The main reason for further testing is the possibility to create a universal method for creation of the parametric model of the human long bone(s), which will produce highly usable geometrical models.

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